

CC	specifically bound by an antibody expressed by clones as mentioned in (I)
CC	; producing (I); and a composition (II) comprising several anti-
CC	botulinum neurotoxin antibodies, where each antibody is specific for a
CC	different epitope of a botulinum neurotoxin and the combination of
CC	antibodies show greater toxin neutralisation than the single antibodies
CC	in surplus. The following are disclosed: a pharmaceutical composition
CC	comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC	BONT/A antibody and for neutralising a botulinum neurotoxin which
CC	involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC	specific for a different epitope of the botulinum neurotoxin and the
CC	combination of antibodies shows greater toxin neutralisation than the
CC	single antibodies in surplus. (I) is useful for diagnosing the botulinum
CC	or for treating pathologies associated with botulinum neurotoxin
CC	poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC	enables rapid detection or diagnosis of botulinism. This is the amino acid
CC	sequence of a mouse light chain variable fragment anti-botulinum toxin
CC	sCFv.
XX	
XX	Sequence 112 AA;
SQ	
Query Match	100.0%; Score 590; DB 8; Length 112;
Best Local Similarity	100.0%; Pred. No. 1.6e-38;
Matches 112; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Dy	1 DIELTSPAIMSASPGKAVTTTCRASBSYDSYGHSFMQFPOOKPQTSPPLMTYSTSNLAS 60
Db	1 DIELTSPAIMSASPGKAVTTTCRASBSYDSYGHSFMQFPOOKPQTSPPLMTYSTSNLAS 60
Gy	61 GVPRFSGSGSGTSYSLTISRMEAEADAAITYCOOSNEDPYTGSDGDAKNR 112
Db	61 GVPRFSGSGSGTSYSLTISRMEAEADAAITYCOOSNEDPYTGSDGDAKNR 112
RESULT 2	
ID ADR38683	standard; peptide; 107 AA.
AC ADR38683;	
DT 02-DEC-2004	(first entry)
XX	
DE Mouse light chain variable region scFv seqid 85.	
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;	
KV BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;	
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;	
XX light chain variable region; single chain antibody; scFv.	
XX Mus sp.	
OS US2004175385-A1.	
PN	
PD 09-SEP-2004.	
XX	
PF 01-AUG-2003; 2003US-00632706.	
XX	
PR 31-AUG-1998; 98US-00144886.	
PR 01-AUG-2002; 2002US-0400721P.	
XX	
PA (RBGC) UNIV CALIFORNIA.	
P1 Marks JD, Ameradorfer P;	
XX	
DR WPI; 2004-652009/63.	
XX	
PT New isolated antibody that neutralizes botulinum neurotoxin type A,	
PT useful for diagnosing botulinism or for treating pathologies associated	
PT with botulinum neurotoxin poisoning.	
XX	
PS Example 1; SEQ ID NO 85; 110pp; English.	
XX	
CC The invention describes an isolated antibody (I) that specifically binds	
CC to an epitope specifically bound by an antibody expressed by a specific	

CC		clone where (I) binds to and neutralises botulinum neurotoxin type A (BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, I6, J12, B4, 1F7, huC25, Ar1, A2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and INGL, where (I) binds to and neutralises botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I)
CC	(I); producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies show greater toxin neutralisation than the single antibodies in surplus.	
CC	The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralizing BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus.	
CC	(I) is useful for diagnosing the botulism or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of a mouse light chain variable fragment anti-botulinum toxin scfv.	
CC		
XX		
SQ	Sequence 107 AA;	
	Query Match 86.5%; Score 510.5; DB 8; Length 107; Best Local Similarity 91.0%; Pred. No. 2,4e-32; Matches 101; Conservative 1; Mismatches 4; Indels 5; Gaps 1,	
OY	1 DIELTGPALMASAPGKRVTTTCRASSVDSYGHSFMQFOOKFGSPKMYISTSLIAS 60 Db 1 DIELTGSPAIMASAPGERKVTTTCGASSSV-----SYMGWFOOKFGSTPKMIYSTSMLIAS 55	
OY	61 GVPRPFGSGSGTSYSLTISRMEADATAYYCQNSNDPTPTPGSDPAAGNK 111 Db 56 GVPRPFGSGSGTSYSLSITSRMEADATAYYCQNSNEDPTPTPGSDPAAGNK 106	
RESULT 3		
AAR79884	AAR79884 standard; protein; 108 AA.	
XX AC	AAR79884;	
XX DT	02-JUL-1996 (first entry)	
XX DE	Anti-BGFR antibody light chain variable region (Clone L2 8C).	
XX KW	Single chain antibody; antibody; epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;	
KX KW	phage antibody library.	
OS XX	Mus musculus.	
XX OS		
FH FH	Key Location/Qualifiers	
FT FT	Region 1..23 /label= Framework region 1.	
FT FT	Region 24..33 /label= CDRL1.	
FT FT	Region 34..48 /label= Framework region 2.	
FT FT	Region 49..55 /label= CDR2.	
FT FT	Region 56..87 /label= Framework region 3.	
FT FT	Region 88..96 /label= CDR3.	
FT FT	Region 97..108 /label= Framework region 4.	
PB PN	MO9525167-A1	

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XX PD 21-SEP-1995.
XX PF 16-MAR-1995; 95WO-EP000978.
XX PR 17-MAR-1994; 94EP-00104160.
XX PR 02-DEC-1994; 94EP-00118970.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Kettleborough AC, Bendig MW, Ansell KH, Guessow D, Adan J;
XX PI Mitjans F, Rosell E, Blasco F, Piulats J;
XX DR WPI, 1995-336972/43.
XX PT Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
XX PT from phage-antibody libraries, useful for diagnosis and therapy of
XX PT tumours.
XX PS Disclosure; Fig 1A; 93pp; English.
XX SS Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
CC antibodies constructed from anti-EGFR antibody fragments can be used for
CC diagnosis of tumours and assessment of tumour growth in vitro and in
CC vivo. They may also be used in a pharmaceutical composition for the
CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
CC fragments are derived from mice but are humanised so as to cause minimum
CC reaction against them. They are produced using the phage antibody library
XX sequence 108 AA;
SQ
Query Match 78.2%; Score 461.5; DB 2; Length 108;
Best Local Similarity 82.1%; Pred. No. 1.6e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
QY 1 DIELTQSPAIMSASGKRYTTTCRASGVSDYGHSPFQKPGTSPKLTWYTSNLA 60
DB 1 DIELTQSPAIMSASGKRYTTTCRASGVSDYGHSPFQKPGTSPKLTWYTSNLA 55
QY 61 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTGGSDQGNKR 112
DB 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTGGSDQGNKR 107
Db 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTGGSDQGNKR 107

RESULT 4
AA97236
ID AA97236 standard; protein; 108 AA.
XX
XX AA97236;
AC
XX
XX 19-DEC-2000 (first entry)
DT
XX
XX Variable light chain fragment of anti-SI(KDR) antibody.
DE
XX Immunoglobulin; antibody; complementary determining region; CDR; VEGF;
XX Vascular endothelial growth factor; KDR;
XX Kinase insert domain containing receptor; multivalent; monovalent;
XX humanised antibody; chimeric antibody; tumour; diabody; triabody;
XX glioblastoma multiforme; hemangioblastoma; AIDS;
XX central nervous system neoplasms; AIDS associated Kaposi's sarcoma;
XX acquired immune deficiency syndrome; AIDS; human.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX MO200044777-A1.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US002180.
XX
XX 29-JAN-1999; 99US-00240736.
XX
XX 29-JAN-1999; 99US-0117726P.
XX

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XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu Z, Witte L;
XX DR WPI; 2000-505966/45.
XX DR N-PSDB; AAA53768.
XX PT Novel immunoglobulin molecules binding kinase insert domain-containing
XX PT receptor with the same affinity as vascular endothelial growth factor,
XX PT used to reduce tumor growth.
XX PS Claim 4; Page 51; 55pp; English.
XX
XX CC New immunoglobulin molecules are described that bind kinase insert domain
XX CC -containing receptor (KDR) with a comparable affinity to human vascular
XX CC endothelial growth factor (VEGF). The antibodies neutralise KDR
XX CC activation. The immunoglobulin may be a multivalent single chain
XX CC antibody, a monovalent single chain antibody, a diabody, a triabody, a
XX CC humanised antibody or a chimerised antibody. The immunoglobulin molecules
XX CC bind specifically to an extracellular domain of the KDR receptor with the
XX CC same affinity as VEGF. Overexpression of VEGF has been implicated in a
XX CC number of human tumour cell lines including glioblastoma multiforme,
XX CC hemangioblastoma, central nervous system neoplasms and AIDS associated
XX CC Kaposi's sarcoma. The antibodies therefore have applications in treating
XX CC these conditions. This sequence encodes a preferred heavy chain
XX CC complementary determining region of the immunoglobulins of the invention
XX sequence 108 AA;
SQ
Query Match 78.1%; Score 460.5; DB 3; Length 108;
Best Local Similarity 82.1%; Pred. No. 1.9e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
QY 1 DIELTQSPAIMSASGKRYTTTCRASGVSDYGHSPFQKPGTSPKLTWYTSNLA 60
DB 1 DIELTQSPAIMSASGKRYTTTCRASGVSDYGHSPFQKPGTSPKLTWYTSNLA 55
QY 61 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTGGSDQGNKR 112
DB 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTGGSDQGNKR 107
Db 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTGGSDQGNKR 107

RESULT 5
AAB82710
ID AAB82710 standard; protein; 108 AA.
XX
XX AAB82710;
AC
XX
XX 11-SEP-2003 (revised)
DT
XX
XX 15-OCT-2001 (first entry)
DT
XX
XX VEGF antagonist antibody IMC-1C11 light chain variable region.
DE
XX IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
XX Vascular endothelial growth factor; angiogenesis; antiangiogenic;
XX antitumour; neoplasms; collagen-vascular disease; autoimmune disease;
XX tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
XX colon carcinoma; ovarian carcinoma; neuroblastoma;
XX glioblastoma multiforme; melanoma; therapy; light chain.
XX
XX Mus sp.
OS Homo sapiens.
OS Chimeric.
OS
XX Key Location/Qualifiers
XX FT 24..33 //label= CDR-L1
XX FT //note="complementarity determining region 1"
XX FT 49..55 //label= CDR-L2
XX FT //note="complementarity determining region 2"
XX FT 88..96
XX

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FT /label= CDR-L3
 FT /note= "complementarity determining region 3"
 XX
 PN W0200154723-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-US002839.
 XX
 PR 28-JAN-2000; 2000US-0178791P.
 XX
 PR 31-MAR-2000; 2000US-00539692.
 XX
 PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
 XX (IMCL-) IMCLONE SYSTEMS INC.
 PI Kerbel R;
 XX
 DR WPI; 2001-514531/56.
 DR N-PSDB; AAH26406.
 XX
 PT Treating or controlling an angiogenic dependent condition (e.g. a
 PT neoplasm, collagen-vascular or auto-immune disease) in mammal by
 PT administering a combination of an anti-angiogenic molecule and a
 PT chemotherapeutic agent.
 XX
 PS Disclosure; Page 38-39; 42pp; English.
 XX
 CC The present sequence is that of the light chain variable region of IMC-
 CC ICI1, a mouse-human chimeric antibody that has vascular endothelial
 CC growth factor (VEGF) antagonist activity. The antibody, or a fragment of
 CC it, can be used as an anti-angiogenic molecule, together with a
 CC chemotherapeutic agent, for the treatment of an angiogenic dependent
 CC condition in a mammal, especially a human. The invention relates
 CC generally to a method of treating or controlling an angiogenic dependent
 CC condition by administering an anti-angiogenic molecule and a
 CC chemotherapeutic agent, to produce a regression or arrest of the
 CC condition while minimizing or preventing significant toxicity of the
 CC chemotherapeutic agent. The anti-angiogenic molecule inhibits or blocks
 CC the action of a vascular endothelium survival factor such as VEGF or its
 CC receptor, and is especially IMC-ICI1. Conditions that can be treated
 CC include a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung carcinoma,
 CC prostate carcinoma, colon carcinoma, prostate carcinoma, ovarian
 CC carcinoma, neuroblastoma, central nervous system tumour, neuroblastoma,
 CC glioblastoma multiforme or melanoma (all claimed). (Updated on 11-SEP-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 108 AA;
 XX
 QY Query Match 78.1%; Score 460.5; DB 4; Length 108;
 Db Best Local Similarity 82.1%; Pred. No. 1.9e-28;
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
 XX
 QY 1 DIETLQSPALMSASPGKVTITTCRASGVDSYGHSPQWFOQKPGTSPKLMIVSTSLAS 60
 Db 1 DIETLQSPALMSASPGKVTITTCRASGVDSYGHSPQWFOQKPGTSPKLMIVSTSLAS 55
 XX
 QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPTFGSGDQAGNKR 112
 Db 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSVPTFGSGTLEIKR 107
 XX
 RESULT 6
 AA025956
 ID AA025956 standard; protein; 108 AA.
 XX
 AC AA025956;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Mouse anti-KDR pIC1 scFv antibody VL region #1.
 XX
 KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;

KM foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
 KM VEGF; tumour growth; light chain variable region; VL; angiogenesis;
 KM pIC11; scFv antibody.
 XX
 OS Mus musculus.
 XX
 PN US2002064528-A1.
 XX
 PD 30-MAY-2002.
 XX
 PF 12-OCT-2001; 2001US-00976787.
 XX
 PR 28-JAN-2000; 2000US-00493539.
 XX
 PA (ZHUZ/) ZHU Z.
 XX (WITT/) WITTE L.
 PI Zhu Z, Witte L;
 XX
 DR WPI; 2002-589175/63.
 DR N-PSDB; AAD42821.
 XX
 PT Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
 PT insert domain-containing receptor with an affinity comparable to human
 PT vascular endothelial growth factor, and neutralizes activation of KDR.
 XX
 PS Claim 4; Page 11; 34pp; English.
 XX
 CC The present invention relates to novel immunoglobulin molecules that bind
 CC to kinase insert domain-containing receptor (KDR) (a human homologue of
 CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable
 CC to human vascular endothelial growth factor (VEGF) and that neutralises
 CC activation of KDR. Sequences of the invention are useful for neutralising
 CC the activation of KDR, for reducing tumor growth and for inhibiting
 CC angiogenesis. The present sequence is mouse anti-KDR pIC1 scFv antibody
 CC light chain variable region (VL)
 XX
 SQ Sequence 108 AA;
 XX
 QY Query Match 78.1%; Score 460.5; DB 5; Length 108;
 Db Best Local Similarity 82.1%; Pred. No. 1.9e-28;
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
 XX
 QY 1 DIETLQSPALMSASPGKVTITTCRASGVDSYGHSPQWFOQKPGTSPKLMIVSTSLAS 60
 Db 1 DIETLQSPALMSASPGKVTITTCRASGVDSYGHSPQWFOQKPGTSPKLMIVSTSLAS 55
 XX
 QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPTFGSGDQAGNKR 112
 Db 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSVPTFGSGTLEIKR 107
 XX
 RESULT 7
 AA074413
 ID AA074413 standard; peptide; 108 AA.
 XX
 AC AA074413;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Antigen-binding protein light chain variable domain (VH) #1.
 XX
 KW Antigen-binding protein; antibody light chain variable domain;
 KW cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KW vascular endothelial growth factor receptor; VEGF;
 XX cell proliferation inhibitor.
 XX
 OS Mus sp.
 XX
 PN W0200190192-A2.
 XX
 PD 29-NOV-2001.
 XX

PF 24-MAY-2001; 2001WO-US016924.
 XX
 PR 24-MAY-2000; 2000US-0206749P.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Zhu Z;
 XX
 DR WPI; 2002-106189/14.
 DR N-PSDB; AAS20284.
 PT New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumor growth and for inhibiting angiogenesis, comprises a complex of two
 PT polypeptides and two second polypeptides.
 XX
 PS Claim 57; Page 57; 64pp; English.
 CC The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;
 CC reducing endothelial cell proliferation; inhibiting VEGF induced
 CC migration of human leukaemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This sequence represents a light chain variable domain (VH) incorporated
 CC into Fv, an engineered protein containing a heavy chain variable domain
 CC and a light chain variable domain in one polypeptide chain, described in
 CC the method of the invention
 XX
 SQ Sequence 108 AA;
 Query Match 78.1%; Score 460.5; DB 5; Length 108;
 Best Local Similarity 82.1%; Pred. No. 1.9e-28;
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
 QY 1 DIELTQSPAIMSASPGKVTTCRASVSVDYGHSHFMQFOOKPETSFKLWITSNLAAS 60
 DB 1 DIELTQSPAIMSASPGKVTTCRASVSVDYGHSHFMQFOOKPETSFKLWITSNLAAS 55
 QY 61 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTFGSGDOAGNKR 112
 DB 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTFGSGDKLEIKR 107
 RESULT 8
 ABJ26725
 ID ABJ26725 standard; protein; 108 AA.
 XX
 AC ABJ26725;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE VEGF binding related protein SEQ ID No 8.
 XX
 KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
 KW leukaemia cell; vascular endothelial growth factor; tumour;
 XX bispecific antigen-binding protein; mouse; murine.
 OS Mus sp.
 XX
 PN WO2003002144-A1.

XX
 PD 09-JAN-2003.
 XX
 PF 26-JUN-2002; 2002WO-US020332.
 XX
 PR 26-JUN-2001; 2001US-0301299P.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 XX
 PI Zhu Z;
 XX
 DR WPI; 2003-201468/19.
 DR N-PSDB; ABT23303.
 PT New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a second
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for
 PT treating tumors.
 XX
 PS Claim 7; Page 49-50; 98pp; English.
 CC The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells and
 CC migration of leukaemia cells. The antibodies are useful for treating
 CC tumours and for in vivo or in vitro for investigative and diagnostic
 CC methods. This sequence represents a mouse protein relating to the
 CC bispecific antibodies that bind to the VEGF receptors of the invention
 XX
 SQ Sequence 108 AA;
 Query Match 78.1%; Score 460.5; DB 6; Length 108;
 Best Local Similarity 82.1%; Pred. No. 1.9e-28;
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
 QY 1 DIELTQSPAIMSASPGKVTTCRASVSVDYGHSHFMQFOOKPETSFKLWITSNLAAS 60
 DB 1 DIELTQSPAIMSASPGKVTTCRASVSVDYGHSHFMQFOOKPETSFKLWITSNLAAS 55
 QY 61 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTFGSGDOAGNKR 112
 DB 56 GVPARFSGSGSGTSTLTISRMEADATYYCOQSNEDPYTFGSGDKLEIKR 107
 RESULT 9
 ADK18202
 ID ADK18202 standard; peptide; 108 AA.
 XX
 AC ADK18202;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Mouse VEGF receptor light chain variable domain peptide, SEQ ID No 8.
 XX
 KW antibody; antigen binding site; vascular endothelial growth factor;
 KW VEGF receptor; immunoglobulin; tumour; angiogenesis; cytosstatic;
 KW immunostimulant; vaccine; complementarity determining region; variable;
 XX light; mouse; murine.
 OS Mus sp.
 XX
 PN WO2004003211-A1.
 XX
 PD 08-JAN-2004.
 XX
 PF 24-DEC-2002; 2002WO-US041372.
 XX
 PR 26-JUN-2002; 2002WO-US020332.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.

XX PI Zhu Z;
 XX DR WPI, 2004-083065/08.
 XX PT New antibody having a first and second binding sites specific for a first
 XX PT and second vascular endothelial growth factor (VEGF) receptor, useful for
 XX PT reducing tumor growth in a mammal and for inhibiting angiogenesis.
 XX PS Claim 7, SEQ ID NO 8, 99pp; English.
 XX CC The invention relates to a novel antibody having a first antigen binding
 XX CC site specific for a first vascular endothelial growth factor (VEGF)
 XX CC receptor and a second antigen specific for a second VEGF receptor. The
 XX CC invention further relates to: an antibody that specifically binds to an
 XX CC extracellular domain of a first VEGF receptor and an extracellular domain
 XX CC of a second VEGF receptor, where binding of the antibody to the first and
 XX CC second VEGF receptor neutralizes activation of that VEGF receptor; a
 XX CC method for making the antibody by co-expressing in a host cell a
 XX CC recombinant DNA construct encoding a first polypeptide having the first
 XX CC immunoglobulin heavy chain domain located to the N-terminus of the second
 XX CC immunoglobulin light chain variable domain; a recombinant DNA construct
 XX CC encoding a second polypeptide having the second immunoglobulin heavy
 XX CC chain variable domain located to the N-terminus of the first
 XX CC immunoglobulin light chain variable domain, for time and in a manner
 XX CC sufficient to allow expression of the polypeptides and formation of the
 XX CC antibody; a method for neutralizing activation of a first VEGF receptor
 XX CC and the second VEGF receptor in a cell by treating a cell with the
 XX CC antibody cited above; a method for reducing tumor growth in a mammal by
 XX CC treating the mammal with the antibody cited above; and a method for
 XX CC inhibiting angiogenesis in a mammal by treating the mammal with the
 XX CC antibody cited above. The antibody has cytostatic and immunostimulant
 XX CC activities. The VEGF receptor antigen can be used to create a vaccine.
 XX CC The antibody is useful for reducing tumor growth in a mammal and for
 XX CC inhibiting angiogenesis. This sequence represents a VEGF receptor
 XX CC variable light chain peptide of the invention.
 XX SQ Sequence 108 AA;
 XX Query Match 78.1%; Score 460.5; DB 8; Length 108;
 XX Best Local Similarity 82.1%; Pred. No. 1.9e-28;
 XX Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
 QY 1 DIETGSPAIMSASPERKVTITTCRASGVDSYGHSPFMWFOQKPGTSPKLMYSTSLAS 60
 DB 1 DIETGSPAIMSASPERKVTITTCRASGVDSYGHSPFMWFOQKPGTSPKLMYSTSLAS 55
 QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFSGDQAGNKR 112
 DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSRSSYPFTFSGTKLEIKR 107
 XX RESULT 10
 XX AAE25960
 XX ID AAE25960 standard; protein; 240 AA.
 XX AC AAE25960;
 XX XX
 XX DT 15-NOV-2002 (first entry)
 XX XX
 XX DE KDR binding immunoglobulin related mouse protein #1.
 XX XX
 XX MM Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;
 XX MM foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
 XX MM VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;
 XX MM pIC11; scFv antibody.
 XX XX
 XX OS Mus sp.
 XX XX US2002064528-A1.
 XX XX PN 30-MAY-2002.
 XX PD
 XX XX

PF 12-OCT-2001; 2001US-00976787.
 XX XX
 XX PR 28-JAN-2000; 2000US-00493539.
 XX XX
 XX PA (ZHUZ/) ZHU Z.
 XX PA (WITTE/) WITTE L.
 XX XX
 XX PI Zhu Z, Witte L,
 XX XX
 XX DR WPI, 2002-589175/63.
 XX DR N-PSDB; AAD42824.
 XX XX
 XX PT Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
 XX PT insert domain-containing receptor with an affinity comparable to human
 XX PT vascular endothelial growth factor, and neutralizes activation of KDR.
 XX PS Disclosure, Page 16-17, 34pp; English.
 XX XX
 XX CC The present invention relates to novel immunoglobulin molecules that bind
 XX CC to kinase insert domain-containing receptor (KDR) (a human homologue of
 XX CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable
 XX CC to human vascular endothelial growth factor (VEGF) and that neutralises
 XX CC activation of KDR. Sequences of the invention are useful for neutralising
 XX CC the activation of KDR, for reducing tumour growth and for inhibiting
 XX CC angiogenesis. The present sequence is KDR binding immunoglobulin related
 XX CC mouse protein
 XX XX
 XX SQ Sequence 240 AA;
 XX Query Match 78.1%; Score 460.5; DB 5; Length 240;
 XX Best Local Similarity 82.1%; Pred. No. 4.2e-28;
 XX Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
 QY 1 DIETGSPAIMSASPERKVTITTCRASGVDSYGHSPFMWFOQKPGTSPKLMYSTSLAS 60
 DB 133 DIETGSPAIMSASPERKVTITTCRASGVDSYGHSPFMWFOQKPGTSPKLMYSTSLAS 187
 QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFSGDQAGNKR 112
 DB 188 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSRSSYPFTFSGTKLEIKR 239
 XX RESULT 11
 XX AAU74419
 XX ID AAU74419 standard; protein; 240 AA.
 XX AC AAU74419;
 XX XX
 XX DT 26-MAR-2002 (first entry)
 XX XX
 XX DE Antigen-binding protein, single chain variable fragment version #1.
 XX XX
 XX MM Antigen-binding protein, single chain variable fragment; scFv; antigen;
 XX MM cytostatic; angiogenesis inhibitor; tumour; leukemia; antibody;
 XX MM vascular endothelial growth factor receptor; VEGF;
 XX MM cell proliferation inhibitor.
 XX XX
 XX OS Mus sp.
 XX OS Synthetic.
 XX OS
 XX XX
 XX FH Key
 XX FT Region
 XX FT Location/Qualifiers
 XX FT 1..117
 XX FT /label= VH
 XX FT /note= "heavy chain variable domain. Specifically claimed
 XX FT in claim 57"
 XX FT 118..132
 XX FT /label= Linker
 XX FT /note= "15 amino acid linker joins the VH and VL regions
 XX FT of the single chain variable fragment protein. Encoded by
 XX FT AAS20285"
 XX FT 133..240
 XX FT /label= VL
 XX FT /note= "light chain variable domain. Specifically claimed
 XX FT Region
 XX FT 133..240
 XX FT
 XX FT

in claim 57"

FT XX Mus sp.
 FN WO200190192-A2.
 PD 29-NOV-2001.
 PP 24-MAY-2001; 2001WO-US016924.
 PR 24-MAY-2000; 2000US-0206749P.
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PI Zhu Z;
 P1
 P2 WPI; 2002-106189/14.
 PT New bispecific immunoglobulin-like antigen-binding protein for reducing
 PT tumor growth and for inhibiting angiogenesis, comprises a complex of two
 PT polypeptides and two second polypeptides.
 PS Claim 63; Page 62; 64pp; English.

XX The invention describes an antigen-binding protein (I) comprising a
 CC complex of two polypeptides (P1) and two second polypeptides (P2) which
 CC are stably associated in an immunoglobulin like complex. P1 has an
 CC antigen-binding site located to the N terminus of immunoglobulin (Ig)
 CC light chain constant domain (CL domain), and P2 has an antigen-binding
 CC site located to the N terminus of the CH1 domain. (I) is useful for:
 CC neutralising the activation of a vascular endothelial growth factor
 CC (VEGF) receptor; reducing tumour growth; inhibiting VEGF-induced
 CC migration of human leukemia cells; blocking interaction of a protein and
 CC its ligand; promoting interactions between immune cells and target cells;
 CC and in vivo and in vitro for investigative, diagnostic or treatment
 CC methods. The design of (I) provides for efficient production so that
 CC substantially all of the antigen-binding proteins produced are assembled
 CC in the desired configuration. (I) is bivalent and bispecific, homogeneous
 CC and in tetrameric form. The heavy chain constant domains which constitute
 CC the FC region (e.g., CH2 and CH3 for an IGG molecule) of a natural
 CC antibody and which provide other antibody functions can be present. There
 CC is no requirement for processing in vitro to obtain the complete product.
 CC This is the amino acid sequence of a single chain variable fragment
 CC (scFv), an engineered protein containing a variable light and variable
 CC heavy domain on one polypeptide, described in the method of the invention

XX Sequence 240 AA;

Query Match 78.1%; Score 460.5; DB 5; Length 240;
 Best Local Similarity 82.1%; Pred. No. 4.2e-28;
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETQSPAIMASGEGKVTTCRASBSVDYGHSMFOOKPGTSPKLTWYTSNLAAS 60
 DB 133 DIETQSPAIMASGEGKVTTCRASBSV-----SYMFMFOOKPGTSPKLTWYTSNLAAS 187
 QY 61 GVPAFFSGSGSGTSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 112
 DB 188 GVPAFFSGSGSGTSLTISRMEADATYYCOQRSYPTFTGSGTKLEIKR 239

RESULT 12

ABJ26731 ID ABJ26731 standard; protein; 240 AA.

XX ABJ26731;

XX 01-MAY-2003 (first entry)

DE VEGF binding related protein SEQ ID No 27.

XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
 KW leukemia cell; vascular endothelial growth factor; tumour;
 KW bispecific antigen-binding protein; mouse; murine.

XX Mus sp.

FN WO2003002144-A1.

PD 09-JAN-2003.

PP 26-JUN-2002; 2002WO-US020332.

PR 26-JUN-2001; 2001US-0301239P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

P1 WPI; 2003-201468/19.

PT New bispecific antibodies having antigen-binding sites specific for a
 PT first vascular endothelial growth factor (VEGF) receptor and for a second
 PT VEGF receptor, useful for inhibiting migration of leukemia cells, or for
 PT treating tumors.

PS Disclosure; Page 55-56; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding
 CC site specific for a first vascular endothelial growth factor (VEGF)
 CC receptor and a second antigen-binding site specific for a second VEGF
 CC receptor. The bispecific antigen-binding proteins block activation of the
 CC VEGF receptor and are useful for reducing or inhibiting VEGF-induced
 CC cellular functions such as mitogenesis of vascular endothelial cells and
 CC migration of leukemia cells. The antibodies are useful for treating
 CC tumours and for in vivo or in vitro for investigative and diagnostic
 CC methods. This sequence represents a mouse protein relating to the
 CC bispecific antibodies that bind to the VEGF receptors of the invention

XX Sequence 240 AA;

Query Match 78.1%; Score 460.5; DB 6; Length 240;
 Best Local Similarity 82.1%; Pred. No. 4.2e-28;
 Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETQSPAIMASGEGKVTTCRASBSVDYGHSMFOOKPGTSPKLTWYTSNLAAS 60
 DB 133 DIETQSPAIMASGEGKVTTCRASBSV-----SYMFMFOOKPGTSPKLTWYTSNLAAS 187
 QY 61 GVPAFFSGSGSGTSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 112
 DB 188 GVPAFFSGSGSGTSLTISRMEADATYYCOQRSYPTFTGSGTKLEIKR 239

RESULT 13

ADK18221 ID ADK18221 standard; protein; 240 AA.

XX ADK18221;

XX 06-MAY-2004 (first entry)

DE Mouse kinase insert domain-containing receptor scFv protein, SEQ ID 27.

XX antibody; antigen binding site; vascular endothelial growth factor;
 KW VEGF receptor; immunoglobulin; tumour; angiogenesis; cytostatic;
 KW immunostimulant; vaccine; KDR; kinase insert domain-containing receptor;
 KW scFv; mouse; murine.

XX Mus sp.

PN WO2004003211-A1.

PD 08-JAN-2004.

PP 24-DEC-2002; 2002WO-US041372.

```
PR 26-JUN-2002; 2002WO-US020332.
XX
PA (IMCL-) IMCLONE SYSTEMS INC.
XX
PI Zhu Z;
XX
DR WPI; 2004-083065/08.
XX
PT New antibody having a first and second binding sites specific for a first
PT and second vascular endothelial growth factor (VEGF) receptor, useful for
PT reducing tumor growth in a mammal and for inhibiting angiogenesis.
XX
PS Disclosure; SEQ ID NO 27; 99p; English.
XX
CC The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen specific for a second VEGF receptor. The
CC invention further relates to: an antibody that specifically binds to an
CC extracellular domain of a first VEGF receptor and an extracellular domain
CC of a second VEGF receptor, where binding of the antibody to the first and
CC second VEGF receptor neutralizes activation of that VEGF receptor; a
CC method for making the antibody by co-expressing in a host cell a
CC recombinant DNA construct encoding a first polypeptide having the first
CC immunoglobulin heavy chain domain located to the N-terminus of the second
CC immunoglobulin light chain variable domain; a recombinant DNA construct
CC encoding a second polypeptide having the second immunoglobulin heavy
CC chain variable domain located to the N-terminus of the first
CC immunoglobulin light chain variable domain, for time and in a manner
CC sufficient to allow expression of the polypeptides and formation of the
CC antibody; a method for neutralizing activation of a first VEGF receptor
CC and the second VEGF receptor in a cell by treating a cell with the
CC antibody cited above; a method for reducing tumor growth in a mammal by
CC treating the mammal with the antibody cited above; and a method for
CC inhibiting angiogenesis in a mammal by treating the mammal with the
CC antibody cited above. The antibody has cytostatic and immunostimulant
CC activities. The VEGF receptor antigen can be used to create a vaccine.
CC The antibody is useful for reducing tumor growth in a mammal and for
CC inhibiting angiogenesis. This sequence represents a kinase insert domain-
CC containing receptor scfv protein of the invention.
XX
SQ Sequence 240 AA;
Query Match 78.1%; Score 460.5; DB 8; Length 240;
Best Local Similarity 82.1%; Pred. No. 4.2e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
QY 1 DIELTOSPAIMASAPKRYVTTTCASASVDYSGHFMQFOQKGTSPKIMYSTNLAS 60
DB 133 DIELTOSPAIMASAPKRYVTTTCASASSV-----SYNHWFOQKGTSPKIMYSTNLAS 187
QY 61 GVPARFSGSGSGTYSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 112
DB 188 GVPARFSGSGSGTYSLTISRMEADATYYCOQRSSTPTFGSGTKLEIKR 239
RESULT 14
ID AAB70842 standard; protein; 330 AA.
XX
AC AAB70842;
XX
DT 11-SEP-2003 (revised)
DT 25-JUN-2001 (first entry).
XX
DE SNV-env leader/human 7B2-scFv fusion construct.
XX
KM T lymphocyte; antibody; single chain variable antibody; scFv; human;
KM cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
KM gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
KM acquired immune deficiency syndrome; severe combined immune deficiency;
KM T cell lymphoma; fusion construct.
XX
QS Homo sapiens.
```

```
OS Spleen necrosis virus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Protein 1..45
FT Protein /label= SNV-env_leader
FT Protein 46..330
FT Protein /label= 7B2-scFv
XX
PN DE19946142-A1.
XX
PD 29-MAR-2001.
XX
PF 27-SEP-1999; 99DE-01046142.
XX
PK 27-SEP-1999; 99DE-01046142.
XX
PA (BUND ) BUNDESREPUBLIK DRUT PAUL-EHRLICH-INST.
XX
PI Cichutek K, Engelstaedter M;
XX
DR WPI; 2001-246140/26.
DR N-PSDB; AAF61511.
XX
PT Cell-targeting vector selective for T lymphocytes, useful in gene therapy
PT of e.g. acquired immune deficiency syndrome, encodes a single-chain
PT variable antibody fragment.
XX
PS Claim 1; Fig 3; 18pp; German.
XX
CC This invention describes a novel cell-targeting vector (A) containing a
CC DNA sequence (i) encoding a single-chain variable antibody fragment
CC (scFv). The products of the invention have antiviral, cytostatic and
CC immunostimulant activity and can be used in gene therapy, immunization
CC and diagnosis particularly of T cell-associated diseases, specifically
CC acquired immune deficiency syndrome (AIDS), severe combined immune
CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
CC human B cells, and 1000 fold selectivity over other human cells. A vector
CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
CC fragment, fully defined in the specification. It was used to transform
CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
CC determine transfection. The viral titer (infectious units/ml) was over
CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa.
CC showing the high selectivity for human T cells. This sequence represents
CC the SNV-env leader/human 7B2-scFv fusion construct used in the
CC construction of novel cell targeting vectors described in the invention.
CC (Updated on 11-SEP-2003 to standardise O6 field)
XX
SQ Sequence 330 AA;
Query Match 78.1%; Score 460.5; DB 4; Length 330;
Best Local Similarity 82.1%; Pred. No. 5.8e-28;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;
QY 1 DIELTOSPAIMASAPKRYVTTTCASASVDYSGHFMQFOQKGTSPKIMYSTNLAS 60
DB 181 DIELTOSPAIMASAPKRYVTTTCASASSV-----SYNHWFOQKGTSPKIMYSTNLAS 235
QY 61 GVPARFSGSGSGTYSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 112
DB 236 GVPARFSGSGSGTYSLTISRMEADATYYCOQRSSTPTFGSGTKLEIKR 287
RESULT 15
ID AAE13144 standard; protein; 106 AA.
XX
AC AAE13144;
XX
DT 11-SEP-2003 (revised)
```

```

DT 28-JAN-2002 (first entry)
XX Humanised antibody light chain fragment.
DE
XX Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
XX cytoskeletal; light chain; myelocytic leukaemia; lymphocytic; erythrocytic;
XX monocytic; multiple myeloma; lymphoid cell; Hodgkin's disease; mouse;
XX human; chimeric.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
XX WO200174296-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010504.
XX
XX 31-MAR-2000; 2000US-00540770.
XX
XX (INCL-) IMCLONE SYSTEMS INC.
XX (CORR ) CORNELL RES FOUND INC.
XX
XX Witte L, Rafii S;
XX
XX MPI: 2001-662942/76.
XX N-PSDB; AAD21670.
XX
XX Inhibiting growth of non-solid tumor cells useful to treat bone marrow
XX tumors such as leukemias or multiple myeloma comprises treatment with an
XX antagonist of a vascular endothelial growth factor receptor.
XX
XX Claim 8; Page 16; 68pp; English.
XX
XX The invention relates to a method for inhibiting the growth of non-solid
XX tumor cells that are stimulated by a ligand of vascular endothelial
XX growth factor receptor (VEGFR) in mammals particularly humans. The method
XX involves treating the mammals with humanised VEGFR monoclonal antibodies
XX (antagonists). Humanised monoclonal antibody comprises humanised mouse
XX variable region joined to human constant region, where the humanised
XX mouse variable region contains mouse complementarity determining region
XX (CDR) grafted into human variable region. The method is useful for
XX treating leukemias such as acute or chronic myelocytic leukaemia, acute
XX or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
XX multiple myelomas and lymphoid cells, particularly those related to non-
XX Hodgkin's and Hodgkin's disease. The present sequence is humanised
XX antibody light chain fragment used in the exemplification of the
XX invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 106 AA;

```

Query Match 77.4%; Score 456.5; DB 4; Length 106;
Best Local Similarity 85.7%; Pred. No. 3.9e-28;
Matches 90; Conservative 3; Mismatches 7; Indels 5; Gaps 1;

```

QY 1 DIELTSPAIMSASPEKVTTCRASESVSYGHSFWMFOOKRGTSPKLMITSTSNLAS 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DIELTSPAIMSASPEKVTTCRASESVSYGHSFWMFOOKRGTSPKLMITSTSNLAS 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSG 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPYTFGSG 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: November 21, 2005, 12:19:54
Job time : 151.949 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 / Search time 27.2821 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-86

Perfect score: 590
Sequence: 1 DIEITQSPAIMSASPGKEKVT.....QOSNEDPYTGGSDQGNKR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	429.5	72.8	107 2 PC4405	Ig kappa chain V r
2	427.5	72.5	140 2 PL0013	Ig kappa chain pre
3	424.5	71.9	106 2 B54378	Ig light chain V r
4	422.5	71.6	130 2 A32513	Ig kappa chain pre
5	419.5	71.1	107 2 A42848	Ig light chain V r
6	416.5	70.6	107 2 A30562	Ig kappa chain V r
7	411.5	69.7	107 2 B30562	Ig kappa chain V r
8	409.5	68.4	130 2 S04573	Ig kappa chain pre
9	407.5	68.1	100 2 S28590	Ig kappa chain V r
10	407.5	68.1	107 2 PD0011	Ig kappa chain V r
11	407.5	68.1	120 2 S6536	Ig light chain V r
12	406.5	68.9	130 1 JL0079	Ig kappa chain pre
13	405.5	68.7	103 2 S29591	Ig kappa chain V r
14	404.5	68.6	130 2 B32456	Ig kappa chain pre
15	404.5	68.6	235 2 S25058	Ig kappa chain m
16	402.5	68.2	105 2 S26338	Ig kappa chain V r
17	401.5	68.1	132 2 B45049	Ig kappa chain V r
18	401.5	68.1	104 2 S05268	Ig kappa chain pre
19	401	68.0	108 2 G30560	Ig kappa chain V r
20	401	68.0	111 1 KVM537	Ig kappa chain V r
21	400.5	67.9	107 2 PT0406	Ig kappa chain V r
22	399.5	67.7	99 2 D38601	Ig kappa chain V r
23	399.5	67.7	106 2 PS0071	Ig kappa chain V r
24	399.5	67.7	108 2 PL0278	Ig kappa chain V r
25	398.5	67.5	91 2 S17630	Ig kappa chain V r
26	397.5	67.4	91 2 S17626	Ig kappa chain V r
27	397	67.3	108 2 S38720	Ig light chain V r
28	395.5	67.0	93 2 S17641	Ig kappa chain V r
29	395.5	67.0	99 2 PH1058	Ig light chain V r

30	395.5	67.0	108 2 PL0277	Ig kappa chain V r
31	395.5	67.0	108 2 PL0276	Ig kappa chain V r
32	394.5	66.9	97 2 S26341	Ig light chain V r
33	394.5	66.9	99 2 PH1059	Ig light chain V r
34	392.5	66.5	97 2 PH1084	Ig light chain V r
35	392.5	66.5	106 2 PL0082	Ig kappa chain V r
36	382.5	66.5	113 2 S03410	Ig kappa chain pre
37	381.5	66.4	97 2 PH1085	Ig light chain V r
38	381.5	66.4	99 2 S29585	Ig kappa chain V r
39	391.5	66.4	107 2 S11118	Ig kappa chain V r
40	391	66.3	131 1 KVM5M6	Ig kappa chain pre
41	390.5	66.2	106 2 PS0070	Ig kappa chain V r
42	390	66.1	98 2 PH1061	Ig light chain V r
43	389.5	66.0	108 2 PS0069	Ig kappa chain V r
44	388.5	65.8	106 2 G27887	Ig kappa chain V r
45	388.5	65.8	123 2 S05269	Ig kappa chain pre

ALIGNMENTS

RESULT 1

PC4405
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
C/Accession: PC4405
R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A/Title: Generation of a phage display library of the immunoglobulin repertoire from hum
A/Reference number: PC4405
A/Molecule type: mRNA
A/Residues: 1-107 <DEN>
A/Cross-references: UNIPROT:O8K1F0; UNIPARC:UP100001767B
A/Experimental source: spleen cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:18-89/Domain: immunoglobulin homology <IMM>

Query Match 72.8%, Score 429.5, DB 2, Length 107,
Best Local Similarity 75.9%, Pred. No. 3.8e-30;
Matches 85; Conservative 7; Mismatches 15; Indels 5; Gaps 1;

QY	1	DIEITQSPAIMSASPGKEKVTTCRASGVDSYGHSPQWFOOKRPTSKYIYTSNLS	60
DB	1	DIEITQSPAIMSASPGKEKVTTCRASGVDSYGHSPQWFOOKRPTSKYIYTSNLS	55
QY	61	GVPAFGSGSGSGTSLTISRMEADATYCCOQSNEDPYTGGSDQGNKR	112
DB	56	GVPAFGSGSGSGTSLTISRMEADATYCCOQSNEDPYTGGSDQGNKR	107

RESULT 2

PL0013
Ig kappa chain precursor V region (4C11) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
R/Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kleber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A/Title: Structural basis of stimulatory anti-idiotypic antibodies.
A/Reference number: PL0011; MUID:88142863; PMID:3125424
A/Accession: PL0013
A/Molecule type: mRNA
A/Residues: 1-140 <CHS>
A/Cross-references: UNIPARC:UP100001767A6
A/Experimental source: cell line 4C11
C/Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterodimer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>
F:138-111/Domain: immunoglobulin homology <IMM>

F146-55/Region: complementarity-determining 1
F171-77/Region: complementarity-determining 2
F110-118/Region: complementarity-determining 3
F110-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 72.5%; Score 427.5; DB 2; Length 140;
Best Local Similarity 76.4%; Pred. No. 7.4e-30;
Matches 89; Conservative 3; Mismatches 16; Indels 5; Gaps 1;

Db 2 IELTQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 61
24 IVLQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 78

Query 62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 112
Db 79 VPARFSGSGSGTSTLTISRMEADATYYCQSNSTPPTFGSGTKLEMR 129

RESULT 3
B54378
Ig light chain V region anti-triplex DNA - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: B54378
R/Agazte, Y.M.; Lee, J.S.; Burkholder, G.D.
J. Biol. Chem. 269, 7019-7023, 1994

A/Title: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescent
A/Reference number: A54378; MUID:94165109; PMID:7509814
A/Accession: B54378
A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 1-106 <AGA>
A/Cross-references: UNIPARC:UPI00001767AC; GB:568985; NID:9545746; PIDN:AA030096.1; PID:
A/Experimental source: spleen and myeloma cell line MOPC 315.43
A/Note: sequence inconsistent with nucleotide translation
A/Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBIPI:144175)

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F16-89/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 424.5; DB 2; Length 106;
Best Local Similarity 81.7%; Pred. No. 1e-29;
Matches 85; Conservative 3; Mismatches 11; Indels 5; Gaps 1;

Db 2 IELTQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 61
2 IVLQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 56

Query 62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSG 105
Db 57 VPARFSGSGSGTSTLTISRMEADATYYCQSNSTPPTFGAG 100

RESULT 4
A33213
Ig kappa chain precursor V region (MRL22) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C/Accession: A32513
R/Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchesal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A/Title: Immunoglobulin kappa light chain variable region gene complex organization and
A/Reference number: A94689; MUID:88331394; PMID:3138286
A/Accession: A32513
A/Molecule type: DNA
A/Residues: 1-130 <KOF>

A/Cross-references: UNIPARC:UPI0000114D9C; GB:M20834; NID:9196943; PIDN:AAA38846.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F18-113/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 422.5; DB 2; Length 130;
Best Local Similarity 79.8%; Pred. No. 1.8e-29;

Matches 83; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

Query 2 IELTQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 61
Db 24 IVLQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 80

Query 62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSG 105
Db 81 VPARFSGSGSGTSTLTISRMEADATYYCQSNSTPPTFGSG 124

RESULT 5
A42848
Ig light chain V region - mouse (fragment)

N/Alternate names: I6 anti-tumor antibody
C/Species: Mus musculus (house mouse)
C/Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C/Accession: A42848; S31902
R/Fell, H.P.; Gayle, M.A.; Yellon, D.; Schieven, G.L.; Marken, J.S.; Aruffo,
J. Biol. Chem. 267, 15552-15558, 1992

A/Title: Chimeric I6 anti-tumor antibody. Genomic construction, expression, and character
A/Reference number: A42848; MUID:92348410; PMID:1639794
A/Accession: A42848
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-107 <FEL>
A/Cross-references: UNIPARC:UPI0000115334; EMBL:M90690
A/Note: sequence extracted from NCBI backbone (NCBIN:109958, NCBIPI:109959)

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F16-89/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 419.5; DB 2; Length 107;
Best Local Similarity 74.8%; Pred. No. 2.8e-29;
Matches 83; Conservative 9; Mismatches 14; Indels 5; Gaps 1;

Query 2 IELTQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 61
Db 2 IVLQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 56

Query 62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 112
Db 57 VPARFSGSGSGTSTLTISRMEADATYYCQSNSTPPTFGAGTKLEMR 107

RESULT 6
A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C/Accession: A30562
R/Sikder, S.K.; Borden, P.; Gruneo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
U. Immunol. 142, 888-893, 1989
A/Title: Amino acid substitutions in V-H CDR2 change the idio type but not the antigen-bir
A/Reference number: A30562; MUID:89110066; PMID:2464031
A/Accession: A30562
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <STK>

A/Cross-references: UNIPARC:UPI00001767B0
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F16-89/Domain: immunoglobulin homology <IMM>

Query Match 70.6%; Score 416.5; DB 2; Length 107;
Best Local Similarity 75.7%; Pred. No. 5e-29;
Matches 84; Conservative 5; Mismatches 17; Indels 5; Gaps 1;

Query 2 IELTQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 61
Db 2 IVLQSPALMSASPGKRVTTTCRASBSYDSYGHSPFQMPQKPGTSPKMTYSTNSIAG 56

Query 62 VPARFSGSGSGTSTLTISRMEADATYYCQSNEDPYTFGSGDQGNKR 112

Db 57 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 107

RESULT 7

IG kappa chain V region (27.10.2) - mouse (fragment)
 B30562
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
 C/Accession: B30562
 R/Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
 U. Immunol. 142, 888-893, 1989
 A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
 A/Reference number: A30562; MUID:89110066; PMID:2464031
 A/Accession: B30562
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-107 <STK>
 A/Cross-references: UNIPARC:UPI00001767BA
 C/Suprafamily: immunoglobulin V region; immunoglobulin
 C/Keywords: heterotetramer; immunoglobulin
 F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 411.5; DB 2; Length 107;
 Best Local Similarity 73.9%; Pred. No. 1.3e-28;
 Matches 82; Conservative 6; Mismatches 18; Indels 5; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASBSVDYSGHSPQKPGTSPKLTWYTSNLSAG 61
 Db 2 IVLQSPAIMSASPEKVTMTCSASSV-----SYMHWYQKSGTSPKRWYDTSKLSAG 56
 Qy 62 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 112
 Db 57 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 107

RESULT 8

IG kappa chain precursor V region (MRL-histone 7L) - mouse (fragment)
 S04573
 C/Species: Mus musculus (house mouse)
 C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
 C/Accession: S04573
 R/Kofler, R.; Noonan, D.J.; Strichal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; Th
 Eur. J. Immunol. 17, 91-95, 1987
 A/Title: Molecular analysis of the murine lupus-associated anti-self response: involvement
 A/Reference number: S04573; MUID:87133856; PMID:3102255
 A/Accession: S04573
 A/Molecule type: mRNA
 A/Residues: 1-130 <KOP>
 A/Cross-references: UNIPARC:UPI0000115DFE; EMBL:X14620; NID:952031; PIDN:CAA32773.1; PID
 A/Note: the authors translated the codon AGC for residue 47 as Asn
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-22/Domain: signal sequence #status predicted <SIG>
 F/23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F/38-113/Domain: immunoglobulin homology <IMM>

Query Match 69.4%; Score 409.5; DB 2; Length 130;
 Best Local Similarity 76.9%; Pred. No. 2.4e-28;
 Matches 80; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASBSVDYSGHSPQKPGTSPKLTWYTSNLSAG 61
 Db 24 IVLQSPAIMSASPEKVTMTCSASSV---KYLHWYQKSGTSPKRWYDTSNLSAG 80
 Qy 62 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 105
 Db 81 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 124

RESULT 9
 S29590
 IG kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S29590

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29590

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-100 <KNV>

A/Cross-references: UNIPARC:UPI0000115F56; EMBL:X59093; NID:952225; PIDN:CAA41819.1; PID:

A/Title: Isolation and structural characterization of trimeric cyanobacterial photosystem

C/Keywords: heterotetramer; immunoglobulin

F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 407.5; DB 2; Length 100;

Best Local Similarity 77.9%; Pred. No. 2.7e-28;

Matches 81; Conservative 5; Mismatches 13; Indels 5; Gaps 1;

Qy 2 IELTQSPAIMSASPEKVTTCRASBSVDYSGHSPQKPGTSPKLTWYTSNLSAG 61
 Db 2 IVLQSPAIMSASPEKVTMTCSASSV-----SYMHWYQKSGTSPKRWYDTSKLSAG 56
 Qy 62 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 105
 Db 57 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 100

RESULT 10

IG kappa chain V region (VLR10, anti-AFP) - mouse (fragment)
 PD0011
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jan-2000
 C/Accession: PD0011
 R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
 Chinese Biochem. J. 12, 648-653, 1996
 A/Title: Generation of a phage display library of the immunoglobulin repertoire from hume
 A/Reference number: PC4405
 A/Accession: PD0011
 A/Contents: Spleen
 A/Residues: 1-107 <DEN>
 A/Cross-references: UNIPARC:UPI00001767AA
 C/Suprafamily: immunoglobulin V region; immunoglobulin homology
 F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 407.9; DB 2; Length 107;
 Best Local Similarity 73.2%; Pred. No. 2.9e-28;
 Matches 82; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPEKVTTCRASBSVDYSGHSPQKPGTSPKLTWYTSNLSAG 60
 Db 1 DIELTQSPAIMSASPEKVTMTCSASSI-----SYMHWYQKSGTSPKRWYDTSKLSAG 55
 Qy 61 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 112
 Db 56 VPARFSGSGSGTSLTISRMKADATYYCQWSSNPYTGCGTKLEIKR 107

RESULT 11

IG light chain V region - mouse (fragment)
 S66536
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S66536
 R/Tsotis, G.; Haase, W.; Engel, A.; Michel, H.
 Eur. J. Biochem. 231, 823-830, 1995
 A/Title: Isolation and structural characterization of trimeric cyanobacterial photosystem
 A/Reference number: S66536; MUID:95377318; PMID:7649183
 A/Accession: S66536
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-120 <TSI>

A/Cross-references: UNIPARC:UPI0000113780; EMBL:X88903; NID:g895870; PIDN:CAA61365.1; P4
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/16-91/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 407.5; DB 2; Length 120;
Best Local Similarity 71.4%; Pred. No. 3.3e-28;
Matches 80; Conservative 8; Mismatches 21; Indels 3; Gaps 1;

QY 1 IELTOSPAIMASPGKVTTCRASVSVDYSGHSFMQWFOQKPGTSPKLMYSTSLASG 60
Db 1 IELTOSPAIMASPGKVTTCRASVSVDYSGHSFMQWFOQKPGTSPKLMYSTSLASG 57

QY 61 GVPARFSGSGSGTSTLTISRMEDATATYCCQSNEDPYTFGSGDOAGNKR 112
Db 58 GVPARFSGSGSGTSTLTISRMEDATATYCCQSGSSIPFTFGGTLEIKR 109

RESULT 12

IG kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence_revision 03-Aug-1996 #text_change 16-Jul-1999

C/Accession: U0079; A49044; B49044

R/Kaartinen, M.; Rocca-Serra, J.; Maekela, O.

Mol. Immunol. 25, 859-865, 1988

A/Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reac

A/Reference number: J10076; MUID:89096973; PMID:3211160

A/Accession: J10079

A/Molecule type: mRNA

A/Residues: 1-130 <KAA>

A/Cross-references: UNIPARC:UPI000017371F; GB:M2792; NID:g197159

A/Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6

A/Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10

R/Milestone, C.; Ewen, J.; Urvais, J.M.; Gonzalez-Fernandez, A.; Ghelardi, R.

Eur. J. Immunol. 22, 1627-1634, 1992

A/Title: Non-random features of the repertoire expressed by the members of one V kappa g

A/Reference number: A49044; MUID:92289826; PMID:1601044

A/Accession: A49044

A/Molecule type: DNA

A/Residues: 1-25 <MTI>

A/Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:g520214; PIDN:AAB22331.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

A/Cross-references: UNIPARC:UPI000011885; GB:S37664; NID:g520215; PIDN:AAB22332.1; PID:

A/Experimental source: BALB/c germ-line

A/Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit

C/Accession: B49044

A/Molecule type: DNA

A/Residues: 114-116 <MTI2>

RESULT 13

IG kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S29591

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29591

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-103 <KAV>

A/Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; NID:g52227; PIDN:CAA41820.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-88/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 405.5; DB 2; Length 103;
Best Local Similarity 77.9%; Pred. No. 4.2e-28;
Matches 81; Conservative 5; Mismatches 13; Indels 5; Gaps 1;

QY 2 IELTOSPAIMASPGKVTTCRASVSVDYSGHSFMQWFOQKPGTSPKLMYSTSLASG 61
Db 1 IELTOSPAIMASPGKVTTCRASVSVDYSGHSFMQWFOQKPGTSPKLMYSTSLASG 55

QY 62 VPARFSGSGSGTSTLTISRMEDATATYCCQSNEDPYTFGSG 105
Db 56 VPARFSGSGSGTSTLTISRMEDATATYCCQSNEDPYTFGSG 99

RESULT 14

IG kappa chain precursor V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 26-Oct-1989 #sequence_revision 26-Oct-1989 #text_change 21-Jan-2000

C/Accession: B32456

R/Dombrink-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.

J. Biol. Chem. 264, 4513-4522, 1989

A/Title: Variable region primary structures of a high affinity anti-fluorescein immunogl

A/Reference number: A32456; MUID:89174706; PMID:2494173

A/Accession: B32456

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-130 <DOM>

A/Cross-references: UNIPARC:UPI00001148B9; GB:J04610; NID:g556313; PIDN:AAA50296.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/38-113/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 404.5; DB 2; Length 130;
Best Local Similarity 77.5%; Pred. No. 6.4e-28;
Matches 79; Conservative 7; Mismatches 13; Indels 3; Gaps 1;

QY 4 IELTOSPAIMASPGKVTTCRASVSVDYSGHSFMQWFOQKPGTSPKLMYSTSLASG 63
Db 26 IELTOSPAIMASPGKVTTCRASVSVDYSGHSFMQWFOQKPGTSPKLMYSTSLASG 82

QY 64 ARFSGSGSGTSTLTISRMEDATATYCCQSNEDPYTFGSG 105
Db 83 ARFSGSGSGTSTLTISRMEDATATYCCQSNEDPYTFGSG 124

RESULT 15

IG kappa chain - mouse

C/Species: Mus musculus (house mouse)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C/Accession: S25058

R/Fischer, R.; Voss, A.; Nierbach, M.; Munkler, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A/Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A/Reference number: S25057
A/Accession: S25058
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-235 <PIS>
A/Cross-references: UNIPARC:UPI0000116096; EMBL:X67211; NID:G54828; PIDN:CNA47650.1; PIR
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/38-111/Domain: immunoglobulin homology <IMM>

Query Match 68.6%; Score 404.5; DB 2; Length 235;
Best Local Similarity 74.8%; Pred. No. 1.2e-27;
Matches 83; Conservative 5; Mismatches 18; Indels 5; Gaps 1;

QY	2	IELTQSPAIMSAPGEKVTTCRASBSVDYSGHSFMQWFOQKPGTSPCLMWTSTNLSG	61
DB	24	IVLTQSPAIMSAPGEKVTTCRASBSV-----SKMWTQQKSGTSPKRWIYDTSKLASG	78
QY	62	VPARFSGSGSGTSTSLTISRMEABDAATYCCQSNEDPYTFSGDQGNKR	112
DB	79	VGRFSGSGSGTSTSLTISRMEABDAATYCCQSSNPLTFGAGTKLELR	129

Search completed: November 21, 2005, 12:22:12
Job time : 28.2821 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: November 21, 2005, 11:45:55 / Search time 165.744 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-86
Perfect score: 590
Sequence: 1 DIETQSPAINMSASPGKVT.....QGSNEDPYTGGSDQGNKR 112

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first: 45 summaries

Database: UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	447.5	75.8	112 2	Q8K1F2_MOUSE
2	429.5	72.8	114 2	Q8K1F1_MOUSE
3	423.5	71.6	112 2	Q8K1F3_MOUSE
4	413	70.0	131 2	Q8L1C3_MOUSE
5	411.5	69.7	134 2	Q8VDD0_MOUSE
6	405.5	68.7	235 2	Q5B6V6_MOUSE
7	402.5	68.2	237 2	Q569Y8_MOUSE
8	401.5	68.1	235 2	Q5XFE8_MOUSE
9	401	68.0	111 1	KVJH_MOUSE
10	396	67.1	111 1	KVJH_MOUSE
11	395.5	67.0	106 2	Q9U4I0_MOUSE
12	394.5	66.9	107 1	KV6F_MOUSE
13	394.5	66.9	107 1	KV6G_MOUSE
14	394.5	66.9	107 1	KV6J_MOUSE
15	391	66.3	131 1	KVJ1_MOUSE
16	389.5	66.0	107 1	KV6I_MOUSE
17	389.5	66.0	112 2	Q8K1F0_MOUSE
18	389	65.9	111 1	KV3K_MOUSE
19	388.5	65.8	107 1	KV6H_MOUSE
20	381	64.6	111 1	KV3L_MOUSE
21	379	64.2	111 1	KV3M_MOUSE
22	378	64.1	111 1	KV3O_MOUSE
23	377	63.9	97 2	Q9J176_MOUSE
24	375.5	63.6	108 1	KV6K_MOUSE
25	375	63.6	111 2	Q8L1U6_MOUSE
26	374	63.4	132 1	KV3P_MOUSE
27	372	63.1	111 1	KV3N_MOUSE
28	371	62.9	111 1	KV3Q_MOUSE
29	370.5	62.8	107 1	KV6E_MOUSE
30	369.5	62.6	107 1	KV6A_MOUSE
31	368	62.4	111 1	KV3A_MOUSE

32	367.5	62.3	107 1	KV6C_MOUSE	P01677 mus musculus
33	367	62.2	112 1	KV3G_MOUSE	P01659 mus musculus
34	366.5	62.1	107 1	KV6D_MOUSE	P01678 mus musculus
35	364.5	61.8	112 1	KV3B_MOUSE	P01655 mus musculus
36	363	61.5	111 1	KV3D_MOUSE	P03977 mus musculus
37	359	60.8	111 1	KV3C_MOUSE	P01656 mus musculus
38	359	60.8	111 2	Q920E9_MOUSE	Q920E9 mus musculus
39	353.5	59.9	110 1	KV3P_MOUSE	P01668 mus musculus
40	352.5	59.7	107 1	KV6E_MOUSE	P01678 mus musculus
41	352	59.7	111 1	KV3S_MOUSE	P01670 mus musculus
42	350	59.3	111 1	KV3R_MOUSE	P01670 mus musculus
43	350	59.3	111 1	KV3T_MOUSE	P01672 mus musculus
44	348.5	59.1	129 1	KV4A_MOUSE	P01680 mus musculus
45	348	59.0	236 2	Q6PIH7_HUMAN	Q6PIH7 homo sapien

ALIGNMENTS

RESULT 1		ALIGNMENTS	
ID	Q8K1F2_MOUSE	PRELIMINARY;	PRT; 112 AA.
AC	Q8K1F2		
DT	01-OCT-2002 (TREMBLrel. 22, Created)		
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Anti-VIPase light chain variable region (Fragment).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN-BALB/c; TISSUE=Hypermuritized spleen;		
RA	Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;		
RT	"Two murine natural polyclonal autoantibodies are encoded by		
RT	nonmutated germ-line genes."		
RL	Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).		
DR	EMBL; AF516283; AAM64201.1; -; Genomic DNA.		
DR	PIR; H33932; H33932.		
DR	HSSP; P01837; 25C8.		
DR	SMR; Q8K1F2; 2-112.		
DR	Ensembl; ENSMUSG0000064150; Mus musculus.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003596; Ig_V.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
FT	NON_TER		
FT	NON_TER		
FT	SEQUENCE		
FT	112 AA; 11953 MW; 4716887PADB543ED CRC64;		
Query Match			
Best Local Similarity 75.8%; Score 447.5; DB 2; Length 112;			
Matches 90; Conservative 4; Mismatches 13; Indels 5; Gaps 1;			
QY	1 DIETQSPAINMSASPGKVTTCRASEVDYGHSPFQPGKPTGPTLWTYSNLS 60		
DB	1 DIVLTQSPAINMSASPGKVTTCNASSV-----SYMWFQPKPTGPTLWTYSNLS 55		
QY	61 GVPARFSGSGSTYSLTISRMEADATVYCOGSNEDPYTGGSDQGNKR 112		
DB	56 GVPARFSGSGSTYSLTISRMEADATVYCOGSNEDPYTGGSDQGNKR 107		
RESULT 2			
ID	Q8K1F1_MOUSE	PRELIMINARY;	PRT; 114 AA.


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FT CHAIN 23 >131 Immunoglobulin gamma-3 kappa chain.
FT NON TER 131
SQ SEQUENCE 131 AA; 14083 MW; 5E8356595466E9E CRC64;

Query Match 70.0%; Score 413; DB 2; Length 131;
Best Local Similarity 79.0%; Pred. No. 4,8e-33;
Matches 83; Conservative 7; Mismatches 11; Indels 4; Gaps 2;

QY 2 IELTOSPAIMASGPKKVTTCRASBSYDYSYGHSMQWFOQKPGTSPKLMYISTSNLASG 61
DB 24 IYLTGSPAIMASGPKKVTTCRASBSYDYSYGHSMQWFOQKPGTSPKLMYISTSNLASG 80

QY 62 VPARFSGSGSGTSTSLTISRMEDADATYYCOQSNEDP-YTFSGG 105
DB 81 VPARFSGSGSGTSTSLTISRMEDADATYYCOQYDSSPSITFGAG 125

RESULT 5
OS8VDD0 MOUSE PRELIMINARY; PRT; 134 AA.
ID OS8VDD0
AC OS8VDD0
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-MOG 212 variable light chain (Fragment).
GN Name=Gm1502; Synonyms=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=BALB/c;
RC Sembl P.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP Cation A.J.; Brownlee G.G.; Staudt L.M.; Gerhard W.;
RT Structural and functional implications of a restricted antibody
RT response to a defined antigenic region on the influenza virus
RT hemagglutinin.
RL EMBL J. 5:1577-1587 (1986).
RL EMBL AL16331; CAC94866.1; -; mRNA.
DR PIR; G27887; G27887.
DR HSSP; F01834; IMIM.
DR SMR; Q8VDD0; 23-134.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR MGI; MGI:2686348; Gm1502.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 134
SQ SEQUENCE 134 AA; 14525 MW; CFP8E2236E2D0CF CRC64;

Query Match 69.7%; Score 411.5; DB 2; Length 134;
Best Local Similarity 73.9%; Pred. No. 7e-33;
Matches 82; Conservative 6; Mismatches 18; Indels 5; Gaps 1;

QY 2 IELTOSPAIMASGPKKVTTCRASBSYDYSYGHSMQWFOQKPGTSPKLMYISTSNLASG 61
DB 24 IYLTGSPAIMASGPKKVTTCRASBSYDYSYGHSMQWFOQKPGTSPKLMYISTSNLASG 78

QY 62 VPARFSGSGSGTSTSLTISRMEDADATYYCOQSNEDP-YTFSGG 112
DB 79 VPARFSGSGSGTSTSLTISRMEDADATYYCOQYDSSPSITFGAG 129

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RESULT 6
OS8EV6 MOUSE PRELIMINARY; PRT; 235 AA.
ID OS8EV6
AC OS8EV6
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Igr-C protein.
GN Name=Igr-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Colon;
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L.; Felting E.A.; Grouse L.H.; Derge U.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusik K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Schetz T.B.;
RA Brownstein M.J.; Ueda T.B.; Toshiyuki S.; Carninci P.; Prange C.;
RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Bonak S.A.; McGowan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Kettelman M.; Madan A.; Rodriguez S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;
RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA Butterfield Y.S.N.; Krzywinski M.I.; Skalska J.; Small D.E.;
RA Scherch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091738; AA91738.1; -; mRNA.
DR SMR; OS8EV6; 23-235.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-8e; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 25719 MW; BEFE4ABDD578252 CRC64;

Query Match 68.7%; Score 405.5; DB 2; Length 235;
Best Local Similarity 73.9%; Pred. No. 5,4e-32;
Matches 82; Conservative 5; Mismatches 19; Indels 5; Gaps 1;

QY 2 IELTOSPAIMASGPKKVTTCRASBSYDYSYGHSMQWFOQKPGTSPKLMYISTSNLASG 61
DB 24 IYLTGSPAIMASGPKKVTTCRASBSYDYSYGHSMQWFOQKPGTSPKLMYISTSNLASG 78

QY 62 VPARFSGSGSGTSTSLTISRMEDADATYYCOQSNEDP-YTFSGG 112
DB 79 VPARFSGSGSGTSTSLTISRMEDADATYYCOQYDSSPSITFGAG 129

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ID KV3H MOUSE STANDARD; PRT; 111 AA.
 AC P01660;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-II region PC 3741/TEPC 111.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE (PC 3741).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.B.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 RL [2]
 RP PROTEIN SEQUENCE (TEPC 111).
 RX MEDLINE=79012520; PubMed=99744;
 RA McKeon D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 CC -1- MISCELLANEOUS: The PC 3741 and TEPC 111 sequences are identical.
 CC -----
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 CC -----
 CC PIR: A83204; KMS37.
 DR HSSP; P01665; 10NZ.
 DR Ensemble; ENSMUSG0000060064; Mus musculus.
 DR InterPro; IPR007110; I9-1-like.
 DR InterPro; IPR003596; I9-V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin domain;
 KM Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 38 Complementarity-determining-1.
 FT REGION 39 53 Framework-2.
 FT REGION 54 60 Complementarity-determining-2.
 FT REGION 61 92 Framework-3.
 FT REGION 93 101 Complementarity-determining-3.
 FT REGION 102 111 Framework-4.
 FT DISULFID 23 92 By similarity.
 FT NON TER 111
 SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
 Query Match 68.0%; Score 401; DB 1; Length 111;
 Best Local Similarity 70.5%; Pred. No. 6.2e-32;
 Matches 74; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 Oy 1 DIETOSPAIMASPEKTTTCRASSEVDYGHSPFMQFOOKPGTSPKLTMTYSTNLS 60
 Db 1 NIVLTQSPASLAVSLQGRATISCRASESDVSGNSFMHWYQOKPQPPKLLTYLASNLS 60
 1 DIVLTQSPASLAVSLQGRATISCRASESDVSGNSFMHWYQOKPQPPKLLTYLASNLS 60
 61 GVPARFSGSGSGTSTLTISRMKADDAATYYCOQSNEDPYTGGG 105
 61 GVPARFSGSGSGRTDFTLTINPVKADVAATYYCOQSNEDPYTGGG 105
 Db 61 GVPARFSGSGSGRTDFTLTINPVKADVAATYYCOQSNEDPYTGGG 105
 RESULT 10
 KV3J MOUSE STANDARD; PRT; 111 AA.
 ID KV3J MOUSE STANDARD; PRT; 111 AA.
 AC P01662;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig kappa chain V-III region ABPC 22/PC 6245.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP PROTEIN SEQUENCE (ABPC 22).
 RX MEDLINE=79012520; PubMed=99744;
 RA McKeon D.J., Bell M., Potter M.;
 RT "Mechanisms of antibody diversity: multiple genes encode structurally
 RT related mouse kappa variable regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 RL [2]
 RP PROTEIN SEQUENCE (PC 9245).
 RX MEDLINE=79073152; PubMed=103003;
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.B.;
 RT "Rearrangement of genetic information may produce immunoglobulin
 RT diversity.";
 RL Nature 276:785-790(1978).
 RL -1- MISCELLANEOUS: The ABPC22 and PC9241 sequences are identical.
 CC -----
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 CC -----
 CC HSSP; P01665; 10NZ.
 DR SMR; P01662; 1-111.
 DR Ensemble; ENSMUSG0000060064; Mus musculus.
 DR InterPro; IPR007110; I9-1-like.
 DR InterPro; IPR003596; I9-V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Direct protein sequencing; Immunoglobulin domain;
 KM Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 38 Complementarity-determining-1.
 FT REGION 39 53 Framework-2.
 FT REGION 54 60 Complementarity-determining-2.
 FT REGION 61 92 Framework-3.
 FT REGION 93 101 Complementarity-determining-3.
 FT REGION 102 111 Framework-4.
 FT DISULFID 23 92 By similarity.
 FT NON TER 111
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;
 Query Match 67.1%; Score 396; DB 1; Length 111;
 Best Local Similarity 70.5%; Pred. No. 1.9e-31;
 Matches 74; Conservative 13; Mismatches 18; Indels 0; Gaps 0;
 Oy 1 DIETOSPAIMASPEKTTTCRASSEVDYGHSPFMQFOOKPGTSPKLTMTYSTNLS 60
 Db 1 NIVLTQSPASLAVSLQGRATISCRASESDVSGNSFMHWYQOKPQPPKLLTYLASNLS 60
 1 DIVLTQSPASLAVSLQGRATISCRASESDVSGNSFMHWYQOKPQPPKLLTYLASNLS 60
 61 GVPARFSGSGSGTSTLTISRMKADDAATYYCOQSNEDPYTGGG 105
 61 GVPARFSGSGSGRTDFTLTINPVKADVAATYYCOQSNEDPYTGGG 105
 Db 61 GVPARFSGSGSGRTDFTLTINPVKADVAATYYCOQSNEDPYTGGG 105
 RESULT 11
 Q9U410 MOUSE PRELIMINARY; PRT; 106 AA.
 ID Q9U410 MOUSE PRELIMINARY; PRT; 106 AA.
 AC Q9U410;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30
 DE Immunoglobulin light chain variable region (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

```

OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12567627;
RA Song X.T., Feng Z.O., Qiu Z.N., Li Y.O., Yu X.C., Xiong Y., Yin C.C.,
  Huang H.L., Guan X.H.;
RA "Cloning and sequence analysis of the light chain variable region
  gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
  japonicum";
RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
  18:257-259(2000).
DR EMBL; AF207620; AAF19434.1; -; Genomic_DNA.
DR HSSP; P01679; 2PBJ.
DR SMR; Q9U410; 4.106.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 67.0%; Score 395.5; DB 2; Length 106;
Best Local Similarity 77.5%; Pred. No. 2,1e-31;
Matches 79; Conservative 6; Mismatches 12; Indels 5; Gaps 1;

QY 4 LTGSPAIMSASPGKRVTTTCRASBSVDSYGHSMQMFQOKRGTSPKMITYSTNLSAGV 63
  |||||::|||:|||||
DB 4 LTGSPAIMSASPGKRVTTTCRASBSVDSYGHSMQMFQOKRGTSPKMITYSTNLSAGV 58
  |||||::|||:|||||

QY 64 ARPSGSGSGTSYSLTISRMEADATYCCOQSNDEPTFGSG 105
  |||||::|||:|||||
DB 59 VRPSGSGSGTSYSLTISRMEADATYCCOQSNDEPTFGSG 100
  |||||::|||:|||||

RESULT 12
KV6F_MOUSE STANDARD; PRT; 107 AA.
ID P04940;
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.;
RA "RNA sequences define an unusually restricted Igg response to 2-
  phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
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CC -----
DR EMBL; K00735; AAA38680.1; -; mRNA.
DR HSSP; P01679; 2PBJ.
DR SMR; P04940; 1.107.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 67.0%; Score 395.5; DB 2; Length 106;
Best Local Similarity 77.5%; Pred. No. 2,1e-31;
Matches 79; Conservative 6; Mismatches 12; Indels 5; Gaps 1;

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FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 105 Framework-4.
FT DISUPID 23 87 By similarity.
FT NON_TER 107
FT SEQUENCE 107 AA; 11561 MW; 6F694284BCFA68B6 CRC64;

Query Match 66.9%; Score 394.5; DB 1; Length 107;
Best Local Similarity 71.2%; Pred. No. 2,6e-31;
Matches 79; Conservative 9; Mismatches 18; Indels 5; Gaps 1;

QY 2 IELTOSPAIMSASPGKRVTTTCRASBSVDSYGHSMQMFQOKRGTSPKMITYSTNLSAG 61
  |||||::|||:|||||
DB 2 IELTOSPAIMSASPGKRVTTTCRASBSVDSYGHSMQMFQOKRGTSPKMITYSTNLSAG 56
  |||||::|||:|||||

QY 62 VPARFSGSGSGTSYSLTISRMEADATYCCOQSNDEPTFGSGDOAGNR 112
  |||||::|||:|||||
DB 57 VPARFSGSGSGTSYSLTISRMEADATYCCOQSNDEPTFGSGDOAGNR 107
  |||||::|||:|||||

RESULT 13
KV6G_MOUSE STANDARD; PRT; 107 AA.
ID P04941;
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.;
RA "RNA sequences define an unusually restricted Igg response to 2-
  phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
CC -----
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CC -----
DR EMBL; K00737; AAA38682.1; -; mRNA.
DR HSSP; Q01W12; 1AY1.
DR SMR; P04941; 1.103.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT DISUPID 23 87 By similarity.
FT NON_TER 107
FT SEQUENCE 107 AA; 11557 MW; 72488DA9EF354934 CRC64;

Query Match 66.9%; Score 394.5; DB 1; Length 107;

```

Best Local Similarity 71.2%; Pred. No. 2.6e-31;
Matches 79; Conservative 9; Mismatches 18; Indels 5; Gaps 1;

QY 2 IELTOSPAIMASGKGVTTTCRASSEVDYSGHSPFMQPGPTSPKMTYSTNLSAG 61
Db 2 ILTQSPAIMASGKGVTTTCRASSEVDYSGHSPFMQPGPTSPKMTYSTNLSAG 56

QY 62 VPAFSGSGSGTSLTISRMEDATYYCCQSNEDPTFGSDQAGNKR 112
Db 57 VPAFSGSGSGTSLTISRMEDATYYCCQSNEDPTFGSDQAGNKR 107

RESULT 14
KV6J_MOUSE STANDARD; PRT; 107 AA.

AC P04974; 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaerlsten M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
RL -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC removed.

CC EMBL; K00744; AAA38689.1; -; mRNA.
DR HSSP; P04944; 1-106.
DR SMR; P04944; 1-106.
DR Ensemble; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11613 MW; A38290781F3C30D3 CRC64;

Query Match 66.9%; Score 394.5; DB 1; Length 107;
Best Local Similarity 71.2%; Pred. No. 2.6e-31;
Matches 79; Conservative 8; Mismatches 19; Indels 5; Gaps 1;

QY 2 IELTOSPAIMASGKGVTTTCRASSEVDYSGHSPFMQPGPTSPKMTYSTNLSAG 61
Db 2 ILTQSPAIMASGKGVTTTCRASSEVDYSGHSPFMQPGPTSPKMTYSTNLSAG 56

QY 62 VPAFSGSGSGTSLTISRMEDATYYCCQSNEDPTFGSDQAGNKR 112
Db 57 VPAFSGSGSGTSLTISRMEDATYYCCQSNEDPTFGSDQAGNKR 107

RESULT 15
KV3I_MOUSE STANDARD; PRT; 131 AA.

AC P01661; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP PROTEIN SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burslein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to the
RT variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled expression
RT of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RL [2]
RP PROTEIN SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP SEQUENCE REVISION.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC PIR; B90412; KWSM6.
DR HSSP; P01665; 10NZ.
DR SMR; P01661; 21-131.
DR Ensemble; ENSMUSG00000060064; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
FT REGION 1 20 Immunoglobulin V region; Signal.
FT CHAIN 21 131 Ig kappa chain V-III region MOPC 63.
FT REGION 21 43 Framework-1.
FT REGION 44 58 Complementarity-determining-1.
FT REGION 59 73 Framework-2.
FT REGION 74 80 Complementarity-determining-2.
FT REGION 81 112 Framework-3.
FT REGION 113 121 Framework-4.
FT REGION 122 131 Complementarity-determining-3.
FT DISULFID 43 112 By similarity.
FT NON TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212BC9F0D8C880A CRC64;

Query Match 66.3%; Score 391; DB 1; Length 131;
Best Local Similarity 69.5%; Pred. No. 7.4e-31;
Matches 73; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 1 IELTOSPAIMASGKGVTTTCRASSEVDYSGHSPFMQPGPTSPKMTYSTNLSAG 60
Db 21 NIVLTQSPALAVSLGQRTTISCRASSEVDYSGHSPFMQPGPTSPKMTYSTNLSAG 80

Qy 61 GVPARFSGSGGTYSYLTISRMBAADATYYCOOSNEDPYTFGSG 105
Db 81 GVPARFSGSGSRIDFTLIDVEADDAATYYCOONNEDPWTFGSG 125

Search completed: November 21, 2005, 12:04:04
Job time : 166.744 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 ; Search time 42.2564 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-86

Perfect score: 590
Sequence: 1 DIELTQSPALMSASGKRVT.....QGSNEDPYTGGSDQAGNKR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	456.5	77.4	106	2	US-09-798-689-8 Sequence 8, Appl
2	456.5	77.4	238	2	US-09-798-689-21 Sequence 21, Appl
3	449.5	76.2	108	2	US-09-171-945-9 Sequence 9, Appl
4	449.5	76.2	108	2	US-09-910-059-9 Sequence 9, Appl
5	449.5	76.2	235	2	US-09-171-945-17 Sequence 17, Appl
6	449.5	76.2	235	2	US-09-910-059-17 Sequence 17, Appl
7	448.5	76.0	256	2	US-09-526-738A-2 Sequence 2, Appl
8	448.5	76.0	256	2	US-09-526-738A-2 Sequence 2, Appl
9	447.5	75.8	129	1	US-08-438-562-2 Sequence 4, Appl
10	447.5	75.8	129	1	US-08-438-562-2 Sequence 4, Appl
11	447.5	75.8	129	1	US-08-438-562-2 Sequence 4, Appl
12	442.5	75.0	108	2	US-09-726-219A-240 Sequence 92, Appl
13	442.5	75.0	108	2	US-09-726-219A-240 Sequence 92, Appl
14	439.5	74.5	105	2	US-08-434-000A-12 Sequence 12, Appl
15	439.5	74.5	105	2	US-09-312-157-12 Sequence 12, Appl
16	439.5	74.3	108	2	US-09-717-888-12 Sequence 12, Appl
17	438.5	74.3	108	2	US-09-726-219A-244 Sequence 244, App
18	438.5	74.3	108	2	US-09-196-522-244 Sequence 244, App
19	438.5	74.3	270	1	US-08-652-507-2 Sequence 2, Appl
20	438.5	74.3	553	1	US-08-661-052-16 Sequence 16, Appl
21	438.5	74.3	553	1	US-09-188-082-16 Sequence 16, Appl
22	438.5	74.3	553	2	US-09-364-088-16 Sequence 16, Appl
23	438.5	74.3	553	2	US-09-102-716-16 Sequence 16, Appl
24	437.5	74.2	110	2	US-09-726-219A-237 Sequence 237, App
25	437.5	74.2	110	2	US-09-196-522-237 Sequence 237, App
26	436.5	74.0	110	2	US-09-726-219A-255 Sequence 255, App
27	436.5	74.0	110	2	US-09-196-522-255 Sequence 255, App

28	436.5	74.0	281	2	US-09-423-439-44 Sequence 44, Appl
29	436.5	74.0	666	2	US-09-423-439-51 Sequence 51, Appl
30	430.5	73.0	107	1	US-08-211-202-3 Sequence 3, Appl
31	430.5	73.0	246	1	US-08-469-486-57 Sequence 57, Appl
32	430.5	73.0	246	1	US-08-469-558-57 Sequence 57, Appl
33	429.5	72.8	106	1	US-07-634-278-1 Sequence 1, Appl
34	429.5	72.8	106	1	US-07-634-278-1 Sequence 1, Appl
35	429.5	72.8	106	1	US-08-477-728-1 Sequence 1, Appl
36	429.5	72.8	106	1	US-08-477-728-1 Sequence 1, Appl
37	429.5	72.8	106	1	US-08-474-040-1 Sequence 1, Appl
38	429.5	72.8	106	1	US-08-474-040-1 Sequence 1, Appl
39	429.5	72.8	106	1	US-08-487-200-1 Sequence 1, Appl
40	429.5	72.8	106	1	US-08-487-200-1 Sequence 1, Appl
41	429.5	72.8	106	1	US-08-488-113B-163 Sequence 163, App
42	429.5	72.8	106	1	US-08-477-484B-163 Sequence 163, App
43	429.5	72.8	106	1	US-08-107-669D-49 Sequence 49, Appl
44	429.5	72.8	106	1	US-08-472-788A-83 Sequence 83, Appl
45	429.5	72.8	106	1	US-08-477-531B-49 Sequence 49, Appl

ALIGNMENTS

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RESULT 1
US-09-798-689-8
; Sequence 8, Application US/09798689
; Patent No. 6811779
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
; FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
; Patent No. 6811779
; CURRENT APPLICATION NUMBER: US/09/798, 689
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/401,163
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 08/967,113
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 08/706,804
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/476,533
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/326,552
; PRIOR FILING DATE: 1994-10-20
; PRIOR APPLICATION NUMBER: 08/196,041
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 8
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
US-09-798-689-8

Query Match      77.4% Score 456.5; DB 2; Length 106;
Best Local Similarity 85.7%; Pred. No. 1;6e-37;
Matches 90; Conservative 3; Mismatches 7; Indels 5; Gaps 1;

QY      1 DIELTQSPALMSASGKRVTTTCRASEVDYIGHSPMWFQOKPCTPLWTSTNLS 60
DB      1 DIELTQSPALMSASGKRVTTTCSASSV-----SYHMFQOKPCTPLWTSTNLS 55
QY      61 GVPARFSGSGSTSYLTISRMEADATYTCQGSNEDPYTFGSG 105
DB      56 GVPARFSGSGSTSYLTISRMEADATYTCQGSNEDPYTFGSG 100

RESULT 2
US-09-798-689-21
; Sequence 21, Application US/09798689
; Patent No. 6811779
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/ GENERAL INFORMATION:
/ APPLICANT: Rockwell, Patricia
/ APPLICANT: Goldstein, Neil I.
/ TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
/ TITLE OF INVENTION: Combined with Radiation and Chemotherapy
/ FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
/ Patent No. 681179
/ CURRENT APPLICATION NUMBER: US/09/798,689
/ CURRENT FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 09/401,163
/ PRIOR FILING DATE: 1999-09-22
/ PRIOR APPLICATION NUMBER: 08/967,113
/ PRIOR FILING DATE: 1997-11-10
/ PRIOR APPLICATION NUMBER: 08/706,804
/ PRIOR FILING DATE: 1996-09-03
/ PRIOR APPLICATION NUMBER: 08/476,533
/ PRIOR FILING DATE: 1995-06-07
/ PRIOR APPLICATION NUMBER: 08/326,552
/ PRIOR FILING DATE: 1994-10-20
/ PRIOR APPLICATION NUMBER: 08/196,041
/ PRIOR FILING DATE: 1994-02-10
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 21
/ LENGTH: 238
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-798-689-21

Query Match 77.4%; Score 456.5; DB 2; Length 238;
Best Local Similarity 85.7%; Pred. No. 4,2e-37;
Matches 90; Conservative 3; Mismatches 7; Indels 5; Gaps 1;

QY 1 DILTOSPAIMASPEKVTTCRASBSVDSYGHSMQFOOKRGTSPLKMTYSTNLAS 60
Db 133 DILTOSPAIMASPEKVTTCRASBSVDSYGHSMQFOOKRGTSPLKMTYSTNLAS 187

QY 61 GVPARFSGSGSGTSTLTISRMEADATYTCQOSNEDPYTFGSG 105
Db 188 GVPARFSGSGSGTSTLTISRMEADATYTCQORSTYPLTFAGTKLELKR 232

RESULT 3
US-09-171-945-9
/ Sequence 9, Application US/09171945
/ Patent No. 6277599
/ GENERAL INFORMATION:
/ APPLICANT: Emery, Stephen
/ APPLICANT: Copley, Clive Graham
/ APPLICANT: Edge, Michael Derek
/ TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
/ TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
/ FILE REFERENCE: Monoclonal Antibody to CEA
/ CURRENT APPLICATION NUMBER: US/09/171,945
/ PRIOR APPLICATION NUMBER: GB9703103.3
/ PRIOR FILING DATE: 1997-02-14
/ PRIOR APPLICATION NUMBER: GB9609405.7
/ PRIOR FILING DATE: 1996-05-04
/ PRIOR APPLICATION NUMBER: PCT/GB97/01165
/ PRIOR FILING DATE: 1997-04-29
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-9

Query Match 76.2%; Score 449.5; DB 2; Length 108;
Best Local Similarity 80.4%; Pred. No. 8e-37;
Matches 90; Conservative 5; Mismatches 12; Indels 5; Gaps 1;
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Matches 90; Conservative 5; Mismatches 12; Indels 5; Gaps 1;

QY 1 DILTOSPAIMASPEKVTTCRASBSVDSYGHSMQFOOKRGTSPLKMTYSTNLAS 60
Db 1 DILTOSPAIMASPEKVTTCRASBSVDSYGHSMQFOOKRGTSPLKMTYSTNLAS 55

QY 61 GVPARFSGSGSGTSTLTISRMEADATYTCQOSNEDPYTFGSGDQAGNKR 112
Db 56 GVPARFSGSGSGTSTLTISRMEADATYTCQORSTYPLTFAGTKLELKR 107

RESULT 4
US-09-910-059-9
/ Sequence 9, Application US/0910059
/ Patent No. 6903203
/ GENERAL INFORMATION:
/ APPLICANT: Copley, Clive G
/ APPLICANT: Edge, Michael Derek
/ APPLICANT: Emery, Stephen Charles
/ TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
/ TITLE OF INVENTION: Their Therapeutic use in an Adept System
/ FILE REFERENCE: 1991-209
/ CURRENT APPLICATION NUMBER: US/09/910,059
/ PRIOR APPLICATION NUMBER: 2001-07-23
/ PRIOR FILING DATE: 1998-10-29
/ PRIOR APPLICATION NUMBER: PCT/GB97/01165
/ PRIOR FILING DATE: 1997-04-29
/ PRIOR APPLICATION NUMBER: GB 9703103.3
/ PRIOR FILING DATE: 1997-02-14
/ PRIOR APPLICATION NUMBER: GB9609405.7
/ PRIOR FILING DATE: 1996-05-04
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: Patentln version 3.1
/ SEQ ID NO 9
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-910-059-9

Query Match 76.2%; Score 449.5; DB 2; Length 108;
Best Local Similarity 80.4%; Pred. No. 8e-37;
Matches 90; Conservative 5; Mismatches 12; Indels 5; Gaps 1;

QY 1 DILTOSPAIMASPEKVTTCRASBSVDSYGHSMQFOOKRGTSPLKMTYSTNLAS 60
Db 1 DILTOSPAIMASPEKVTTCRASBSVDSYGHSMQFOOKRGTSPLKMTYSTNLAS 55

QY 61 GVPARFSGSGSGTSTLTISRMEADATYTCQOSNEDPYTFGSGDQAGNKR 112
Db 56 GVPARFSGSGSGTSTLTISRMEADATYTCQORSTYPLTFAGTKLELKR 107

RESULT 5
US-09-171-945-17
/ Sequence 17, Application US/09171945
/ Patent No. 6277599
/ GENERAL INFORMATION:
/ APPLICANT: Emery, Stephen
/ APPLICANT: Copley, Clive Graham
/ APPLICANT: Edge, Michael Derek
/ TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
/ TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
/ FILE REFERENCE: Monoclonal Antibody to CEA
/ CURRENT APPLICATION NUMBER: US/09/171,945
/ PRIOR APPLICATION NUMBER: GB9703103.3
/ PRIOR FILING DATE: 1998-10-29
/ PRIOR APPLICATION NUMBER: GB9703103.3
/ PRIOR FILING DATE: 1997-02-14
/ PRIOR APPLICATION NUMBER: GB9609405.7
/ PRIOR FILING DATE: 1996-05-04
/ PRIOR APPLICATION NUMBER: PCT/GB97/01165
/ PRIOR FILING DATE: 1997-04-29
/ NUMBER OF SEQ ID NOS: 131
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1 SOFTWARE: Patentin Ver. 2.1
2 SEQ ID NO 17
3 LENGTH: 235
4 TYPE: PR1
5 ORGANISM: Artificial Sequence
6 FEATURE:
7 OTHER INFORMATION: Description of Artificial Sequence: humanized
8 US-09-171-945-17

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Query Match	76.2%;	Score 449.5;	DB 2;	Length 235;
Best Local Similarity	80.4%;	Pred. No. 2e-36;		
Matches 90;	Conservative 5;	Mismatches 12;	Indels 5;	Gaps 1.

Oy

1 DIETQSPAIMSASPGKVTYTTTCRASESDYSYGSMQRQQKPETS PKLMIYSTNLAS 60
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Dd

23 DIELTQSPAIMASPGKVTITCSASSV---TYMNFQOKPETS PKLMIYSTNLAS 77

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Qy      61 GVPARFSSGGSGTSTSLTISRHEADATYYCCQSNEDPYTFGSGDQGNKR 112
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RESULT 6
US-09-910-059-17
; Sequence 17, Application US/09910059

OTHER INFORMATION: chimaeric light chain sequence
US-09-910-059-17

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Qy      61  GVPARFSSGSGTYSYLTISRMEADATYYCQSNEDYTFGSGDDAGNKR 112
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Db      78  GVPARFSSGSGTYSYLTISRMEADATYYCQQRSTYPLTFGAGTKLBIR 129

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RESULT 7
US-09-526-738A-2
; Sequence 2, Application US/09526738A
; Patent No. 6630584
; GENERAL INFORMATION:
; APPLICANT: RMOI UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
; APPLICANT: LTD.

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? TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P3
? FILE REFERENCE: 1196336
? CURRENT APPLICATION NUMBER: US/09/526,738A
? CURRENT FILING DATE: 2000-03-16
? NUMBER OF SEQ ID NOS: 9
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 2
? LENGTH: 256
? TYPE: PRT
? ORGANISM: Humanus
? US-09-526-738A-2
?
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Query Match	76.0%;	Score 448.5;	DB 2;	Length 256;
Best Local Similarity	80.4%;	Pred. No. 2.8e-36;		
Matches 90; Conservative	4;	Mismatches 13;	Indels 5;	Gaps 1;

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QY      61  GVPARFSGSGGCTSYLTISMEAEADATYYCCQSNEDPYVPGSGDGAGNKR 112
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; Sequence 4, Application US/09526738A

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Best Local Similarity	80.4%	Pred. No. 1.8e-36		
Matches 90; Conservative	4	Mismatches 13	Indels 5	Gaps 1

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QY      61  GVPARFSGSGGSTSLTISRKEADADATYYCQQSNEDPYTFGSGDQAGNKR 112
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US-08-116-778E-2
 ; Sequence 2, Application US/08116778E
 ; Patent No. 5830470
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAMURA, KAZUYASU
 ; APPLICANT: KOIKE, MASAMICHI
 ; APPLICANT: SHITARA, KENYA
 ; APPLICANT: HANAII, NOBUO
 ; APPLICANT: KIYAWA, YOSHIOISA
 ; APPLICANT: HASEGAWA, MAOMORU
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHAYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD
 ;

CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778S
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig peptide
LOCATION: -22..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-116-778S-2
Query Match 75.8%; Score 447.5; DB 1; Length 129;
Best Local Similarity 81.1%; Pred. No. 1.5e-36;
Matches 90; Conservative 3; Mismatches 13; Indels 5; Gaps 1;
QY 2 IELTQSPALMSASGGERVTTTCRASBSVDYSGHSFMQFQOKPPTSPRLMISTSNLASG 61
Db 24 IVLTQSPALMSASGGERVTTTCRASBSVDYSGHSFMQFQOKPPTSPRLMISTSNLASG 78
QY 62 VPARFSGSGGTSYSLTISRMEADATYYCQGSNEDPYTFGSGDQGNKR 112
Db 79 VPARFSGSGGTSYSLTISRMEADATYYCQGSNEDPYTFGSGDQGNKR 129
RESULT 10
US-08-438-562-2
Sequence 2, Application US/08438562
Patent No. 5874255
GENERAL INFORMATION:

APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUMANA, YOSHITISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: NIXON & VANDERHYTE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: sig peptide
LOCATION: -22..-1
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE TO TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
FEATURE:
NAME/KEY: domain
LOCATION: 24..33
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 1"
FEATURE:
NAME/KEY: domain
LOCATION: 49..55
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 2"
FEATURE:
NAME/KEY: domain
LOCATION: 88..96
IDENTIFICATION METHOD: BY SIMILARITY
IDENTIFICATION METHOD: WITH KNOWN SEQUENCE OR TO AN ESTABLISHED
IDENTIFICATION METHOD: CONSENSUS
OTHER INFORMATION: /product= "HYPERVARIABLE REGION 3"
US-08-438-562-2
Query Match 75.8%; Score 447.5; DB 1; Length 129;
Best Local Similarity 81.1%; Pred. No. 1.5e-36;
Matches 90; Conservative 3; Mismatches 13; Indels 5; Gaps 1;

PROTEINS IN PLANTS AND THEIR USES

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
Storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/312.157

FILING DATE: 14-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/434,000

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Guise, Jeffrey W.

REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/127

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 552-8400

TELEFAX: (619) 552-0159

TELEX: 67-351

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 105 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

DESCRIPTION: Guy's 13 Kappa

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-312-157-12

Query Match 74.5%; Score 439.5; DB 2; Length 105;

Best Local Similarity 81.9%; Pred. No. 7.4e-36;
Matches 86; Conservative 3; Mismatches 11; Indels 5; Gaps 1;

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|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIVMTQSPAIMSASGEGVTTTCRASGVDSYGHSPOMFOOKPCTSPKMTYSTNLAS 55
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GVPAFFSGSGSTSYSLTISRMEADATYYCCQSNEDPYTFGSG 105
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 56 GVPAFFSGSGSTSYSLTISRMEADATYYCHQRTSYPTTGGG 100
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Search completed: November 21, 2005, 12:07:35
Job time : 43.2564 secs

his rage black (up)

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 / Search time 138.667 Seconds
(without alignments)
337.478 Million cell updates/sec

Title: US-10-632-706-86

Perfect score: 590
Sequence: 1 DIETQSPAINASPGKVT.....QGSNEDPYTGGSDQGNKR 112

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590	100.0	112	4	US-10-632-706-86
2	562	95.3	112	3	US-09-144-886-89
3	510.5	86.5	107	4	US-10-632-706-85
4	494.5	83.8	107	3	US-09-144-886-88
5	460.5	78.1	108	3	US-09-976-787-8
6	460.5	78.1	108	3	US-09-865-198-8
7	460.5	78.1	108	5	US-10-482-630-8
8	460.5	78.1	108	5	US-10-203-398-8
9	460.5	78.1	108	5	US-10-778-910-8
10	460.5	78.1	108	5	US-10-809-387-8
11	460.5	78.1	240	3	US-09-976-787-28
12	460.5	78.1	240	3	US-09-865-198-27
13	460.5	78.1	240	5	US-10-482-630-27
14	460.5	78.1	240	5	US-10-778-910-27
15	460.5	78.1	240	5	US-10-809-387-28
16	460.5	77.4	106	3	US-09-976-787-24
17	460.5	77.4	106	3	US-09-865-198-23
18	460.5	77.4	106	3	US-09-988-689-8
19	460.5	77.4	106	3	US-10-482-630-23
20	460.5	77.4	106	5	US-10-778-910-23
21	460.5	77.4	106	5	US-10-809-387-24
22	460.5	77.4	238	3	US-09-976-787-29
23	460.5	77.4	238	3	US-09-865-198-28
24	460.5	77.4	238	3	US-09-865-198-21
25	460.5	77.4	238	5	US-10-482-630-28
26	460.5	77.4	238	5	US-10-778-910-28
27	460.5	77.4	238	5	US-10-809-387-29

28	449.5	76.2	108	3	US-09-910-049-9	Sequence 9, Appl
29	449.5	76.2	235	3	US-09-910-049-17	Sequence 17, Appl
30	448.5	76.0	256	4	US-10-247-488-2	Sequence 2, Appl
31	448.5	76.0	258	4	US-10-247-488-4	Sequence 4, Appl
32	443.5	75.2	109	3	US-09-144-886-91	Sequence 91, Appl
33	442.5	75.0	108	4	US-10-803-622-240	Sequence 240, App
34	442.5	75.0	108	4	US-10-803-622-240	Sequence 240, App
35	439.5	74.5	105	3	US-09-982-107-12	Sequence 12, Appl
36	439.5	74.5	105	3	US-10-781-989-12	Sequence 12, Appl
37	439.5	74.5	109	4	US-10-312-316-50	Sequence 50, Appl
38	439.5	74.5	109	4	US-10-632-706-88	Sequence 88, Appl
39	438.5	74.3	108	4	US-10-803-622-244	Sequence 244, App
40	438.5	74.3	108	4	US-10-803-622-244	Sequence 244, App
41	438.5	74.3	110	5	US-10-688-255-4	Sequence 4, Appl
42	438.5	74.3	244	5	US-10-609-671-2	Sequence 2, Appl
43	438.5	74.3	669	3	US-09-807-721-2	Sequence 2, Appl
44	437.5	74.2	107	4	US-10-232-187-4	Sequence 4, Appl
45	437.5	74.2	110	4	US-10-803-622-237	Sequence 237, App

ALIGNMENTS

```
RESULT 1
US-10-632-706-86
; Sequence 86, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOBER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-8951200S
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody
US-10-632-706-86
Query Match 100.0%; Score 590; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.3e-44;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIETQSPAINASPGKVTTCRASEVDYGHSEFMQFOOKPSTPLMTYTSNLAS 60
DB 1 DIETQSPAINASPGKVTTCRASEVDYGHSEFMQFOOKPSTPLMTYTSNLAS 60
QY 61 GVPARFSGSGSTSYLTISIRMEADATYYCQGSNEDPYTGGSDQGNKR 112
DB 61 GVPARFSGSGSTSYLTISIRMEADATYYCQGSNEDPYTGGSDQGNKR 112
RESULT 2
US-09-144-886-89
; Sequence 89, Application US/09144886
; Patent No. US2002015114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amersdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
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/ CURRENT FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 98
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 89
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Bont/A clone
/ OTHER INFORMATION: 3C3 region VL epitope 2
US-09-144-886-89

Query Match          95.3%; Score 562; DB 3; Length 112;
Best Local Similarity 95.5%; Pred. No. 9,5e-42;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 60
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Db 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 60

Qy 61 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSNEDPTTFGSGDQAGNK 112
    |||
Db 61 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSSSYPTTFGSGDQAGNK 112

RESULT 3
US-10-632-706-85
/ Sequence 85, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ APPLICANT: AMERSOORFER, PETER
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ TITLE OF INVENTION: NEUROTOXINS
/ FILE REFERENCE: 407T-8951200S
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ CURRENT FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 85
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody
US-10-632-706-85

Query Match          86.5%; Score 510.5; DB 4; Length 107;
Best Local Similarity 91.0%; Pred. No. 3e-37;
Matches 101; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 60
    |||
Db 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 55

Qy 61 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSNEDPTTFGSGDQAGNK 111
    |||
Db 56 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSNEDPTTFGSGDQAGNK 106

RESULT 4
US-09-144-886-88
/ Sequence 88, Application US/09144886
/ Patent No. US20020155114A1
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D
/ APPLICANT: Amersdorfer, Peter
/ TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
/ TITLE OF INVENTION: Botulinum Neurotoxins
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/ FILE REFERENCE: 2500.117USO
/ CURRENT APPLICATION NUMBER: US/09/144,886
/ CURRENT FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 98
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 88
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Bont/A clone
/ OTHER INFORMATION: 2G5 region VL epitope 2
US-09-144-886-88

Query Match          83.8%; Score 494.5; DB 3; Length 107;
Best Local Similarity 87.4%; Pred. No. 7.6e-36;
Matches 97; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 60
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Db 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 55

Qy 61 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSNEDPTTFGSGDQAGNK 111
    |||
Db 56 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSSSYPTTFGSGDQAGNK 106

RESULT 5
US-09-976-787-8
/ Sequence 8, Application US/09976787
/ Patent No. US20020064528A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ APPLICANT: White, Larry
/ TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
/ FILE REFERENCE: 11245/46505
/ CURRENT APPLICATION NUMBER: US/09/976,787
/ CURRENT FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 09/493,539
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/117,726
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 8
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-976-787-8

Query Match          78.1%; Score 460.5; DB 3; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

Qy 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 60
    |||
Db 1 DIELTQSPAIMSASPGKRVTTTCRASISYDSYGHSPFMWFQKPGTSPKLMISTSNLAS 55

Qy 61 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSNEDPTTFGSGDQAGNK 112
    |||
Db 56 GVPARFSGSGSGTSTSLTISRMEAEADATYYCCQSSSYPTTFGSGDQAGNK 107

RESULT 6
US-09-865-198-8
/ Sequence 8, Application US/09865198
/ Patent No. US20020103345A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ APPLICANT: Bispecific Immunoglobulin-like Antigen Binding Proteins and Method
/ TITLE OF INVENTION: Production
/ FILE REFERENCE: 11245/47102
/ CURRENT APPLICATION NUMBER: US/09/865,198
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CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 8
LENGTH: 108
TYPE: PRT
ORGANISM: Mouse
US-09-865-198-8

Query Match 78.1%; Score 460.5; DB 3; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASBGEKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60
DB 1 DIELTOSPAIMASBGEKVTTCRASBSV-----SYMMFOOKPQTSPLKMIYSTSNLAS 55
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNR 112
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSYPFTFGSGTKLEIKR 107

RESULT 7

US-10-482-630-8
Sequence 8, Application US/10482630
Publication No. US20040242851A1
GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors
FILE REFERENCE: 11245/48502
CURRENT APPLICATION NUMBER: US/10/482,630
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: PCT/US02/20332
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/301,299
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 137
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 8
LENGTH: 108
TYPE: PRT
ORGANISM: Mouse
US-10-482-630-8

Query Match 78.1%; Score 460.5; DB 5; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASBGEKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60
DB 1 DIELTOSPAIMASBGEKVTTCRASBSV-----SYMMFOOKPQTSPLKMIYSTSNLAS 55
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNR 112
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSYPFTFGSGTKLEIKR 107

RESULT 8

US-10-203-399B-8
Sequence 8, Application US/10203399B
Publication No. US20040248781A1
GENERAL INFORMATION:

APPLICANT: Kerbel, Robert
TITLE OF INVENTION: Therapeutic Method for Reducing Angiogenesis
FILE REFERENCE: 11245/47002
CURRENT APPLICATION NUMBER: US/10/203,399B
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/178,791
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 09/539,692
PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: PCT/US01/02839
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 108
TYPE: PRT
ORGANISM: Mouse
US-10-203-399B-8

Query Match 78.1%; Score 460.5; DB 5; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASBGEKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60
DB 1 DIELTOSPAIMASBGEKVTTCRASBSV-----SYMMFOOKPQTSPLKMIYSTSNLAS 55
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNR 112
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSYPFTFGSGTKLEIKR 107

RESULT 9

US-10-778-910-8
Sequence 8, Application US/10778910
Publication No. US20040259156A1
GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Method
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/10/778,910
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: US/09/865,198
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 8
LENGTH: 108
TYPE: PRT
ORGANISM: Mouse
US-10-778-910-8

Query Match 78.1%; Score 460.5; DB 5; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASBGEKVTTCRASBSVDYSGHSPMQFOOKPQTSPLKMIYSTSNLAS 60
DB 1 DIELTOSPAIMASBGEKVTTCRASBSV-----SYMMFOOKPQTSPLKMIYSTSNLAS 55
QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNR 112
DB 56 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSSYPFTFGSGTKLEIKR 107

RESULT 10

US-10-809-387-8
Sequence 8, Application US/10809387
Publication No. US20050214860A1
GENERAL INFORMATION:

APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46506
CURRENT APPLICATION NUMBER: US/10/809,387
CURRENT FILING DATE: 2004-03-23
PRIOR APPLICATION NUMBER: 09/976,787
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/493,539

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/ PRIOR FILING DATE: 2000-01-28
/ SOFTWARE: WordPerfect 8.0 for Windows
/ PRIOR APPLICATION NUMBER: 60/117,726
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 8
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-809-387-8

Query Match      78.1%; Score 460.5; DB 5; Length 108;
Best Local Similarity 82.1%; Pred. No. 7.4e-33;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 60
DB 1 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 55
61 GVPARFSGSGSGTSTSLTISRMEADATYYCOOSNEDPPTFGSGDQAGNR 112
GVPARFSGSGSGTSTSLTISRMEADATYYCOORSSYPTFGSGTKLEIKR 107

RESULT 11
US-09-976-787-28
/ Sequence 28, Application US/09976787
/ Patent No. US20020064528A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ APPLICANT: Witte, Larry
/ TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
/ FILE REFERENCE: 11245/46505
/ CURRENT APPLICATION NUMBER: US/09/976,787
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 09/493,539
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/117,726
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 28
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-976-787-28

Query Match      78.1%; Score 460.5; DB 3; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 60
DB 133 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 187
61 GVPARFSGSGSGTSTSLTISRMEADATYYCOOSNEDPPTFGSGDQAGNR 112
GVPARFSGSGSGTSTSLTISRMEADATYYCOORSSYPTFGSGTKLEIKR 239

RESULT 12
US-09-865-198-27
/ Sequence 27, Application US/09865198
/ Patent No. US20020103345A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Bispesific Immunoglobulin-Like Antigen Binding Proteins and Metho
/ FILE REFERENCE: 11245/47102
/ CURRENT APPLICATION NUMBER: US/09/865,198
/ PRIOR FILING DATE: 2001-05-24
/ PRIOR APPLICATION NUMBER: US 60/206,749
/ PRIOR FILING DATE: 2000-05-24
```

```
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 27
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Mouse
US-09-865-198-27

Query Match      78.1%; Score 460.5; DB 3; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 60
DB 133 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 187
61 GVPARFSGSGSGTSTSLTISRMEADATYYCOOSNEDPPTFGSGDQAGNR 112
GVPARFSGSGSGTSTSLTISRMEADATYYCOORSSYPTFGSGTKLEIKR 239

RESULT 13
US-10-482-630-27
/ Sequence 27, Application US/10482630
/ Publication No. US20040242851A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Bispesific Antibodies That Bind to VEGF Receptors
/ FILE REFERENCE: 11245/48502
/ CURRENT APPLICATION NUMBER: US/10/482,630
/ PRIOR FILING DATE: 2003-12-23
/ PRIOR APPLICATION NUMBER: PCT/US02/20332
/ PRIOR FILING DATE: 2002-06-26
/ PRIOR APPLICATION NUMBER: US 60/301,299
/ PRIOR FILING DATE: 2001-06-26
/ NUMBER OF SEQ ID NOS: 137
/ SOFTWARE: WordPerfect 8.0 for Windows
/ SEQ ID NO 27
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Mouse
US-10-482-630-27

Query Match      78.1%; Score 460.5; DB 5; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 60
DB 133 DIELTOSPAINMSAPGKRVTTTCRASBSYDSYGHSMQFQKRGTSPKLMIYSTSNLAS 187
61 GVPARFSGSGSGTSTSLTISRMEADATYYCOOSNEDPPTFGSGDQAGNR 112
GVPARFSGSGSGTSTSLTISRMEADATYYCOORSSYPTFGSGTKLEIKR 239

RESULT 14
US-10-778-910-27
/ Sequence 27, Application US/10778910
/ Publication No. US20040259156A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhu, Zhenping
/ TITLE OF INVENTION: Bispesific Immunoglobulin-Like Antigen Binding Proteins and Methoc
/ FILE REFERENCE: 11245/47102
/ CURRENT APPLICATION NUMBER: US/10/778,910
/ PRIOR FILING DATE: 2004-02-13
/ PRIOR APPLICATION NUMBER: US/09/865,198
/ PRIOR FILING DATE: 2001-05-24
/ PRIOR APPLICATION NUMBER: US 60/206,749
/ PRIOR FILING DATE: 2000-05-24
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: WordPerfect 8.0 for Windows
```


SEQ ID NO 27
LENGTH: 240
TYPE: PRT
ORGANISM: Mouse
US-10-778-910-27

Query Match 78.1%; Score 460.5; DB 5; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETQSPAIMSAPGKVTTCRAESVDSYGHSPQWFOQKPGTSPKLMYSTSNLAS 60
133 DIETQSPAIMSAPGKVTTCRAESSV-----SYMHWFOQKPGTSPKLMYSTSNLAS 187

QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPTFGSGDQAGNR 112
DB 188 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSSSYPTFGSGTKLEIKR 239

RESULT 15

US-10-809-387-28
Sequence 28, Application US/10809387
Publication No. US20050214860A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
APPLICANT: Wille, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46506
CURRENT APPLICATION NUMBER: US/10/809,387
PRIOR FILING DATE: 2004-03-23
PRIOR APPLICATION NUMBER: 09/976,787
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 28
LENGTH: 240
TYPE: PRT
ORGANISM: Mouse
US-10-809-387-28

Query Match 78.1%; Score 460.5; DB 5; Length 240;
Best Local Similarity 82.1%; Pred. No. 1.7e-32;
Matches 92; Conservative 4; Mismatches 11; Indels 5; Gaps 1;

QY 1 DIETQSPAIMSAPGKVTTCRAESVDSYGHSPQWFOQKPGTSPKLMYSTSNLAS 60
DB 133 DIETQSPAIMSAPGKVTTCRAESSV-----SYMHWFOQKPGTSPKLMYSTSNLAS 187

QY 61 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSNEDPTFGSGDQAGNR 112
DB 188 GVPARFSGSGSGTSTSLTISRMEADATYYCCQSSSYPTFGSGTKLEIKR 239

Search completed: November 21, 2005, 12:33:33
Job time : 139.667 secs

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1 CURRENT APPLICATION NUMBER: US/11/174,186
2 CURRENT FILING DATE: 2005-07-01
3 PRIOR APPLICATION NUMBER: US 60/288,564
4 PRIOR FILING DATE: 2001-05-03
5 NUMBER OF SEQ ID NOS: 42
6 SOFTWARE: PatentIn version 3.3
7 SEQ ID NO 1
8 LENGTH: 106
9 TYPE: PRT
10 ORGANISM: Artificial
11 FEATURES:
12 OTHER INFORMATION: KS VK mouse
13 US-11-174-186-1

Query Match 66.9%; Score 394.5; DB 7; Length 106;
Best Local Similarity 76.0%; Pred. No. 3.7e-21;
Matches 79; Conservative 5; Mismatches 15; Indels 5; Gaps 1;
Qy 2 IEILOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 61
Db 2 ILILOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 56
Qy 62 VPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSG 105
Db 57 FPARFSGSGSGTSTSLTISRMEADATYYCHRGSGPYTFGSG 100

RESULT 3

US-11-077-978-1
1 Sequence 1, Application US/11077978
2 Publication No. US2005024433A1
3 GENERAL INFORMATION:
4 APPLICANT: Yasaki, Paul J.
5 APPLICANT: Sherman, Mark A.
6 APPLICANT: Shively, John B.
7 APPLICANT: Raubitschek, Andrew A.
8 APPLICANT: Wu, Anna M.
9 TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
10 FILE REFERENCE: 54435.8012 US01
11 CURRENT APPLICATION NUMBER: US/11/077,978
12 CURRENT FILING DATE: 2005-03-11
13 NUMBER OF SEQ ID NOS: 27
14 SOFTWARE: PatentIn version 3.2
15 SEQ ID NO 1
16 LENGTH: 111
17 TYPE: PRT
18 ORGANISM: Artificial
19 FEATURES:
20 OTHER INFORMATION: Artificially constructed variable light chain of M5A and M5B
21 OTHER INFORMATION: humanized antibodies
22 US-11-077-978-1

Query Match 65.8%; Score 388; DB 7; Length 111;
Best Local Similarity 67.6%; Pred. No. 1e-20;
Matches 71; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
Qy 1 DIELOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 60
Db 1 DIELOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 60
Qy 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSG 105
Db 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSG 105

RESULT 4

US-11-174-186-8
1 Sequence 8, Application US/11174186
2 Publication No. US20050244418A1
3 GENERAL INFORMATION:
4 APPLICANT: Gillies, Stephen
5 APPLICANT: Lo, Kin-Ming
6 APPLICANT: Qian, Xiang

1 TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
2 FILE REFERENCE: LEX-019
3 CURRENT APPLICATION NUMBER: US/11/174,186
4 CURRENT FILING DATE: 2005-07-01
5 PRIOR APPLICATION NUMBER: US 60/288,564
6 PRIOR FILING DATE: 2001-05-03
7 NUMBER OF SEQ ID NOS: 42
8 SOFTWARE: PatentIn version 3.3
9 SEQ ID NO 8
10 LENGTH: 106
11 TYPE: PRT
12 ORGANISM: Artificial
13 FEATURES:
14 OTHER INFORMATION: VK7 light chain
15 US-11-174-186-8

Query Match 65.5%; Score 386.5; DB 7; Length 106;
Best Local Similarity 74.0%; Pred. No. 1.2e-20;
Matches 77; Conservative 6; Mismatches 16; Indels 5; Gaps 1;
Qy 2 IEILOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 61
Db 2 ILILOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 56
Qy 62 VPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSG 105
Db 57 FPARFSGSGSGTSTSLTISRMEADATYYCHRGSGPYTFGSG 100

RESULT 5

US-11-174-186-42
1 Sequence 42, Application US/11174186
2 Publication No. US20050244418A1
3 GENERAL INFORMATION:
4 APPLICANT: Gillies, Stephen
5 APPLICANT: Lo, Kin-Ming
6 APPLICANT: Qian, Xiang
7 TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
8 FILE REFERENCE: LEX-019
9 CURRENT APPLICATION NUMBER: US/11/174,186
10 CURRENT FILING DATE: 2005-07-01
11 PRIOR APPLICATION NUMBER: US 60/288,564
12 PRIOR FILING DATE: 2001-05-03
13 NUMBER OF SEQ ID NOS: 42
14 SOFTWARE: PatentIn version 3.3
15 SEQ ID NO 42
16 LENGTH: 213
17 TYPE: PRT
18 ORGANISM: Artificial
19 FEATURES:
20 OTHER INFORMATION: light chain
21 US-11-174-186-42

Query Match 65.3%; Score 385.5; DB 7; Length 213;
Best Local Similarity 68.8%; Pred. No. 2.3e-20;
Matches 77; Conservative 9; Mismatches 21; Indels 5; Gaps 1;
Qy 1 DIELOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 60
Db 1 DIELOSFAIMSASPGKVTTCRASBSVDSYGHSPFQMPQKPGTSPKLIYSTSNLASG 55
Qy 61 GVPARFSGSGSGTSTSLTISRMEADATYYCOQSNEDPYTFGSGDQAGNKR 112
Db 61 GVPARFSGSGSGTSTSLTISRMEADATYYCHRGSGPYTFGSGTLEIKR 107

RESULT 6

US-11-174-186-9
1 Sequence 9, Application US/11174186
2 Publication No. US20050244418A1
3 GENERAL INFORMATION:
4 APPLICANT: Gillies, Stephen
5 APPLICANT: Lo, Kin-Ming

APPLICANT: Qian, Xing1
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT FILING DATE: 2005-07-01
CURRENT APPLICATION NUMBER: US/11/174.186
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: VK8 light chain
US-11-174-186-9

Query Match 64.7% Score 381.5; DB 7; Length 106;
Best Local Similarity 71.4%; Pred. No. 2.6e-20;
Matches 75; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASASGEKVTTCRASBSVDYGHSMQFOOKPSTPKLMIYSTSNLAS 60
DB 1 EIVLTQSPATLSLSEGERVTLTCSASSV-----SYLMVYQKPGSSSPKRWIPTDSKLAS 55
QY 61 GVPARFSGSGGTSTLTISRMEADATYYCCQSNEDPYTFGSG 105
DB 56 GVPARFSGSGGTSTLTISRMEADATYYCQWSPPFLTGAGTKLELR 100

RESULT 7
US-10-512-184-36
Sequence 36, Application US/10512184
Publication No. US20050244901A1

GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512.184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1.
SEQ ID NO 36
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with
OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match 62.8% Score 370.5; DB 1; Length 248;
Best Local Similarity 67.0%; Pred. No. 2.4e-19;
Matches 75; Conservative 9; Mismatches 23; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASASGEKVTTCRASBSVDYGHSMQFOOKPSTPKLMIYSTSNLAS 60
DB 141 DIVLTQSPATLSLSEGERVTLTCSASSV-----NYIYVQWSGTSPPKRWIPTDSKLAS 195
QY 61 GVPARFSGSGGTSTLTISRMEADATYYCCQSNEDPYTFGSGQDQGNKR 112
DB 196 GVPARFSGSGGTSTLTISRMEADATYYCQWSPPFLTGAGTKLELR 247

RESULT 8
US-10-512-184-50
Sequence 50, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.

TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 615
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fusion protein
OTHER INFORMATION: comprising the leader peptide - chitinase - linker
OTHER INFORMATION: - scFv SS2 - cmvC/H16c.
US-10-512-184-50

Query Match 62.8% Score 370.5; DB 1; Length 615;
Best Local Similarity 67.0%; Pred. No. 4.6e-19;
Matches 75; Conservative 9; Mismatches 23; Indels 5; Gaps 1;

QY 1 DIELTOSPAIMASASGEKVTTCRASBSVDYGHSMQFOOKPSTPKLMIYSTSNLAS 60
DB 482 DIVLTQSPATLSLSEGERVTLTCSASSV-----NYIYVQWSGTSPPKRWIPTDSKLAS 536
QY 61 GVPARFSGSGGTSTLTISRMEADATYYCCQSNEDPYTFGSGDQGNKR 112
DB 537 GVPARFSGSGGTSTLTISRMEADATYYCQWSPPFLTGAGTKLELR 588

RESULT 9
US-11-174-186-15
Sequence 15, Application US/11174186
Publication No. US20050244418A1

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xing1
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174.186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288.564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VK5
US-11-174-186-15

Query Match 62.6% Score 369.5; DB 7; Length 106;
Best Local Similarity 68.3%; Pred. No. 1.6e-19;
Matches 71; Conservative 11; Mismatches 17; Indels 5; Gaps 1;

QY 2 IELTOSPAIMASASGEKVTTCRASBSVDYGHSMQFOOKPSTPKLMIYSTSNLASG 61
DB 2 ILTQSPATLSLSEGERVTLTCSASSV-----SYLMVYQKPGSSSPKRWIPTDSKLASG 56
QY 62 VPARFSGSGGTSTLTISRMEADATYYCCQSNEDPYTFGSG 105
DB 57 PPARFSGSGGTSTLTISRMEADATYYCQWSPPFLTGAGTKLELR 100

RESULT 10
US-11-174-186-16
Sequence 16, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:

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/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 16
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: KS VK mouse
US-11-174-186-16
```

```
Query Match 62.5%; Score 368.5; DB 7; Length 106;
Best Local Similarity 62.3%; Pred. No. 1.8e-19;
Matches 72; Conservative 10; Mismatches 17; Indels 5; Gaps 1;
```

```
QY 2 IELTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLASG 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 ILTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLASG 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VPARFSGSGGTSYSLTISRMEADATYYCOQSNEDPYTFGSG 105
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 57 FPARFSGSGGTSYSLTISRMEADATYYCHORSGYPTTFGSG 100
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 11

```
US-11-077-978-4
/ Sequence 4, Application US/11077978
/ Publication NO. US20050244333A1
/ GENERAL INFORMATION:
/ APPLICANT: Yazaki, Paul J.
/ APPLICANT: Sherman, Mark A.
/ APPLICANT: Shively, John E.
/ APPLICANT: Raubitschek, Andrew A.
/ APPLICANT: Wu, Anna M.
/ TITLE OF INVENTION: A Humanized Anti-CRA T84.66 Antibody and Uses Thereof
/ FILE REFERENCE: 54435, 8012, US01
/ CURRENT APPLICATION NUMBER: US/11/077, 978
/ CURRENT FILING DATE: 2005-03-11
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: IMCBA
/ DATABASE ENTRY DATE: 2002-09-09
/ RELEVANT RESIDUES: (1)..(111)
US-11-077-978-4
```

```
Query Match 60.8%; Score 359; DB 7; Length 111;
Best Local Similarity 61.9%; Pred. No. 7.8e-19;
Matches 65; Conservative 15; Mismatches 25; Indels 0; Gaps 0;
```

```
QY 1 DIELTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLAS 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 DILTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLAS 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 GVPARFSGSGGTSYSLTISRMEADATYYCOQSNEDPYTFGSG 105
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 GIPARFSGSGGTSYSLTISRMEADATYYCOQSNEDPYTFGSG 105
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 12
US-11-174-186-10

```
/ Sequence 10, Application US/11174186
/ Publication NO. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 10
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: KS VK veneered
US-11-174-186-10
```

```
Query Match 60.8%; Score 358.5; DB 7; Length 106;
Best Local Similarity 66.3%; Pred. No. 8.1e-19;
Matches 69; Conservative 11; Mismatches 19; Indels 5; Gaps 1;
```

```
QY 2 IELTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLASG 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 ILTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLASG 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VPARFSGSGGTSYSLTISRMEADATYYCOQSNEDPYTFGSG 105
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 57 FPARFSGSGGTSYSLTISRMEADATYYCHORSGYPTTFGSG 100
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 13

```
US-11-174-186-14
/ Sequence 14, Application US/11174186
/ Publication NO. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xiang
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 14
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: KS de-immunized VK4
US-11-174-186-14
```

```
Query Match 60.8%; Score 358.5; DB 7; Length 106;
Best Local Similarity 66.3%; Pred. No. 8.1e-19;
Matches 69; Conservative 11; Mismatches 19; Indels 5; Gaps 1;
```

```
QY 2 IELTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLASG 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 ILTQSPALMSAPGKRYTTTCRASSVDSYGHSPFQWQPKRGTSPKLMIYSTSLASG 56
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 VPARFSGSGGTSYSLTISRMEADATYYCOQSNEDPYTFGSG 105
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 57 FPARFSGSGGTSYSLTISRMEADATYYCHORSGYPTTFGSG 100
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 14

Search completed: November 21, 2005, 12:33:50
Job time : 3.15128 secs

US-11-174-186-12
; Sequence 12, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xing
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VK2
US-11-174-186-12

Query Match 60.4%; Score 356.5; DB 7; Length 106;
Best Local Similarity 65.4%; Pred. No. 1,le-18;
Matches 68; Conservative 12; Mismatches 19; Indels 5; Gaps 1;

QY 2 IELTQSPALMSASPEKXTTTCRASEVDSYGHSPQWFOOKRGTSFKLMTYSTSNLASG 61
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 2 IVLTPSPALMSASPEKXTTTCRASEVDSYGHSPQWFOOKRGTSFKLMTYSTSNLASG 56
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 62 VPARFSGSGSGTSTLTISRMEDADATYCCQSNEDPYTFGSG 105
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 57 FPARFSGSGSGTSTLTISRMEDADATYCCQSNEDPYTFGSG 100
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 15
US-11-174-186-13
; Sequence 13, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xing
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS-deimmunized VK3
US-11-174-186-13

Query Match 60.3%; Score 355.5; DB 7; Length 106;
Best Local Similarity 65.4%; Pred. No. 1,3e-18;
Matches 68; Conservative 12; Mismatches 19; Indels 5; Gaps 1;

QY 2 IELTQSPALMSASPEKXTTTCRASEVDSYGHSPQWFOOKRGTSFKLMTYSTSNLASG 61
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 2 IVLTPSPALMSASPEKXTTTCRASEVDSYGHSPQWFOOKRGTSFKLMTYSTSNLASG 56
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
QY 62 VPARFSGSGSGTSTLTISRMEDADATYCCQSNEDPYTFGSG 105
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 57 FPARFSGSGSGTSTLTISRMEDADATYCCQSNEDPYTFGSG 100
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 143.255 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-87

Perfect score: 553
Sequence: 1 DTBLTQSPAIMSASPERKVT.....QWSSNPLTFGSGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003s: *
7: geneseqp2004s: *
8: geneseqp2005s: *
9: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	100.0	107	8	ADR38685
2	518	93.7	109	8	ADR38686
3	516	93.3	107	8	ADR38673
4	516	93.3	129	5	ABR75616
5	515	93.1	107	9	ADW86126
6	515	93.1	210	8	ADU86565
7	515	93.1	210	8	ADU86571
8	510	92.2	108	8	ADU74993
9	506	91.5	107	8	ADR38670
10	506	91.5	244	2	AAR79867
11	505	91.3	242	2	AAR79871
12	502	90.8	106	5	ABG32682
13	502	90.8	106	5	AAE27810
14	502	90.8	128	2	AAR27050
15	501	90.6	106	4	AAE69673
16	501	90.6	106	4	ADU47720
17	501	90.6	128	8	AAE69655
18	501	90.6	128	8	ADU47747
19	499	90.2	242	2	AAR79870
20	499	90.2	242	2	AAR79872
21	498.5	90.1	108	8	ADW86127
22	498.5	90.1	214	8	ADU86519
23	497	89.9	106	8	ADU6879
24	496	89.7	246	2	AAR79869

25	491.5	88.9	117	3	AAV93891
26	489	88.4	108	2	AAR21293
27	489	88.4	259	9	AAE29819
28	488	88.2	110	6	AAE33326
29	488	88.2	110	9	ADZ21524
30	488	88.2	110	9	ADZ21532
31	488	88.2	128	2	AAR12327
32	488	88.2	244	2	AAR79868
33	488	88.2	244	2	AAR79873
34	488	88.2	260	9	ADZ21541
35	488	88.2	281	6	AAE33333
36	488	88.2	281	9	ADZ21537
37	486	87.9	110	9	ADZ21534
38	486	87.9	128	4	AAE65521
39	486	87.9	260	9	ADZ21542
40	486	87.9	304	9	ADX69520
41	485	87.7	107	4	ADW80852
42	485	87.7	108	2	AAR21301
43	484	87.5	246	9	ADW64805
44	484	87.5	246	9	ADW64803
45	484	87.5	252	8	ADH77287

ALIGNMENTS

RESULT 1
ADR38685
ID ADR38685 standard; peptide; 107 AA.

AC ADR38685;

DT 02-DEC-2004 (first entry)

DE Mouse light chain variable region scFv seqid 87.

KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;

KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;

KW light chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PP 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PP 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marks JD, Ameresdorfer P;

XX WPI; 2004-652009/63.

PS New isolated antibody that neutralizes botulinum neurotoxin type A,

PT useful for diagnosing botulism or for treating pathologies associated

PT with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 87; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds

to an epitope specifically bound by an antibody expressed by a specific

clone where (I) binds to and neutralizes botulinum neurotoxin type A

(BoNT/A). An isolated antibody (I) that specifically binds to an epitope

specifically bound by an antibody expressed by a clone chosen from clone

S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, A1, Ar2, WRI (V), WRI (T), 3-1,

3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum

neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)

comprising BoNT/A neutralising epitope having an epitope that is

specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin
 CC scFv.
 CC
 CC Sequence 107 AA;
 SQ
 Query Match 100.0%; Score 553; DB 8; Length 107;
 Best Local Similarity 100.0%; Pred. No. 2.1e-34;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 QY 1 DTSLTQSPALMSAPGPKVTTTCGASSSVSYMYVQOKPGSSPRLTYDTSNLSAGVPVR 60
 DB 1 DTSLTQSPALMSAPGPKVTTTCGASSSVSYMYVQOKPGSSPRLTYDTSNLSAGVPVR 60
 QY 61 FSGSGSGTSTSLTISRMEADDAATYYCOQMSNPLTFGSGTKLEIKR 107
 DB 61 FSGSGSGTSTSLTISRMEADDAATYYCOQMSNPLTFGSGTKLEIKR 107
 Db
 RESULT 2
 ADR38686
 ID ADR38686 standard; peptide; 109 AA.
 AC ADR38686;
 DT 02-DEC-2004 (first entry)
 DE Mouse light chain variable region scFv seqid 88.
 XX
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KM light chain variable region; single chain antibody; scFv.
 OS
 XX Mus sp.
 XX
 XX US2004175385-A1.
 XX
 XX 09-SEP-2004.
 XX
 XX 01-AUG-2003; 2003US-00632706.
 XX
 XX 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX PA
 XX Marks JD, Amerdorfer P;
 PI
 DR WPI; 2004-652009/63.
 XX
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX
 XX Example 1; SEQ ID NO 88, 110pp; English.
 XX
 XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific

clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, G39, IC6, JD12, B4, IF3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin
 CC scFv.
 CC
 CC Sequence 109 AA;
 SQ
 Query Match 93.7%; Score 518; DB 8; Length 109;
 Best Local Similarity 94.5%; Pred. No. 9.3e-32;
 Matches 103; Conservative 1; Mismatches 3; Indels 2; Gaps 1;
 CC
 QY 1 DTSLTQSPALMSAPGPKVTTTCGASSSV--SYMYVQOKPGSSPRLTYDTSNLSAGVP 58
 DB 1 DTSLTQSPALMSAPGPKVTTTCGASSSVSYMYVQOKPGSSPRLTYDTSNLSAGVP 60
 QY 59 VRFSGSGSGTSTSLTISRMEADDAATYYCOQMSNPLTFGSGTKLEIKR 107
 DB 61 VRFSGSGSGTSTSLTISRMEADDAATYYCOQMSNPLTFGSGTKLEIKR 109
 Db
 RESULT 3
 ADR38673
 ID ADR38673 standard; peptide; 107 AA.
 AC ADR38673;
 DT 02-DEC-2004 (first entry)
 DE Mouse light chain variable region scFv seqid 75.
 XX
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KM light chain variable region; single chain antibody; scFv.
 OS
 XX Mus sp.
 XX
 XX US2004175385-A1.
 XX
 XX 09-SEP-2004.
 XX
 XX 01-AUG-2003; 2003US-00632706.
 XX
 XX 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX PA
 XX Marks JD, Amerdorfer P;
 PI
 DR WPI; 2004-652009/63.
 XX
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,

PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

PS Example 1, SEQ ID NO 75, 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C35, 1C6, 3D12, B4, 1F3, huc25, At1, At2, WR1(Y), WR1(T), 3-1,
 CC 3-8, 3-10 and IMN1, where (I) binds to and neutralises botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC , producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin
 CC scFv.

SQ Sequence 107 AA;

Query Match 93.3%; Score 516; DB 8; Length 107;
 Best Local Similarity 94.4%; Pred. No. 1.3e-31;
 Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DTELTPAINMSASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLMSGVPR 60

DB 1 DTELTPAINMSASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLMSGVPR 60

QY 61 FSGSGSTSYSLTISRMEADAAATYYCOQWSNPPLTFSSGRTLEIKR 107

DB 61 FSGSGSTSYSLTISRMEADAAATYYCOQWSNPPLTFSSGRTLEIKR 107

RESULT 4

ID ABB75616 standard; protein; 129 AA.

AC ABB75616;

DT 10-JUN-2002 (first entry)

DE Anti-RANK ligand mAb 19H22 light chain variable region.

XX RANK ligand; RANK-L; monoclonal antibody; mAb; 19H22; antibody;
 XX complementarity determining region; CDR; rheumatoid arthritis;
 XX osteoporosis; bone cancer; metastasis; osteoarthritis;
 XX psoriasis; inflammatory bowel disease; multiple sclerosis; diabetes;
 XX cyclostatic; antiarthritic; antiinflammatory; osteopathic; antidiabetic;
 XX antirheumatic; immunosuppressive; antipsoriatic; neuroprotective;
 XX light chain; VL; mouse.

XX Mus musculus.

XX Key Location/Qualifiers

FT 24..33 /label= CDR1

FT /note= "complementarity determining region 1"

FT 49..55 /label= CDR2

FT /note= "complementarity determining region 2"

FT 88..96 /label= CDR3

FT /note= "complementarity determining region 3"

XX WO200215846-A2.

XX 28-FEB-2002.

XX 21-AUG-2001; 2001WO-US026161.

XX 21-AUG-2000; 2000US-0226524P.

XX 07-SEP-2000; 2000US-0220639P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Sweet RW, Tornetta MA, Truneh A, Wattam TA;

XX WPI; 2002-242022/29.

XX N-PSDB; ABL53530.

XX A mouse monoclonal antibody 19H22 for treating or preventing osteopenic
 XX disease including rheumatoid arthritis and osteoporosis.

XX Claim 6; Page 7; 45pp; English.

XX The present sequence is that of the light chain variable region of
 CC claimed anti-human RANK ligand (RANK-L) murine monoclonal antibody (mAb)
 CC 19H22 (isotype IgG2b/kappa). The mAb is produced by hybridoma cells
 CC obtained by immunising C57BL/6 mice with human RANK-L protein, and fusing
 CC spleen cells with X63-Ag8.653 myeloma cells. 19H22 mAb is specific for
 CC human RANK-L, having a binding affinity characterised by a dissociation
 CC constant of about 10 power -10 M. RANK-L is a member of the tumour
 CC necrosis factor family of proteins and a key regulator of the immune
 CC system, bone development and homeostasis. The invention provides altered,
 CC fragment, antibodies comprising the light and heavy chain variable
 CC regions of 19H22, and antibodies comprising the complementarity
 CC determining regions of 19H22. These are used in methods for the
 CC diagnosis, treatment and prevention of osteopenic diseases, including
 CC rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer,
 CC wear debris induced osteolysis or osteoarthritis, and immune diseases
 CC including psoriasis, insulin dependent diabetes, inflammatory bowel
 CC disease or multiple sclerosis. Methods are also provided for the
 CC recombinant production of the antibodies, using isolated nucleic acids
 CC and transfected host (preferably mammalian) host cells, and a method of
 CC diagnosing conditions associated with Th1 T-cell activity or osteoclast
 CC development and activation, in particular those listed above

SQ Sequence 129 AA;

Query Match 93.3%; Score 516; DB 5; Length 129;
 Best Local Similarity 96.2%; Pred. No. 1.6e-31;
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTQSPAINMSASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLMSGVPR 63

DB 4 LTQSPAINMSASGKGVTTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLMSGVPR 63

QY 64 GSGGTSYSLTISRMEADAAATYYCOQWSNPPLTFSSGRTLEIKR 107

DB 64 GSGGTSYSLTISRMEADAAATYYCOQWSNPPLTFSSGRTLEIKR 107

RESULT 5

ID ADM86126 standard; protein; 107 AA.

AC ADM86126;

DT 21-APR-2005 (first entry)

```
DE Novel cytotoxic conjugate-related mouse aY1 protein region SeqID#46.
XX cytotoxin; immunconjugate; cytostatic; immunosuppressive; virucide;
XX apoptosis stimulation; cancer; ovary tumor; uterine cervix tumor;
XX endometrial carcinoma; breast tumor; pancreas tumor; Cag glycotope;
KM autoimmune disease; graft rejection; viral infection; D86;
KM antibody engineering; aY1.
XX
XX Mus musculus.
OS
XX MOZ005009369-A2.
PN
XX 03-FEB-2005.
PD
XX
XX 21-JUL-2004; 2004MO-US023340.
PP
XX
XX 21-JUL-2003; 2003US-0488447P.
PR
XX
XX (IMMU-) IMMUNOGEN INC.
PA
XX
XX Payne G, Chun P, Tavares DJ;
PI
XX
XX WPI, 2005-142544/15.
DR
XX
XX Cytotoxic conjugate useful for treating cancer, autoimmune diseases,
PT graft rejections or viral infections, comprises cell binding agent and
PT cytotoxic agent.
PS
XX
XX Example 12; SEQ ID NO 46; 179pp; English.
XX
XX This invention relates to a novel cytotoxic conjugate which comprises a
CC cell binding agent and a cytotoxic agent, where the cell binding agent
CC binds to Cag glycotope. Preferably, the cell binding agent is the murine
CC anti-Cag monoclonal antibody D86 or their epitope-binding fragments or a
CC humanized version of the same. The cytotoxic agent is chosen from
CC maytansinoid compounds, taxoid compounds, CC-1065 compounds, dolastatin
CC compounds, daunorubicin compounds or doxorubicin compounds. The invention
CC may be useful for the production of compounds with a cytostatic,
CC immunosuppressive or virucide activity acting as stimulators of
CC apoptosis. The invention is useful for inhibiting growth of a cell
CC expressing Cag glycotope and may be used for treating a subject having a
CC cancer (for example serous ovarian carcinoma, endometriod ovarian
CC carcinoma, neoplasm of the uterine cervix, neoplasm of the endometrium,
CC neoplasm of the vulva, breast carcinoma, pancreatic tumor or tumor of the
CC uterellum), in which Cag glycotope is expressed or overexpressed. In
CC addition, the invention may be useful for treating autoimmune diseases,
CC graft rejections or viral infections. The present sequence is that of a
CC region of the mouse aY1 protein which was used to demonstrate homology
CC with a region of the mouse D86 antibody light chain protein during the
CC exemplification of the invention.
XX
XX
SQ Sequence 107 AA;
XX
XX Query Match 93.1%; Score 515; DB 9; Length 107;
XX Best Local Similarity 91.6%; Pred.No.1,5e-31;
XX Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0
QY 1 DTETLQSPALMSASGKGYTTCSASSSYMYWYOQKGSSPRLIITYDSTNLASGVPR 60
Db 1 DIQMGTSPALMSASGKGYTTCSSASSSYMYWYOQKGSSPRLIITYDSTNLASGVPR 60
QY 61 FSGSGSSTYSYLTIISRMEDAAATYYCQOWSNPLTFSGGTKLELR 107
Db 61 FSGSGSSTYSYLTIISRMEDAAATYYCQOWSNPLTFPGAGTKLELR 107
RESULT 6
ADU86565
ID ADU86565 standard; protein; 210 AA.
JC
XX ADU86565;
XX
PT 10-FEB-2005 (first entry)
```

XX	Immunoglobulin variable domain protein seqid 54.
DE	
XX	antiinflammatory; antibacterial; virucide; cytostatic; antipsoriatic;
XX	antidiabetic; vasotropic; vaccine; protein purification; protein folding;
KW	diagnosis; inflammation; immune disorder; allergic hypersensitivity;
KW	infection; autoimmune disease; asthma; psoriasis;
KW	insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
KW	systemic lupus erythematosus; myasthenia gravis; hematological disease;
KW	neoplasm; immunoglobulin; variable region.
XX	
OS	Homo sapiens.
XX	
XX	WO2004101790-A1.
PN	
PD	
XX	25-NOV-2004.
XX	
PF	14-MAY-2004; 2004WO-GB002102.
XX	
PR	14-MAY-2003; 2003US-0470340P.
PR	17-MAR-2004; 2004US-0554021P.
XX	
XX	(DOMA-) DOMANTIS LTD.
PA	
XX	
PI	Jaspers LG, Jones PC, Famm KHU, Wincer GP;
DR	WPI, 2004-821888/81.
PT	
PT	Recovering a polypeptide that unfolds reversibly from a repertoire of
PT	polypeptides for treating e.g., cancer, by unfolding a portion of the
PT	displayed polypeptides and refolding a portion of the unfolded
PT	polypeptides.
XX	
PS	Disclosure; SEQ ID NO 54; 222pp; English.
XX	
XX	The invention describes a method of recovering a polypeptide that unfolds
CC	reversibly from a repertoire of polypeptides that unfolds reversibly and
CC	has a common selectable characteristic that distinguishes folded
CC	polypeptides from unfolded or misfolded polypeptides. The method
CC	comprises: providing a polypeptide display system comprising the
CC	repertoire of displayed polypeptides; unfolding at least a portion of the
CC	displayed polypeptides; refolding at least a portion of the unfolded
CC	polypeptides; and recovering at least one polypeptide that unfolds
CC	reversibly and has the selectable characteristic from the refolded
CC	portion. The method is useful in recovering a polypeptide that unfolds
CC	reversibly from a repertoire of polypeptides that unfolds reversibly. The
CC	library or repertoire is useful for selecting a polypeptide comprising an
CC	antibody variable domain that unfolds reversibly or a polypeptide that
CC	refolds reversibly and comprising an antibody format. The polypeptide is
CC	useful in the manufacture of a medicament for diagnosing, creating or
CC	preventing a disease or medical condition mediated by a cytokine,
CC	cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
CC	as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
CC	viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
CC	I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
CC	erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
CC	tumor. This is the amino acid sequence of an immunoglobulin variable
CC	region associated with the protein purification method of the invention.
XX	
XX	Sequence 210 AA:
QY	
Query Match	93.1%; Score 515; DB 8; Length 210;
Best Local Similarity	91.6%; Pred. No. 2.9e-31;
Matches	98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
DB	
1	DTBLTQSPALMSASRGRKVTTCASSSVSYMYVYQOKPPSSPRLTYDTSNLASGYPVR 60
1	:::.....
1	DIQMTQSPALMSASPGKRVTTTCASSSVSYMYVYQOKPPSSPRLTYDTSNLASGYPVR 60
1	DIQMTQSPALMSASPGKRVTTTCASSSVSYMYVYQOKPPSSPRLTYDTSNLASGYPVR 60
61	PSGSGSGTSYSLTISRMEADPAATYYCCQMSNPFLTSGSGTKLELR 107
61	PSGSGSGTSYSLTISRMEADPAATYYCCQMSNPFLTSGSGTKLELR 107
61	PSGSGSGTSYSLTISRMEADPAATYYCCQMSNPFLTSGSGTKLELR 107
61	PSGSGSGTSYSLTISRMEADPAATYYCCQMSNPFLTSGSGTKLELR 107

RESULT 7
ADU86571
ID ADU86571 standard; protein: 210 AA.
AC ADU86571;
XX 10-FEB-2005 (first entry)
XX
DE Immunoglobulin variable domain protein seqid 60.
XX
KW antinflammatory; antibacterial; virucide; cytostatic; antipsoriatic;
KW antidiabetic; vasotropic; vaccine; protein purification; protein folding;
KW diagnosis; inflammation; immune disorder; allergic hypersensitivity;
KW infection; autoimmune disease; asthma; psoriasis;
KW insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
KW systemic lupus erythematosus; myasthenia gravis; hematological disease;
KW neoplasm; immunoglobulin; variable region.
XX
XX Homo sapiens.
XX OS
XX MO2004101790-A1.
XX PN
XX 25-NOV-2004.
XX PD
XX 14-MAY-2004; 2004WO-GB002102.
XX PF
XX 14-MAY-2003; 2003US-0470340P.
XX PR 17-MAR-2004; 2004US-0554021P.
XX PT
XX (DOMA-) DOMANTIS LTD.
XX PA
XX Jeppers LS, Jones PC, Famm KHJ, Winter GP;
XX WPI; 2004-821886/81.
XX DR
XX Recovering a polypeptide that unfolds reversibly from a repertoire of
XX PT polypeptides for treating e.g., cancer, by unfolding a portion of the
XX PT displayed polypeptides and refolding a portion of the unfolded
XX PT polypeptides.
XX
XX Disclosure; SEQ ID NO 60; 222pp; English.
XX PS
XX The invention describes a method of recovering a polypeptide that unfolds
XX CC reversibly from a repertoire of polypeptides that unfolds reversibly and
XX CC has a common selectable characteristic that distinguishes folded
XX CC polypeptides from unfolded or misfolded polypeptides. The method
XX CC comprises: providing a polypeptide display system comprising the
XX CC repertoire of displayed polypeptides; unfolding at least a portion of the
XX CC displayed polypeptides; refolding at least one polypeptide that unfolds
XX CC reversibly and has the selectable characteristic from the refolded
XX CC portion. The method is useful in recovering a polypeptide that unfolds
XX CC reversibly from a repertoire of polypeptides that unfolds reversibly. The
XX CC library or repertoire is useful for selecting a polypeptide comprising an
XX CC antibody variable domain that unfolds reversibly or a polypeptide that
XX CC refolds reversibly and comprising an antibody format. The polypeptide is
XX CC useful in the manufacture of a medicament for diagnosing, treating or
XX CC preventing a disease or medical condition mediated by a cytokine,
XX CC cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
XX CC as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
XX CC viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
XX CC I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
XX CC erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
XX CC tumor. This is the amino acid sequence of an immunoglobulin variable
XX CC region associated with the protein purification method of the invention.
XX
XX Sequence 210 AA;
SQ

Query Match 93.1%; Score 515; DB 8; Length 210;
Best Local Similarity 91.6%; Pred. No. 2, 9e-31;
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 DTELSTSPAIMSASPGKVTTCSSASSVSYMYWYOOKPGSSPRLLYDTSNLASGVPR 60
DB 1 DIQMTSPAIMSASPGKVTMTCSASSVSYMYWYOOKPGSSPRLLYDTSNLASGVPR 60
QY 61 FSGSGSGTSTSLTISRMEADAAATYYCQWSSNPLTFGSGTKLELR 107
DB 61 FSGSGSGTSTSLTISRMEADAAATYYCQWSTYPLTFGAQTKLELR 107
RESULT 8
ADT74993
ID ADT74993 standard; protein: 108 AA.
XX
XX ADT74993;
AC
XX 13-JAN-2005 (first entry)
DT
XX
DE Light chain murine anti-hL-SIGN scFv antibody protein A2LC Seq 39.
XX
XX autoimmune disease; antibody; antigen presenting cell; APC;
KW diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hL-SIGN.
XX
XX Mus sp.
XX OS
XX MO2004091543-A2.
XX PN
XX 28-OCT-2004.
XX PD
XX 04-MAR-2004; 2004WO-US006570.
XX PF
XX 04-MAR-2003; 2003US-0451816P.
XX PR 15-DEC-2003; 2003US-0529500P.
XX PR 28-FEB-2004; 2004US-0548385P.
XX PT
XX (ALEX-) ALEXION PHARM INC.
XX PA
XX Bowditch KS, Kretz-Rommel A, Dakapagari N;
XX WPI; 2004-758274/74.
XX DR
XX
XX Treating an autoimmune disease comprises providing an
XX PT antibody/autoantigen construct containing an autoantigen linked to an
XX PT antibody to a receptor of an antigen presenting cell and administering
XX PT the construct to a subject.
XX
XX Example 9; Fig 8; 71pp; English.
XX PS
XX This invention relates to the novel treatment of an autoimmune disease
XX CC that utilizes an antibody/autoantigen construct. Specifically, it refers
XX CC to a peptide autoantigen that is linked to an antibody raised against an
XX CC antigen presenting cell (APC) receptor. The present invention describes a
XX CC method for treating diabetes mellitus by inducing an immune tolerance to
XX CC an autoantigen, which can be chosen from glutamic acid decarboxylase
XX CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
XX CC from each thereof or beta cell antigens that are linked to an APC
XX CC receptor antibody. In particular, the antibody recognises a receptor
XX CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
XX CC others, which is expressed on the surface of the APC. The antibody/
XX CC autoantigen construct then works to interfere with the interaction
XX CC between the APC and immune cells such as autoreactive T cells, and hence
XX CC inhibits T-cell proliferation. Accordingly, such compositions exhibit
XX CC antidiabetic and immunosuppressive activities and can be used in the
XX CC development of vaccines. Note that the single chain antibodies (scFvs)
XX CC used in this specification contain both variable light and heavy chain
XX CC regions connected by a linker, their short length makes these antibody
XX CC fragments particularly suitable for antigen linkage, and the capacity for
XX CC binding to the receptor is preserved. This polypeptide sequence is a
XX CC light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the
XX CC invention.
XX
XX Sequence 108 AA;
SQ

Query Match 92.2%; Score 510; DB 8; Length 108;
 Best Local Similarity 95.2%; Pred. No. 3.7e-31;
 Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKRVTTTCSASSSVSYMYOQKPGSSPRLLIYDTSNLASGVPRFSG 63
 DB 4 LTGSPAIMSASPGKRVTTTCSASSSVSYMYOQKPGSSPRLLIYDTSNLASGVPRFSG 63
 QY 64 SGGSGGTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107
 DB 64 SGGSGGTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107

RESULT 9
 ADR38670
 ID ADR38670 standard; peptide: 107 AA.
 AC ADR38670;
 XX 02-DEC-2004 (first entry)
 DT Mouse light chain variable region scFv seqid 72.
 DE
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KM light chain variable region; single chain antibody; scFv.
 OS Mus sp.
 XX US2004175385-A1.
 PN 09-SEP-2004.
 PD 01-AUG-2003; 2003US-00632706.
 PF 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX (REGC) UNIV CALIFORNTA.
 PA Marks JD, Amersdorfer P;
 PI WPI; 2004-652009/63.
 DR
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 PS Example 1; SEQ ID NO 72; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, IC6, 3D12, B4, 1F3, huc25, A1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin

CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin
 CC scFv.
 CC
 SQ Sequence 107 AA;
 QY 91.5%; Score 506; DB 8; Length 107;
 Best Local Similarity 91.6%; Pred. No. 7.4e-31;
 Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 DTELQSPAIMSASPGKRVTTTCSASSSVSYMYOQKPGSSPRLLIYDTSNLASGVPR 60
 DB 1 DTELQSPAIMSASPGKRVTTTCSASSSVSYMYOQKPGSSPRLLIYDTSNLASGVPR 60
 QY 61 FSGSGGTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107
 DB 61 FSGSGGTSYSLTISRMEADATYYCCQWMSNPLTFGSGTKLELR 107

RESULT 10
 AAR79867
 ID AAR79867 standard; protein: 244 AA.
 AC AAR79867;
 XX 02-JUL-1996 (first entry)
 DT Anti-BGFR single chain antibody (Clone 10 D 2).
 DE
 XX Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
 KM tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
 KM phage antibody library.
 OS Mus musculus.
 XX WO9525167-A1.
 PN 21-SEP-1995.
 PD 16-MAR-1995; 95WO-EP000978.
 PF 17-MAR-1994; 94EP-00104160.
 PR 02-DEC-1994; 94EP-00118970.
 XX (MERE) MERCK PATENT GMBH.
 PA Kettleborough AC, Bendig MM, Ansell KH, Guessow D, Adan J;
 PI Miltjans F, Rosell E, Blasco F, Plutats J;
 XX WPI; 1995-336972/43.
 DR N-PSDB; AAT04020.
 DR Anti-BGFR antibodies and single chain Fv antibody fragments - obtained
 PT from phage-antibody libraries, useful for diagnosis and therapy of
 PT tumours.
 PS Claim 4; Page 60-61; 93pp; English.

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
 CC antibodies constructed from anti-BGFR antibody fragments can be used for
 CC diagnosis of tumours and assessment of tumour growth in vitro and in
 CC vivo. They may also be used in a pharmaceutical composition for the
 CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
 CC fragments are derived from mice but are humanised so as to cause minimum
 CC reaction against them. They are produced using the phage antibody
 CC library. They are produced using the phage antibody library. (See
 CC AAT04011-T04026 and AAR79858-R79873)

Query Match 91.5%; Score 506; DB 2; Length 244;
 Best Local Similarity 92.6%; Pred. No. 1.6e-30;

Matches 100; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 DTELTPSAIMASPEKVTTCSSASSSVYMYWYQKRGSSPRLIYDTSNLASGVPR 60
 DB 137 DIELTPSAIMASPEKVTTCSSASSSVYMYWYQKRGSSPRLIYDTSNLASGVPR 196
 QY 61 FSGSGSGTYSLTISRMEADATYCCQWSSNP--LTFSGGTKEIK 106
 DB 197 FSGSGSGTYSLTISRMEADATYCCQWSSNPMTYFGGTKEIK 244

RESULT 11

AAR79871
 ID AAR79871 standard; protein; 242 AA.

AC AAR79871;

DT 02-JUL-1996 (first entry)

DE Anti-EGFR single chain antibody (Clone 7 G 1).

KM Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
 KW tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
 KW phage antibody library.

OS Mus musculus.

XX WO9525167-A1.

PD 21-SEP-1995.

PF 16-MAR-1995; 95WO-EP000978.

PR 17-MAR-1994; 94EP-00104160.
 PR 02-DEC-1994; 94EP-00118970.

PA (MERE) MERCK PATENT GMBH.

PI Kettleborough AC, Bendig MW, Ansell KH, Guesow D, Adan J;
 PI Mitjans F, Rosell E, Blasco F, Pizlats J;

DR WPI, 1995-336972/43.

XX N-PSDB; AAT04024.

PT Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
 PT from phage-antibody libraries, useful for diagnosis and therapy of
 PT tumours.

PS Claim 4; Page 70; 93pp; English.

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
 CC antibodies constructed from anti-EGFR antibody fragments can be used for
 CC diagnosis of tumours and assessment of tumour growth in vitro and in
 CC vivo. They may also be used in a pharmaceutical composition for the
 CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
 CC fragments are derived from mice but are humanised so as to cause minimum
 CC reaction against them. They are produced using the phage antibody
 CC library. They are produced using the phage antibody library. (See
 CC AAT04011-T04024 and AAR79858-R79873)

CC Sequence 242 AA;

Query Match 91.3%; Score 505; DB 2; Length 242;

Best Local Similarity 92.5%; Pred. No. 1.9e-30;

Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DTELTPSAIMASPEKVTTCSSASSSVYMYWYQKRGSSPRLIYDTSNLASGVPR 60

DB 137 DIELTPSAIMASPEKVTTCSSASSSVYMYWYQKRGSSPRLIYDTSNLASGVPR 196

QY 61 FSGSGSGTYSLTISRMEADATYCCQWSSNP-LTFSGGTKEIK 106

DB 197 FSGSGSGTYSLTISRMEADATYCCQWSSNPMTYFGGTKEIK 244

RESULT 12

ABG32682
 ID ABG32682 standard; protein; 106 AA.

XX ABG32682;

DT 29-NOV-2002 (first entry)

DE Murine anti-EGFR antibody, MAb425, VK polypeptide.

KM Mouse; variable kappa light chain; VK; epidermal growth factor receptor;
 KW EGFR; antibody; Her 1; immunogenic; immune system; T cell epitope;
 KW immunogenicity; major histocompatibility complex; MHC; allotype;
 KW MHC class II; antibody therapy; cancer; tumour; murine;
 KW anti-EGFR antibody; MAb425.

OS Mus sp.

XX WO20026058-A1.

PD 29-AUG-2002.

PF 18-FEB-2002; 2002WO-EP001687.

PR 19-FEB-2001; 2001EP-00103954.

PA (MERE) MERCK PATENT GMBH.

PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;

DR WPI, 2002-674898/72.

PT New modified anti-epidermal growth factor receptor antibodies which are
 PT non-immunogenic or less immunogenic compared with non-modified
 PT antibodies, useful for treating cancers or tumors, e.g. tumor of the
 PT breast, heart or lung.

PS Disclosure; Page 20; 47pp; English.

CC The invention discloses a modified antibody (or fragment) directed to the
 CC epidermal growth factor receptor (EGFR or Her 1). The antibody is
 CC substantially non-immunogenic, or less immunogenic, than any original
 CC immunogenically non-modified antibody directed to the same receptor when
 CC exposed to the immune system of a given species and compared with the non
 CC -modified antibody. Compared with a non-modified antibody, the modified
 CC antibody does not have, or has a reduced number, of T cell epitope
 CC sequences and/or major histocompatibility complex (MHC) allotypes having
 CC the ability to bind peptides derived from the non-modified antibody. The
 CC 13-mer T-cell epitope peptide, or a sequence having at least 9
 CC consecutive amino acid residues of the 13-mer T-cell epitope having a
 CC potential MHC class II binding activity, is useful in the manufacture of
 CC an immunogenically modified antibody having substantially no or less
 CC immunogenicity, when used in vivo, compared to the non-modified antibody.
 CC The modified antibody is useful in antibody therapy to treat cancers or
 CC tumours. The modified antibody is substantially non-immunogenic or less
 CC immunogenic than any original immunogenically non-modified antibody
 CC directed to the same receptor when exposed to the immune system of a
 CC given species, has enhanced properties and with reduced or absent
 CC potential to induce an immune response in the human subject. The modified
 CC antibody displays an increased circulation time within the human subject
 CC and would be of particular benefit in chronic or recurring disease
 CC settings. The sequence presented is the murine anti-EGFR antibody,
 CC MAb425, variable kappa light chain (VK) polypeptide

CC Sequence 106 AA;

Query Match 90.8%; Score 502; DB 5; Length 106;

Best Local Similarity 94.2%; Pred. No. 1.5e-30;

Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTPSAIMASPEKVTTCSSASSSVYMYWYQKRGSSPRLIYDTSNLASGVPRFSG 63

Db 4 LTGSPAIMSASPGKVTMTCSASSSVYMWYQOKPSSPRLIYDTSNLASGVPRFSG 63
 QY 64 SGGSTSYSLTISRMEADATYYCOOWSSNPLTFGSGTKLEIK 106
 Db 64 SGGSTSYSLTISRMEADATYYCOOWSSHIFTFGSGTKLEIK 106

RESULT 13

AAE27810
 ID AAE27810 standard; protein; 106 AA.

XX AAE27810;
 XX

DT 13-DBC-2002 (first entry)
 XX

DS Mouse 425 antibody VK protein.
 XX

KM Mouse; fusion protein; immunological; major histocompatibility complex;
 KM MHC; nausea; gastric upset; antibody; VK region.
 XX

OS Mus sp.
 XX

PN WO20026514-A2.
 XX

PD 29-AUG-2002.
 XX

PF 18-FEB-2002; 2002WO-EP001690.
 XX

PR 19-FEB-2001; 2001EP-00103955.
 PR 05-APR-2001; 2001EP-00108291.
 XX

PA (MERE) MERCK PATENT GMBH.
 XX

PI Gallies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S,
 PI Hanlon M, Watkins J, Baker M, May JC;
 XX

DR WPI; 2002-667054/71.
 XX

PT New modified fusion protein with reduced immunogenicity, useful for
 PT combining favorable properties of a composition, comprises an
 PT immunoglobulin molecule linked to a non-immunoglobulin target
 PT polypeptide.
 XX

PS Example 18; Page 68; 92pp; English.
 XX

CC The invention relates to an immunogenically modified fusion protein
 CC derived from a parent fusion protein, comprising first and second
 CC proteins/polypeptides, where the first protein is an immunoglobulin
 CC molecule or its fragment and the second protein is non-immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker
 CC molecule. The immunogenically modified fusion protein is useful in
 CC combining known favourable properties of a composition or in creating new
 CC properties of a composition which elicits biological or pharmacological
 CC efficacy without having undesirable physiological effects such as nausea
 CC or gastric upset. The present sequence is mouse 425 antibody VK protein.
 CC This sequence is used in the exemplification of the invention
 XX

XX Sequence 106 AA;
 SQ

Query Match 90.8%; Score 502; DB 5; Length 106;
 Best Local Similarity 94.2%; Pred. No. 1.5e-30;
 Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKVTMTCSASSSVYMWYQOKPSSPRLIYDTSNLASGVPRFSG 63
 Db 4 LTGSPAIMSASPGKVTMTCSASSSVYMWYQOKPSSPRLIYDTSNLASGVPRFSG 63

QY 64 SGGSTSYSLTISRMEADATYYCOOWSSNPLTFGSGTKLEIK 106
 Db 64 SGGSTSYSLTISRMEADATYYCOOWSSHIFTFGSGTKLEIK 106

Db 64 SGGSTSYSLTISRMEADATYYCOOWSSHIFTFGSGTKLEIK 106

RESULT 14

AAE27050
 ID AAE27050 standard; protein; 128 AA.

XX AAE27050;
 XX

DT 25-MAR-2003 (revised)
 DT 01-MAR-1993 (first entry)
 XX

DS VLA425 antibody cloned into pUC18.
 XX

XX Monoclonal antibody; complementarity determining region; framework;
 KM antigens; tumour; melanoma; carcinoma; glioma; light; heavy; variable;
 KM chain.
 XX

OS Synthetic.
 XX

PH Key Location/Qualifiers
 FH Peptide 1..22
 FT /note="signal peptide"
 FT Protein 23..128

FT /note="mature peptide"
 FT Region 46..55
 FT /label=CDR1
 FT Region 71..77
 FT /label=CDR2
 FT Region 110..118
 FT /label=CDR3

XX WO9215683-A1.
 XX

PD 17-SEP-1992.
 XX

PF 04-MAR-1992; 92WO-EP000480.
 XX

PR 06-MAR-1991; 91BP-00103389.
 XX

PA (MERE) MERCK PATENT GMBH.
 XX

PI Bendig MM, Kettleborough CA, Saldanha V;
 XX

DR WPI; 1992-331729/40.
 DR N-PADB; AAQ28740.
 XX

PT Human monoclonal antibodies binding to human receptors - for treatment
 PT and diagnosis of tumours, e.g. melanoma and carcinoma.
 XX

PS Disclosure; Fig 2; 89pp; English.
 XX

CC The variable light chain of monoclonal antibody 425 was prepd. from a
 CC synthetic cDNA sequence in which mutatiohs had been made to the 5' and 3'
 CC ends to allow for cloning into HCV expression vectors. Donor splice
 CC sites were recreated in the 3' flanking regions to allow correct splicing
 CC of the variable and constant regions. The 5' sequence was altered to
 CC introduce an initiation codon. The cloned antibody may be used int the
 CC prodn. of reshaped or humanised antibodies which are less immunogenic than
 CC native antibodies and may be used to combat e.g. glioma, melanoma or
 CC carcinoma. See also AAE27299-300 and AAE27037-41. (updated on 25-MAR-2003
 CC to correct PN field.)
 XX

XX Sequence 128 AA;
 SQ

Query Match 90.8%; Score 502; DB 2; Length 128;
 Best Local Similarity 94.2%; Pred. No. 1.8e-30;
 Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASPGKVTMTCSASSSVYMWYQOKPSSPRLIYDTSNLASGVPRFSG 63
 Db 26 LTGSPAIMSASPGKVTMTCSASSSVYMWYQOKPSSPRLIYDTSNLASGVPRFSG 85

QY 64 SGGSTSYSLTISRMEADATYYCOOWSSNPLTFGSGTKLEIK 106
 Db 64 SGGSTSYSLTISRMEADATYYCOOWSSHIFTFGSGTKLEIK 106

Db 86 SGGSTSYSLTISRMEADATYYCOOWSSHIFTFGSGTKLEIK 128

RESULT 15

AAB69673
ID AAB69673 standard; protein; 106 AA.

AC AAB69673;

DT 30-APR-2001 (first entry)

DE Murine mlk-beta1 antibody light chain SEQ ID NO: 58.

XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
XX light chain; graft versus host disease; transplant; autoimmune disease;
XX multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

OS Mus sp.

PN US6180370-B1.

PD 30-JAN-2001.

PF 07-JUN-1995; 95US-00484537.

PR 28-DEC-1988; 88US-00290975.

PR 13-FEB-1989; 89US-00310252.

PR 28-SEP-1990; 90US-00590274.

PR 19-DEC-1990; 90US-00634278.

PA (PROT-) PROTEIN DESIGN LABS INC.

PI Queen Cl, Selick HE;

DR WPI; 2001-190856/19.

PT Producing humanized immunoglobulin, involves producing a cell containing

PT DNA segments encoding humanized heavy and light chain variable regions,

PT and expressing the DNA segments in the cell.

PS Disclosure; Fig 5; 145pp; English.

XX The present invention describes a method of producing humanised

XX immunoglobulins involving expressing in a cell a nucleic acid encoding a

XX humanised version of an immunoglobulin. This is obtained by comparing a

XX donor and human immunoglobulin and producing a combined antibody which

XX contains part of each. These are useful in the treatment of graft-versus-

XX host disease, transplant rejection, autoimmune diseases such as diabetes,

XX rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic

XX lupus erythematosus, herpes infections, CMV virus infections and myeloid

XX leukaemia. The present sequence is an antibody used to demonstrate the

XX method of the invention

XX Sequence 106 AA;

XX Query Match 90.6%; Score 501; DB 4; Length 106;

XX Best Local Similarity 93.2%; Pred. No. 1.7e-30;

XX Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX DB 4 LTQSPAIMSASPGKVTTCSSASSVSYMYWYQOKPGSSPRLIYDTSNLAGVPRFSG 63

XX 4 LTQSPAIMSASPGKVTTCSSASSVSYMYWYQOKPGSSPRLIYDTSNLAGVPRFSG 63

XX 64 SSGSGTYSYSLTISRMEADAATYCCQMSNPITFGSGTLELK 106

XX 64 SSGSGTYSYSLTISRMEADAATYCCQMSNPITFGSGTLELK 106

XX Search completed: November 21, 2005, 12:19:55

XX Job time : 144.255 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 26.0641 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-87

Perfect score: 553
Sequence: 1 DTELQSPAIMSASPGKVT.....QWSSNPITFGSGTKLBIKR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	481	87.0	107 2 PC4405	Ig kappa chain V r
2	473	85.5	107 2 A30562	Ig kappa chain V r
3	472	85.4	107 2 B30562	Ig kappa chain V r
4	471	85.2	130 1 JL0079	Ig kappa chain pre
5	469.5	84.9	108 2 S38720	Ig light chain V r
6	467	84.4	103 2 S29591	Ig kappa chain V r
7	466	84.3	235 2 S25058	Ig kappa chain - m
8	465	84.1	106 2 PS0071	Ig kappa chain V r
9	463	83.7	104 2 B49049	Ig kappa chain V r
10	462	83.5	140 2 PL0013	Ig kappa chain pre
11	460.5	83.3	108 2 G30560	Ig kappa chain V r
12	460	83.0	107 2 A42848	Ig light chain V r
13	459	83.0	107 2 PD0011	Ig kappa chain V r
14	457	82.6	107 2 S11119	Ig kappa chain V r
15	456	82.5	106 2 B54378	Ig light chain V r
16	455	82.3	107 2 S11118	Ig kappa chain V r
17	455	82.3	108 2 S11125	Ig kappa chain V r
18	454	82.1	130 2 A32513	Ig kappa chain pre
19	449	81.2	107 2 S11121	Ig kappa chain V r
20	448	81.0	105 2 S26338	Ig kappa chain V r
21	447	80.8	107 2 PT0406	Ig kappa chain V r
22	443	80.1	106 2 G27887	Ig kappa chain V r
23	442	79.9	107 2 S11117	Ig kappa chain V r
24	442	79.9	113 2 S03410	Ig kappa chain pre
25	442	79.9	120 2 S66336	Ig light chain V r
26	441	79.7	97 2 S26341	Ig light chain V r
27	441	79.7	100 2 S29590	Ig kappa chain V r
28	439	79.4	106 2 PL0082	Ig kappa chain V r
29	438	79.2	107 2 S11112	Ig kappa chain V r

30	438	79.2	132 2 S05268	Ig kappa chain pre
31	437.5	79.1	106 2 S11114	Ig kappa chain V r
32	437	79.0	130 2 S04573	Ig kappa chain pre
33	436	78.8	106 2 PS0070	Ig kappa chain V r
34	435	78.7	97 2 PH1084	Ig light chain V r
35	434	78.5	104 2 JC6076	anti-D-dimer monoc
36	433	78.3	108 2 PL0278	Ig kappa chain V r
37	433	78.3	123 2 S05269	Ig kappa chain pre
38	432	78.1	130 2 B32456	Ig kappa chain pre
39	430	77.8	108 2 PS0069	Ig kappa chain V r
40	429	77.6	108 2 PL0277	Ig kappa chain V r
41	429	77.6	108 2 PL0276	Ig kappa chain V r
42	429	77.6	108 2 S29581	Ig kappa chain V r
43	428	77.4	107 2 S11113	Ig kappa chain V r
44	427	77.2	107 2 S11123	Ig kappa chain V r
45	425	76.9	124 2 S05267	Ig kappa chain pre

ALIGNMENTS

RESULT 1

PC4405
Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004

C/Accession: PC4405
R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.

Chinese Biochem. J. 12, 648-653, 1996
A/Title: Generation of a phage display library of the immunoglobulin repertoire from hum

A/Reference number: PC4405
A/Accession: PC4405

A/Molecule type: mRNA
A/Residues: 1-107 <DEN>

A/Cross-references: UNIPROT:O8KLF0; UNIPARC:UP100001767B8

A/Experimental source: spleen cell
C/Suprafamily: immunoglobulin V region; immunoglobulin homology

F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 481; DB 2; Length 107;
Best Local Similarity 85.0%; Pred. No. 8.9e-35;

Matches 91; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY	1	DTELQSPAIMSASPGKVTTCASSSVSITMYTQKPGSSPLLITDTSILASGVPR	60
DB	1	DIELTQSPAIMSASPGKVTTCASSSISYTHWYQKPGTSPKRWIDTSKLSGVPR	60
QY	61	PSGSGSGTSYSLTISRMEADATYTCOWMSNPITFGSGTKLBIKR	107
DB	61	PSGSGSGTSYSLTISRMEADATYTCOWMDNPITFGSGTKLBIKR	107

RESULT 2

A30562
Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000

C/Accession: A30562
R/Sikder, S.K.; Borden, P.; Gruezo, F.; Akolmar, P.N.; Bhattacharya, S.B.; Morrison, S.L.

J. Immunol. 142, 888-893, 1989
A/Title: Amino acid substitutions in V-H CDR3 change the idotype but not the antigen-bir

A/Reference number: A30562; MUID:89110066; PMID:2464031
A/Status: preliminary

A/Accession: A30562
A/Molecule type: mRNA

A/Cross-references: UNIPARC:UP100001767B0

C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 473; DB 2; Length 107;
Best Local Similarity 87.5%; Pred. No. 4.4e-34;

Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTGSPALMSASPGKRVTTTCGASSSVSYMYRYOQKPGSSPLLLYDTSNLASGVPAFPG 63
Db 4 LTGSPALMSASPGKRVTTTCGASSSVSYMYRYOQKPGSSPLLLYDTSNLASGVPAFPG 63

QY 64 SGGSTSYSLTISRMEADATATTCQWSSNPLTFGSGTKLEIKR 107
Db 64 SGGSTSYSLTISRMEADATATTCQWSSNPLTFGSGTKLEIKR 107

RESULT 3

Ig kappa chain V region (27,10,2) - mouse (fragment)
B30562
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
A/Accession: B30562
R/Sikder, S.K.; Borden, P.; Grzesio, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A>Title: Antio acid substitutions in V-H CDR2 change the idiotype but not the antigen-b-
A/Reference number: A30562; MUID:85110066; PMID:2464031
A/Accession: B30562
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <SIK>

C/Cross-references: UNIPARC:UPI00001767BA
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F/16-89/Domain: Immunoglobulin homology <IMM>

Query Match 85.4%; Score 472; DB 2; Length 107;
Best Local Similarity 86.5%; Pred. No. 5.3e-34;
Matches 90; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTGSPALMSASPGKRVTTTCGASSSVSYMYRYOQKPGSSPLLLYDTSNLASGVPAFPG 63
Db 4 LTGSPALMSASPGKRVTTTCGASSSVSYMYRYOQKPGSSPLLLYDTSNLASGVPAFPG 63

QY 64 SGGSTSYSLTISRMEADATATTCQWSSNPLTFGSGTKLEIKR 107
Db 64 SGGSTSYSLTISRMEADATATTCQWSSNPLTFGSGTKLEIKR 107

RESULT 4

Ig kappa chain precursor V region (anti-phenylloxazalone 6f6) - mouse
JL0079
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
A/Accession: JL0079; A49044; B49044
R/Kaartinen, M.; Rocca-Berra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988
A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-reas
A/Reference number: JL0076; MUID:89069673; PMID:3211160
A/Accession: JL0079
A/Molecule type: mRNA
A/Residues: 1-130 <KKA>

A/Cross-references: UNIPARC:UPI000017371F; GB:M27792; NID:g197159
A/Experimental source: mRNA clones for anti-phenylloxazalone antibody 6f6
A/Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue 10C for residue
R/Milstein, C.; Ben, J.; Urvyle, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1621-1634, 1992
A>Title: Non-random features of the repertoire expressed by the members of one V kappa g
A/Reference number: A49044; MUID:92289826; PMID:1601044
A/Accession: A49044
A/Molecule type: DNA
A/Residues: 1-25 <MTL>

A/Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:g350214; PIDN:AAE22332.1; PID
A/Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIPI:106809)
A/Accession: B49044
A/Molecule type: DNA
A/Residues: 114-116 <MTL2>

A/Cross-references: UNIPARC:UPI000001188B5; GB:S37664; NID:g350215; PIDN:AAE22332.1; PID

A:Experimental source: BAB/c germ-line
A:Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 additional clones
A:Note: sequence extracted from NCBI backbone (NCBI:106807, NCBI:106822)
C:Genetics:
A:Gene: V(kappa)Ox1
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:45-109/Disulfide bonds: #status predicted

Query Match 85.2%; Score 471; DB 1; Length 130;
Best Local Similarity 87.5%; Pred. No. 7, 9e-34;
Matches 91; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTGSPALMSAPGKRVTTTCSASSSVYMYTQOKRGPSPRLIYPTSNLASGVPVPSG 63
DB 26 LTGSPALMSAPGKRVTTTCSASSSVYMYTQOKRGPSPRLIYPTSNLASGVPVPSG 85

OY 64 SGGSTSYSLTISRMEADATYCCQWSSNPITFGSGTLELR 107
DB 86 SGGSTSYSLTISRMEADATYCCQWSSNPITFGSGTLELR 129

RESULT 5
S38720
Ig light chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38720
R:Climans, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38720
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <CIN>
A:Cross-references: UNIPARC:UPI0000117544; EMBL:X76023; NID:9416104; PIDN:CAA53610.1; PIDN:CAA53610.2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 469.5; DB 2; Length 108;
Best Local Similarity 88.6%; Pred. No. 8, 8e-34;
Matches 93; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 4 LTGSPALMSAPGKRVTTTCSASSSVYMYTQOKRGPSPRLIYPTSNLASGVPVPSG 63
DB 4 LTGSPALMSAPGKRVTTTCSASSSVYMYTQOKRGPSPRLIYPTSNLASGVPVPSG 63

OY 64 SGGSTSYSLTISRMEADATYCCQWSSNPITFGSGTLELR 107
DB 64 SGGSTSYSLTISRMEADATYCCQWSSNPITFGAGTQLQKR 108

RESULT 6
S29591
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S29591
R:Kawaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S29591
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <KAN>
A:Cross-references: UNIPARC:UPI0000115577; EMBL:X59094; NID:9522227; PIDN:CAA41820.1; PIDN:CAA41820.2

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-88/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 467; DB 2; Length 103;
Best Local Similarity 89.1%; Pred. No. 1.4e-33;
Matches 90; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63
DB 3 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWYDTSKLASGVPRFSG 62

QY 64 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGSGTKLE 104
DB 63 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGAGTKLE 103

RESULT 7
S25058

Ig kappa chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C:Accession: S25058

R: Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific

A:Reference number: S25057

A:Accession: S25058

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-235 <FIS>

A:Cross-references: UNIPARC:UPI0000116096; EMBL:X67211; NID:G54828; PIDN:CAA47650.1; PID

F:38-111/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 466; DB 2; Length 235;
Best Local Similarity 88.5%; Pred. No. 3.9e-33;
Matches 92; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63
DB 26 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWYDTSKLASGVPRFSG 85

QY 64 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGSGTKLE 107
DB 86 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGAGTKLE 129

RESULT 8
PS0071

Ig kappa chain V region (38C13 V8) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C:Accession: PS0071

R: Levy, S.; Campbell, M.J.; Levy, R.

J. Exp. Med. 170, 1-13, 1989

A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement

A:Reference number: A92781; MUID:89310348; PMID:2501443

A:Accession: PS0071

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-106 <LEV>

A:Cross-references: UNIPARC:UPI00001767C9

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 465; DB 2; Length 106;
Best Local Similarity 87.4%; Pred. No. 2.1e-33;
Matches 90; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63

DB 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWYDTSKLASGVPRFSG 63

QY 64 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGSGTKLE 106
DB 64 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGATKLE 106

RESULT 9
B49049

Ig kappa chain V region (anti-Idiotypic) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C:Accession: B49049

R: Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.

Eur. J. Immunol. 22, 2893-2899, 1992

A:Title: Molecular analysis of anti-Idiotypic monoclonal antibodies in the HLA-DR antigen

A:Reference number: A49049; MUID:93049629; PMID:1425914

A:Accession: B49049

A:Status: Preliminary

A:Molecule type: nucleic acid

A:Residues: 1-104 <ARM>

A:Cross-references: UNIPARC:UPI00001767AD

A:Experimental source: BALB/c

A:Note: sequence extracted from NCBI backbone (NCBI:118298, NCBI:118299)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-89/Domain: immunoglobulin homology <IMM>

Query Match 83.7%; Score 463; DB 2; Length 104;
Best Local Similarity 88.1%; Pred. No. 3.1e-33;
Matches 89; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63
DB 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWYDTSKLASGVPRFSG 63

QY 64 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGSGTKLE 104
DB 64 SSGSTSYSLTISRMEDADATYYCOQMSNPITFGAGTKLE 104

RESULT 10
P10013

Ig kappa chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: P10013

R: Cheng, H.L.; Sood, A.K.; Ward, R.B.; Kleber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-Idiotypic antibodies.

A:Reference number: P10011; MUID:88142863; PMID:3125424

A:Accession: P10013

A:Molecule type: mRNA

A:Residues: 1-140 <CHR>

A:Cross-references: UNIPARC:UPI00001767A6

A:Experimental source: cell line 4C11

C:Comment: This protein is an anti-Idiotypic antibody that induces an anti-phosphorylcho

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:123-129/Domain: signal sequence status predicted <SIG>

F:23-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F:38-111/Domain: immunoglobulin homology <IMM>

F:46-55/Region: complementarity-determining 1

F:71-77/Region: complementarity-determining 2

F:110-118/Region: complementarity-determining 3

F:130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 83.5%; Score 462; DB 2; Length 140;
Best Local Similarity 87.5%; Pred. No. 5.1e-33;
Matches 91; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRFSG 63

Db 26 LTGSPALMSASPGKHTTITCSASSSVSYMMFQOKDPDTPSKLMIVYSTNLASGVPRFSG 85

QY 64 SGGSTSYSLTISRMEADAAITYYCCQWSSNPLTFGGSTKJELNR 107

Db 86 SGGSTSYSLTISRMEADAAITYYCCQWSSVPRTFGGSTKJELNR 129

RESULT 11

G30560
IG kappa chain V region (35..8.2H) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 23-Mar-1999 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C/Accession: G30560
R/Malinda, T.; Kadat, E.A.
J. Immunol. 142, 863-870, 1989
A/Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal
A/Reference number: A30560; MUID:89110062; PMID:2464028
A/Accession: G30560
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-108 <MAT>
A/Cross-references: UNIPARC:UPI00001767B8
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
C/16-89/Domain: immunoglobulin homology <IMM>

Query Match	83.3%	Score 460.5;	DB 2;	Length 108;
Best Local Similarity	85.7%	Pred. No. 5.2e-33;		
Matches 90;	Conservative .	5;	Mismatches 9;	Indels 1;
				Gaps 1;

```

Oy      4 LTGSPAIMSAPGEEKYTTTCSASSSVSYMYWYQOKPGSSPRLLYDTSNLASGVPRFSG 63
         |||||
         |||||:|||||:|||||
Db      4 LTGSPAIMSAPGEEKYTTTCSASSSVSYMYWYQOKGSSPEKTYIDTSKLASGVPRFSG 63
         |||||
         |||||:|||||:|||||

```

```
Qy      64 SSGSTSYSLTISRMEADATYYCOOMSSN-PLTFGSGTKLELR 107  
        |||||  
Db      64 SSGSTSYSLTISSMEADATYYCOOTRNPPTFGSGTKLEIR 108  
        |||||
```

RESULT 12

A42848
Ig1light chain V region - mouse (fragment)
N/Alternate names: L6 anti-tumor antibody
C/Species: Mus musculus (house mouse)
C/Date: 27-Apr-1993 #sequence revision 18-Nov-1994 #text change 21-Jan-2000
C/Accession: A42848; S33902
R/Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsitch, L.; Schieven, G.L.; Marken, J.S.; Arnfield
J. Biol. Chem. 267, 15552-15558, 1992
A/Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, and character
A/Reference number: A42848; MUID:92348410; PMID:1639794
A/Accession: A42848
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-107 <FEI>
A/Cross-references: UNIPARC:UPI0000115334; EMBL:M90690
A/Note: sequence extracted from NCBI backbone (NCBIN:109958, NCBIPI:109959)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
C/16-89/Domain: immunoglobulin homology <IMM>

Query Match	83.2%	Score 460;	DB 2;	Length 107;
Best Local Similarity	85.6%	Pred. No. 5.7e-33;		
Matches 89; Conservative	7;	Mismatches 8;	Indels 0;	Gaps 0;

4 LTGSPAIMSASPGKVTITTCASASSVSVMYMQOKPGSSPRLLIYDTSNLASGVPRFSG 63
4 LSGSPILSASPGKVTLLCRASSSVSFNNMYQOKPGSSPKPMIATSNLASGVPRFSG 63

QY 64 SSGGTSYSLTISRMEADATYYCOOWSNPLTFGSGTKLELR 107
| | | | | : | | | | | : | | | | | : | | | | |
Db 64 SSGGTSYSLISRVEADATYYCOOWSNPLTFGAGTKLELR 107

RESULT 13
PD0011
Ig kappa chain V region (VLBI, anti-APP) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 10-Jul-1998 #sequence_rev1510 10-Jul-1998 #text_change 21-Jan-2000
C/Accession: PD0011

R: Deng, J.B., Han, H., Su, C.Z., Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A>Title: Generation of a phage display library of the immunoglobulin repertoire from human
A:Reference number: PC4405
A:Contents: Spleen
A:Accession: PD0011
A:Molecule type: mRNA
A:Residues: 1-107 <DEN>
A:Cross-references: UNIPARC:UPI00001767AA
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
P:16-89/Domain: immunoglobulin homology <IMM>

Query Match	83.0%	Score 459	DB 2	Length 107
Best Local Similarity	82.2%	Pred. No. 7e-33		
Matches 88; Conservative	7	Mismatches 12	Indels 0	Gaps 0

QY 1 DTELTPAINSASPGKEVTTCSSASSVSVMWVYQOKGSSPLLIDTISNLASGVPR 60

Db 1 DIELTPAINSASPGKEVTTCSSASSISYMWYQOKGTSPKMWYDTSKLASGVPAK 60

QY 61 FSGSGGTSYSLTISRMEARDAATYYCQWMSNPLFGSGTKLEIKR 107
| | | | | : | | | | | : | | | | |
Db 61 GSGSGGTSYSLTISRVEARDAATYYCQWRDNPFGSGTKLEIKR 107

RESULT 14

```

S1119
Ig kappa chain V region (clone NO6-8.3.1) - mouse (fragment)
CISpecies: Mus musculus (house mouse)
CjDate: 19-Mar-1997 #sequence_rev1sion 23-Aug-1997 #text_change 21-Jan-2000
CjAccession: S1119
R:Karttunen, M.; Grifflths, G.M.; Markham, A.P.; Milstein, C.
Nucleotide 304, 320-324, 1983
A:Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone
A:Reference number: S07331, MUID:83271467; PMID:6877353
A:Accession: S1119
A:Molecule type: mRNA
A:Residues: 1-107 <NAT>
A:Cross-References: UNIPARC:UPI00001767B0
CjSuperfamily: immunoglobulin V region; immunoglobulin homology
P.16-89/Domain: immunoglobulin homology <IMM>

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Query Match	82.6%	Score 457	DB 2	Length 107
Best Local Similarly	84.6%	Pred. No. 1e-32		
Matches 88; Conservative	4	Mismatches	12	Indels 0
				Gaps 0

```

OY      4 LTQSPALMSASPGKEVTTTCSASSSVSYMWYQKPGSSPRLLIYDTSNLASGVPRFSG 63
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4 LTQSPALMSASPGKEVTTTCSASSSVSYMWYQKPGSSPRLLIYDTSNLASGVPRFSG 63

```

Dy 64 SSGTSTSLTISRMEADATYYCQWSSNPLTFGSGTKLEKR 107
| | | | | : | | | | |
Db 64 XGXGTSTSLTISSMFAEDATYYCCQWSSNPLTFGAGTKLEKR 107

RESULT 15

B54378
Ig light chain V region anti-triplex DNA - mouse (fragment)
Cispecies: Mus musculus (house mouse)
Cdate: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
Accession: B54378
RAgazie, Y.M.; Lee, J.S.; Burkholder, G.D.
V Biol. Chem. 269, 7019-7023, 1994
Article: Characterization of a new monoclonal antibody to triplex DNA and immunofluorescence
A:Reference number: A54378; MUID:94165109; PMID:7509814
Accession: B54378

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-106 <AGA>
A/Cross-references: UNIPARC:UPI00001767AC; GB:S68985; NID:G545746; PID:AB30096.1; PID:
A/Experimental source: spleen and myeloma cell line M08C 315.43
A/Note: sequence inconsistent with nucleotide translation
A/Note: sequence extracted from NCBI backbone (NCBIN:144174, NCBI:144175)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:16-89/Domain: immunoglobulin homology <IM>

Query Match 82.5%; Score 456; DB 2; Length 106;
Best Local Similarity 86.4%; Pred. No. 1.3e-32;
Matches 89; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY	4	LTQSPATMSASPGKVTTCSSASSSVYMYOQKRGSSPRLLYDTSNLASGVVPRPSG	63
DB	4	LTQSPATMSASPGKVTTCSSASSSVYMYOQKRGSPKLIYSTSKLASGVVPRPSG	63
QY	64	SGSGTYSGLTISREAEADATYYCQWSSNPITFGSGTKLEIK	106
DB	64	SGSGTYSGLTISREAEADATYYCQWSSNPITFGSGTKLEIK	106

Search completed: November 21, 2005, 12:22:12
Job time : 26.0641 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55; Search time 158.344 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-87
Perfect score: 553
Sequence: 1 DTBLTQSPAINASPGKRVLT.....QQWSSNPITFGSGTKLEIKR 107

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: uniprot_05.80.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	500	90.4	Q9U410_MOUSE	Q9U410 mus musculu
2	489	88.4	KV6K_MOUSE	P04945 mus musculu
3	475	85.9	Q8K1F2_MOUSE	Q8K1F2 mus musculu
4	471	85.2	Q58E6V_MOUSE	Q58E6V mus musculu
5	466	84.3	KV6F_MOUSE	P04940 mus musculu
6	463	83.7	Q8K1F3_MOUSE	Q8K1F3 mus musculu
7	461	83.4	KV6I_MOUSE	P04943 mus musculu
8	460	83.2	KV6G_MOUSE	P04941 mus musculu
9	460	83.2	KV6H_MOUSE	P04942 mus musculu
10	460	83.2	KV6J_MOUSE	P04944 mus musculu
11	457	82.6	Q5XFF8_MOUSE	Q5XFF8 mus musculu
12	456	82.5	Q8K1F0_MOUSE	Q8K1F0 mus musculu
13	452	81.7	Q8VDD0_MOUSE	Q8VDD0 mus musculu
14	443.5	80.2	Q811C3_MOUSE	Q811C3 mus musculu
15	440	79.6	Q8K1F1_MOUSE	Q8K1F1 mus musculu
16	426	77.0	Q569Y8_MOUSE	Q569Y8 mus musculu
17	414	74.9	KV6B_MOUSE	P01678 mus musculu
18	413.5	74.8	Q9J176_MOUSE	Q9J176 mus musculu
19	413	74.8	KV6C_MOUSE	P01677 mus musculu
20	410	74.1	KV6D_MOUSE	P01678 mus musculu
21	408	73.8	KV4A_MOUSE	P01680 mus musculu
22	406	73.4	KV6A_MOUSE	P01675 mus musculu
23	398	72.0	KV6E_MOUSE	P01679 mus musculu
24	390.5	70.6	Q9J178_MOUSE	Q9J178 mus musculu
25	375	67.8	Q9U178_MOUSE	Q9U178 mus musculu
26	364	65.8	KV3L_HUMAN	P18135 homo sapien
27	363.5	65.7	Q6PIH7_HUMAN	Q6PIH7 homo sapien
28	363	65.6	KV3D_HUMAN	P01622 homo sapien
29	361	65.3	KV3M_HUMAN	P18136 homo sapien
30	360.5	65.2	Q569I7_HUMAN	Q569I7 homo sapien
31	360	65.1	KV3B_HUMAN	P01620 homo sapien

32	358.5	64.8	111	1	KV3N_MOUSE	P01666 mus musculu
33	358.5	64.8	244	2	Q65ZC9_HUMAN	Q65ZC9 homo sapien
34	357.5	64.6	108	1	KV1B_HUMAN	P01594 homo sapien
35	355.5	64.3	108	1	KV1O_HUMAN	P01607 homo sapien
36	355.5	64.3	111	1	KV3M_MOUSE	P01665 mus musculu
37	354.5	64.1	108	1	KV1P_HUMAN	P01608 homo sapien
38	354.5	64.1	108	2	Q9U170_HUMAN	Q9U170 homo sapien
39	354.5	64.1	111	1	Q9U170_MOUSE	P01667 mus musculu
40	354.5	64.1	236	2	Q6PIH8_HUMAN	Q6PIH8 homo sapien
41	354.5	64.1	240	2	Q65ZC9_HUMAN	Q65ZC9 homo sapien
42	354	64.0	107	2	Q96SA9_HUMAN	Q96SA9 homo sapien
43	353	63.8	109	1	KV3E_HUMAN	P01623 homo sapien
44	352.5	63.7	108	2	Q9U177_HUMAN	Q9U177 homo sapien
45	352.5	63.7	111	1	KV3K_MOUSE	P01663 mus musculu

ALIGNMENTS

```

RESULT 1
Q9U410_MOUSE
ID Q9U410_MOUSE PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30
DE Immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12567627;
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,
RA Huang H.L., Guan X.H.;
RT "Cloning and sequence analysis of the light chain variable region
RT gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
RT japonicum.";
RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
RL 18:257-259(2000); AAF19434.1; -, Genomic_DNA.
DR EMBL; AF207620; AAF19434.1; -, Genomic_DNA.
DR HSSP; P01679; 2FBJ.
DR SMR; Q9U410; 4-106.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 106
SQ SEQUENCE 106 AA; 11478 MW; F20F5444d6BA63E CRC64;

Query Match 90.4%; Score 500; DB 2; Length 106;
Best Local Similarity 94.2%; Pred. No. 3.6e-42;
Matches 97; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKRVLTTCSSASSSVSYWYQOKRGSFRLLIYDTSNLAGVPVRFSG 63
DB 4 LTQSPAINASPGKRVLTTCSSASSSVSYWYQOKRGSFRLLIYDTSNLAGVPVRFSG 63
QY 64 SSGGTSYSLTTRMEAEADAATYYCOQWSSNPITFGSGTKLEIK 106
DB 64 SSGGTSYSLTTRMEAEADAATYYCOQWSSNPITFGSGTKLEIK 106

RESULT 2
KV6K_MOUSE
ID KV6K_MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (rel. 05, Created)
DT 13-AUG-1987 (rel. 05, Last sequence update)

```

DT 10-MAY-2005 (Ref. 47, last annotation update)
 DE IG kappa chain V-VI region N02-6.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muroidae; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "MnA sequences define an unusually restricted Igg response to 2-
 RT phenylloxazone and its early diversification.";
 RL Nature 304:320-324(1993).
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; K00746; AAA3691.1; -; mRNA.
 DR HSSP; Q91W12; 1A11.
 DR SMR; P04945; 1-108.
 DR Ensembl; ENSMUSG0000062686; Mus musculus.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 98 Framework-4.
 FT REGION 99 108 Complementarity-determining-3.
 FT DISULFID 23 87 By similarity.
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;
 Query Match 88.4%; Score 489; DB 1; Length 108;
 Best Local Similarity 91.4%; Pred. No. 4.7e-41;
 Matches 96; Conservative 4; Mismatches 3; Indels 2; Gaps 1;
 QY 4 LTGSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPRFSG 63
 DB 4 LTGSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPRFSG 63
 QY 64 SSGSTSYSLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 106
 DB 64 SSGSTSYSLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 106
 DB 64 SSGSTSYSLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 108
 RESULT 3
 Q8K1F2_MOUSE
 ID Q8K1F2_MOUSE PRELIMINARY; PRT; 112 AA.
 AC Q8K1F2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DB Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BAIB/C; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 [2]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Terryneck T., Avramas S.;
 RT "Two murine natural polypeptide autoantibodies are encoded by
 RT nonmated germ-line genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
 DR EMBL; AF516283; AAM64201.1; -; Genomic_DNA.
 DR PIR; H33932; H33932.
 DR HSSP; P01837; 25C8.
 DR SMR; Q8K1F2; 2-112.
 DR Ensembl; ENSMUSG0000064150; Mus musculus.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 11953 MW; 4716B87FAD543BD CRC64;
 Query Match 85.9%; Score 475; DB 2; Length 112;
 Best Local Similarity 86.9%; Pred. No. 1.2e-39;
 Matches 93; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 1 DTELTPSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPR 60
 DB 1 DTELTPSPAIMSASPEKRYTTTCASASSVSYMYWYQOKPSSPRLIYDTSNLASGVPR 60
 QY 61 FSGSGSGTSTLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 107
 DB 61 FSGSGSGTSTLTISRMEADATYTCOQMSNP--LTPSGTGLRLK 107
 RESULT 4
 Q58EV6_MOUSE
 ID Q58EV6_MOUSE PRELIMINARY; PRT; 235 AA.
 AC Q58EV6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, last annotation update)
 DE Igk-C protein.
 GN Name=Igk-C;
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muroidae; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausner R.D., Collins F.S., Wagner L., Brenner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hult S.W.,
 RA Datchenko L., Marusik B., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hult S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Feingold J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield Y.S.N., Krzywicki M.I., Skalka U., Smalls D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 [2]

RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC091738; AAH91738.1; -, mRNA.
 DR SMR: O588Y6; 23-235.
 DR GO: GO:0003823; F:antigen binding; IRA.
 DR InterPro: IPR003599; IG_1.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003597; IG_C1.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF07654; CI-sect; 1.
 DR SMART: SM00409; IG; 2.
 DR SMART: SM00407; IGc1; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
 SO SEQUENCE 235 AA; 25719 MW; BR4E4ABDD2578252 CRC64;

Query Match 85.2%; Score 471; DB 2; Length 235;
 Best Local Similarity 86.5%; Pred. No. 7.6e-39;
 Matches 90; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTGSPAINASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRPSG 63
 |||||
 DB 26 LTGSPAINASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWIYDTSKLASGVPRPSG 85
 |||||
 QY 64 SSGSTYSGLTISRMEADATYTCQOWSSNPLTFGSGTKLELKR 107
 |||||
 DB 86 SSGSTYSGLTISRMEADATYTCQOWSSNPLTFGAGTKLELKR 129
 |||||

RESULT 5

KY6F_MOUSE
 ID KY6F_MOUSE STANDARD; PRT; 107 AA.

AC P04940;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-VI region NQ2-17.4.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Marham A.F., Mistein C.;
 RT "mRNA sequences define an unusually restricted IGF response to 2-
 phenylloxazalone and its early diversification";
 RL Nature 304:320-324 (1983).
 CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL: K00735; AAA38680.1; -, mRNA.
 DR HSSP: P04940; 1-107.
 DR Ensemble: ENSMUSG0000062047; Mus musculus.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.

FT REGION 88 96 Complementarity-determining-3.
 FT REGION 97 106 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON TER 107 107
 SO SEQUENCE 107 AA; 11561 MW; 6F694284BCFA68B6 CRC64;

Query Match 84.3%; Score 466; DB 1; Length 107;
 Best Local Similarity 85.6%; Pred. No. 9.2e-33;
 Matches 89; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 LTGSPAINASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPRPSG 63
 |||||
 DB 4 LTGSPAINASPGKVTTCSSASSSVSYMYWYQOKSGSPKRWIYDTSKLASGVPRPSG 63
 |||||
 QY 64 SSGSTYSGLTISRMEADATYTCQOWSSNPLTFGSGTKLELKR 107
 |||||
 DB 64 SSGSTYSGLTISRMEADATYTCQOWSSNPLTFGAGTKLELKR 107
 |||||

RESULT 6

OBK1F3_MOUSE
 ID OBK1F3_MOUSE PRELIMINARY; PRT; 112 AA.

AC O8K1F3;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region. (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Terrynck T., Avrameas S.;
 RT "Two murine natural polyclonal reactive autoantibodies are encoded by
 RT nonmutated germ-line genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
 RA Tillman D.M., You N.T., Hill R.J., Marich T.N.;
 RT "Both Igm and Igg anti-DNA antibodies are the products of clonally
 RT selective B cell stimulation in (NZB x NZW) F1 mice.";

RL J. Exp. Med. 176:761-779 (1992).
 DR EMBL: AF516282; AAM64200.1; -, Genomic_DNA.
 DR PIR: A33933; A33933.
 DR PIR: PH1085; PH1085.
 DR HSSP: P01837; 25C8.
 DR SMR: Q8K1F3; 2-112.
 DR Ensemble: ENSMUSG0000063156; Mus musculus.
 DR InterPro: IPR007110; IG_1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON TER 1 1
 FT NON TER 112 112
 FT NON TER 112 112
 SO SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 83.7%; Score 463; DB 2; Length 112;
 Best Local Similarity 85.0%; Pred. No. 1.9e-38;
 Matches 91; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 DTELTPAINASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLASGVPR 60
 |||||
 DB 1 DVLTPAINASPGKVTTCSSASSSVSYMYWYQOKPGSSPKRWIYDTSNLASGVPR 60
 |||||

Qy 61 FSGSGSGTSTSLTISRMEADDAATYYCOQWSSNPLTFGSGTKLELR 107
 |||||
 Db 61 FSGSGSGTSTSLTISRMEADDAATYYCOQWSSNPLTFGSGTKLELR 107

RESULT 7

KV6I MOUSE

ID KV6I MOUSE STANDARD; PRT; 107 AA.

AC P04943;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG kappa chain V-VI region NQ6-8.3.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."
 RL Nature 304:320-324(1983).
 CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.

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CC -----
 CC EMBL, K00740; AAA38685.1; -; mRNA.
 DR HSSP; P01679; ZPBJ.
 DR SMR; P04943; 1-107.
 DR Ensembl; ENSMUSG0000062047; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE, 1.
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 96 Complementarity-determining-3.
 FT REGION 97 106 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11573 MW; 66948248FCFC86 CRC64;

Query Match 83.4%; Score 461; DB 1; Length 107;
 Best Local Similarity 84.6%; Pred. No. 2.9e-38;
 Matches 88; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 4 LTGSPALMSAPGKVTTCGASSSVSYMYWYQKQKSSPRLLYDTSNLASGVPRFSG 63
 |||||
 Db 4 LTGSPALMSAPGKVTTCGASSSVSYMYWYQKQKSSPRLLYDTSNLASGVPRFSG 63

Qy 64 SSGSGTSTSLTISRMEADDAATYYCOQWSSNPLTFGSGTKLELR 107
 |||||
 Db 64 SSGSGTSTSLTISRMEADDAATYYCOQWSSNPLTFGSGTKLELR 107

RESULT 8

KV6G MOUSE

ID KV6G MOUSE STANDARD; PRT; 107 AA.

AC P04941;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE IG kappa chain V-VI region NQ2-48.2.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."
 RL Nature 304:320-324(1983).
 CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.

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CC -----
 CC EMBL, K00737; AAA38682.1; -; mRNA.
 DR HSSP; Q91W12; IAYI.
 DR SMR; P04941; 1-103.
 DR Ensembl; ENSMUSG0000062047; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE, 1.
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 96 Complementarity-determining-3.
 FT REGION 97 106 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON TER 107
 SQ SEQUENCE 107 AA; 11557 MW; 72488DA9BF54934 CRC64;

Query Match 83.2%; Score 460; DB 1; Length 107;
 Best Local Similarity 84.6%; Pred. No. 3.7e-38;
 Matches 88; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 4 LTGSPALMSAPGKVTTCGASSSVSYMYWYQKQKSSPRLLYDTSNLASGVPRFSG 63
 |||||
 Db 4 LTGSPALMSAPGKVTTCGASSSVSYMYWYQKQKSSPRLLYDTSNLASGVPRFSG 63

Qy 64 SSGSGTSTSLTISRMEADDAATYYCOQWSSNPLTFGSGTKLELR 107
 |||||
 Db 64 SSGSGTSTSLTISRMEADDAATYYCOQWSSNPLTFGSGTKLELR 107

RESULT 9

KV6H MOUSE

ID KV6H MOUSE STANDARD; PRT; 107 AA.

AC P04942;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG kappa chain V-VI region NQ5-61.1.2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone and its early diversification."

RL Nature 304:320-324(1983).
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; K00739; AAA8684.1; -; mRNA.
 DR HSP; P01679; 2PB1.
 DR SMR; P04942; 1-107.
 DR Ensembl; ENSMUSG0000062047; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IG_v.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Hydroloma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 96 Complementarity-determining-3.
 FT REGION 97 106 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11605 MW; CA6C484B0CFB550 CRC64;
 Query Match 83.2%; Score 460; DB 1; Length 107;
 Best Local Similarity 84.6%; Pred. No. 3.7e-38;
 Matches 88; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 Oy 4 LTGSPAIMSAPGKVTTCSSASSSVSYMYVYQKPSPPRLIYDTSNLSGVPRFSG 63
 Db 4 LTGSPAIMSAPGKVTTCSSASSSVSYMYVYQKPSPPRLIYDTSNLSGVPRFSG 63
 Oy 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107
 Db 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107
 RESULT 10
 KV6J MOUSE STANDARD; PRT; 107 AA.
 ID_KV6J_MOUSE
 AC P04944; 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE IG kappa chain V-VI region NQ5-78.2.6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.W., Martham A.P., Milstein C.;
 RA "mRNA sequences define an unusually restricted IgG response to 2-
 RA phenyloxazolone and its early diversification".
 RT Nature 304:320-324(1983).
 RL Nature 304:320-324(1983).
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; K00744; AAA8689.1; -; mRNA.
 DR HSP; Q91W12; IAY1.
 DR SMR; P04944; 1-106.

DR Ensembl; ENSMUSG0000062047; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IG_v.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Hydroloma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 96 Complementarity-determining-3.
 FT REGION 97 106 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11613 MW; A38290781F3C30D3 CRC64;
 Query Match 83.2%; Score 460; DB 1; Length 107;
 Best Local Similarity 84.6%; Pred. No. 3.7e-38;
 Matches 88; Conservative 6; Mismatches 10; Indels 0; Gaps 0;
 Oy 4 LTGSPAIMSAPGKVTTCSSASSSVSYMYVYQKPSPPRLIYDTSNLSGVPRFSG 63
 Db 4 LTGSPAIMSAPGKVTTCSSASSSVSYMYVYQKPSPPRLIYDTSNLSGVPRFSG 63
 Oy 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107
 Db 64 SSGSTSYSLTISRMEDADATYTCQOWSNPLTFGSGTKLELR 107
 RESULT 11
 Q5XF8_MOUSE PRELIMINARY; PRT; 235 AA.
 ID_Q5XF8_MOUSE
 AC Q5XF8; 25-OCT-2004 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=FVB/N; TISSUE=Colon;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max 9.I., Wang J., Hsieh F.,
 RA Ditchenko L., Mardina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitsuki S., Carrin P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Aramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodigues A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Butlerfield Y.S.N., Krzyzinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [2]
 CC NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RA Director MGC Project;
 RL Submitted (OCT-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC084683; AAA8683.1; -; mRNA.

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DR   SMR; Q5XFY8; 23-235.
DR   GO: 0003823; F: antigen binding; IEA.
DR   InterPro; IPR003599; IG.
DR   InterPro; IPR007110; IG_1like.
DR   InterPro; IPR003597; IG_cl.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR003596; IG_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGcl; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM   Hypothetical protein.
SQ   SEQUENCE 235 AA; 25835 MM; 828EBD277FDC667 CRC64;

Query Match      82.6%; Score 457; DB 2; Length 235;
Best Local Similarity 83.7%; Pred. No. 1.9e-37;
Matches 87; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSSPRLIYDTSNLASGVPRFSG 63
DB 26 LTOSPALISGPGKVTTCSSASSSVYMWYQOKPGSSPSPWYATSKLASGVPRFSG 85

64 SGGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
DB 86 SGGSTSYSLTISRMEADATYYCOQWSSNPLTFGAGTRLELR 129

RESULT 12
Q8K1F0 MOUSE PRELIMINARY; PRT; 112 AA.
ID O8K1F0
AC O8K1F0
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RN 2
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyelective autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AF516285; AAM64203.1; -, Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSP; P01837; IOR0.
DR SMK; Q8K1F0; 3-112.
DR Ensemble; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11901 MM; F6644663201AA239 CRC64;

Query Match      82.5%; Score 456; DB 2; Length 112;
Best Local Similarity 84.6%; Pred. No. 9.8e-38;
Matches 88; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSSPRLIYDTSNLASGVPRFSG 63

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DB 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSTSPKRWIYDTSKLASGVPRFSG 63
QY 64 SGGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
DB 64 SGGSTSYSLTISRMEADATYYCOQWSSNPLTFGGTKLELR 107

RESULT 13
O8VDD0 MOUSE PRELIMINARY; PRT; 134 AA.
ID O8VDD0
AC O8VDD0
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-MOG z12 variable light chain (Fragment).
OS Name=Gm1502; Synonyms=anti-MOG kappa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Sembel P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN 2
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Chernajovsky Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN 3
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2427335;
RA Caton A.v., Brownlee G.G., Staudt L.M., Gerhard W.;
RT "Structural and functional implications of a restricted antibody
RT response to a defined antigenic region on the influenza virus
RT haemagglutinin.";
RL EMBO J. 5:1577-1587(1986).
DR EMBL; A016331; CAC94866.1; -, mRNA.
DR PIR; G27887; G27887.
DR HSP; P01834; IMIM.
DR SMK; Q8VDD0; 23-134.
DR Ensemble; ENSMUSG0000062047; Mus musculus.
DR MGI; MGI:2686348; Gm1502.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 134
FT NON_TER 134
SQ SEQUENCE 134 AA; 14525 MM; CDF8E2236E2D0CF CRC64;

Query Match      81.7%; Score 452; DB 2; Length 134;
Best Local Similarity 84.6%; Pred. No. 3e-37;
Matches 88; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 LTOSPAIMASPGKVTTCSSASSSVSYMWYQOKPGSSPRLIYDTSNLASGVPRFSG 63
DB 26 LTOSPALISGPGKVTTCSSASSSVYMWYQOKPGSTSPKRWIYDTSKLASGVPRFSG 85

64 SGGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
DB 86 SGGSTSYSLTISRMEADATYYCHGRSSVPMWFGGTKLELR 129

RESULT 14
O8I1C3 MOUSE PRELIMINARY; PRT; 131 AA.
ID O8I1C3
AC O8I1C3
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

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DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MRL/MpJ-1pr/1pr; TISSUE=Spleen;
RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;
RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephriticgenic monoclonal
RL antibodies derived from an MRL/lpr lupus mouse.";
RL Mol. Immunol. 30:177-182(1993).
DR EMBL; D14629; BAA03482.1; -; mRNA.
DR HSSP; P01679; 2PRJ
DR SMART; Q811C3; 23-131.
DR Ensemble; ENSMUSG0000058987; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Signal.
FT CHAIN 23 >131 Potential.
FT NON TER 131 Immunoglobulin gamma-3 kappa chain.
SQ SEQUENCE 131 AA; 14083 MW; 5E8365695466E98 CRC64;

Query Match 80.2%; Score 443.5; DB 2; Length 131;
Best Local Similarity 84.0%; Pred. No. 2,1e-36;
Matches 89; Conservative 8; Mismatches 6; Indels 3; Gaps 2;

QY 4 LTQSPALMSASPGKVTTCASASSV--SYWYWOQKPGSSPRLTIYDTSNLASGVPRF 61
DB 26 LTQSPALMSASPGKVTTCASASSVSSSYLHWYQKSGASPKLWYTSNLASGVPRF 85
QY 62 SSGSGSGTSTSLTISRMEADATATYCCQWSSNP-LTFGSGTLELR 106
DB 86 SSGSGSGTSTSLTISRMEADATATYCCQYHSPRTFGGTYLELR 131

RESULT 15
Q8K1F1 MOUSE PRELIMINARY; PRT; 114 AA.
AC Q8K1F1_
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Tsuchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RN (2)
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RL nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN (3)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA Tillman D.W., Jon N.T., Hill R.J., Marion T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RL selective B cell stimulation in (NZB x NZM)F1 mice.";
RL J. Exp. Med. 176:761-779(1992).

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DR EMBL; AF516284; AAM64202.1; -; Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PH1058; PH1058.
DR HSSP; P01837; 25C8.
DR SMART; Q8K1F1; 2-114.
DR Ensemble; ENSMUSG0000059896; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1 1
FT NON TER 114 114
SQ SEQUENCE 114 AA; 12163 MW; 8BD9833DBF3EFPD1 CRC64;

Query Match 79.6%; Score 440; DB 2; Length 114;
Best Local Similarity 80.7%; Pred. No. 4e-36;
Matches 88; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 DTELTQSPALMSASPGKVTTCASASSV--SYWYWOQKPGSSPRLTIYDTSNLASGV 58
DB 1 DIVLTQSPALMSASPGKVTTCASASSVSSSYLHWYQKSGASPKLWYTSNLASGV 60
QY 59 VRFSGSGSGTSTSLTISRMEADATATYCCQWSSNP-LTFGSGTLELR 107
DB 61 ARFSGSGSGTSTSLTISRMEADATATYCCQYHSPRTFGGTYLELR 109

Search completed: November 21, 2005, 12:04:05
Job time : 159.344 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 / Search time 40.37 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-87
Perfect score: 553
Sequence: 1 DTETLQSPAIMSAPGHEKVT.....QWSSNPLRTGGTKELKLR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCpus_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	506	91.5	244	1	US-08-553-497A-20 Sequence 20, Appl
2	505	91.3	242	1	US-08-553-497A-28 Sequence 28, Appl
3	502	90.8	128	1	US-07-946-421-26 Sequence 26, Appl
4	501	90.6	106	1	US-07-634-278-58 Sequence 58, Appl
5	501	90.6	106	1	US-08-477-728-58 Sequence 58, Appl
6	501	90.6	106	1	US-08-474-040-58 Sequence 58, Appl
7	501	90.6	106	1	US-08-487-200-58 Sequence 58, Appl
8	501	90.6	106	2	US-08-484-537-58 Sequence 58, Appl
9	501	90.6	128	1	US-07-634-278-31 Sequence 31, Appl
10	501	90.6	128	1	US-08-477-728-31 Sequence 31, Appl
11	501	90.6	128	1	US-08-474-040-31 Sequence 31, Appl
12	501	90.6	128	1	US-08-487-200-31 Sequence 31, Appl
13	501	90.6	128	2	US-08-484-537-31 Sequence 31, Appl
14	499	90.2	242	1	US-08-553-497A-26 Sequence 26, Appl
15	496	89.7	246	1	US-08-553-497A-24 Sequence 24, Appl
16	490.5	88.7	108	2	US-09-232-290-2 Sequence 2, Appl
17	489	88.4	108	2	US-09-126-219A-243 Sequence 243, App
18	489	88.4	108	2	US-09-196-522-243 Sequence 243, App
19	488	88.2	244	1	US-08-553-497A-22 Sequence 22, Appl
20	485	87.7	108	2	US-09-126-219A-251 Sequence 251, App
21	485	87.7	108	2	US-09-196-522-251 Sequence 251, App
22	479	86.6	108	2	US-09-171-945-9 Sequence 9, Appl
23	479	86.6	108	2	US-09-910-059-9 Sequence 9, Appl
24	478	86.4	108	2	US-09-126-219A-253 Sequence 253, App
25	478	86.4	108	2	US-09-196-522-253 Sequence 253, App
26	477	86.3	106	2	US-09-198-689-8 Sequence 8, Appl
27	477	86.3	235	2	US-09-171-945-17 Sequence 17, Appl

28	477	86.3	235	2	US-09-910-039-17 Sequence 17, Appl
29	477	86.3	238	2	US-09-798-689-21 Sequence 21, Appl
30	475	85.9	107	1	US-08-211-202-3 Sequence 3, Appl
31	475	85.9	108	2	US-09-726-219A-241 Sequence 241, App
32	475	85.9	108	2	US-09-196-522-241 Sequence 241, App
33	475	85.9	128	2	US-08-619-491-2 Sequence 2, Appl
34	475	85.9	128	4	PCT-US95-07302-2 Sequence 57, Appl
35	475	85.9	246	1	US-08-469-486-57 Sequence 57, Appl
36	475	85.9	246	1	US-08-469-658-57 Sequence 8, Appl
37	475	85.9	255	2	US-09-553-498-8 Sequence 8, Appl
38	475	85.9	255	2	US-09-618-869-8 Sequence 2, Appl
39	475	85.9	270	1	US-08-652-507-2 Sequence 16, Appl
40	475	85.9	553	1	US-08-661-052-16 Sequence 16, Appl
41	475	85.9	553	2	US-09-188-082-16 Sequence 16, Appl
42	475	85.9	553	2	US-09-364-088-16 Sequence 16, Appl
43	475	85.9	553	2	US-09-102-716-16 Sequence 16, Appl
44	474	85.7	108	2	US-09-726-219A-240 Sequence 240, App
45	474	85.7	108	2	US-09-196-522-240 Sequence 240, App

ALIGNMENTS

RESULT 1
US-08-553-497A-20
Sequence 20, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSOW, DETLEF
APPLICANT: ADAM, JADME
APPLICANT: MITTAMS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIUTATS, JADME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
NUMBER OF SEQUENCES: 30
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANTIGAN, P. C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 91.5%; Score 506; DB 1; Length 244;
Best Local Similarity 92.6%; Pred. No. 6.6e-42;
Matches 100; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 1 DTETLQSPALMSASPEKRYTTTCSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 60
DB 137 DIELTQSPALMSASPEKRYTMTCSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 196

QY 61 FSGSGSGTSTSLTISRMEADATYYCOQMSNP--LTFSGTKLEIK 106
DB 197 FSGSGSGTSTSLTISRMEADATYYCOQMSNPMTTFGQTKLEIK 244

RESULT 2
US-08-553-497A-28
Sequence 28, Application US/08553497A
Patent No. 5844093

GENERAL INFORMATION:
APPLICANT: KETLEBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KATH H.
APPLICANT: GUSNOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESCA
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PUJOLIS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553.497A
FILING DATE: 17-NOV-1995

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-28

Query Match 91.3%; Score 505; DB 1; Length 242;
Best Local Similarity 92.5%; Pred. No. 8.2e-42;
Matches 98; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DTETLQSPALMSASPEKRYTTTCSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 60
DB 137 DIELTQSPALMSASPEKRYTMTCSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPR 196

QY 61 FSGSGSGTSTSLTISRMEADATYYCOQMSNP-LTFSGTKLEIK 106
DB 197 FSGSGSGTSTSLTISRMEADATYYCOQMSNP-LTFGQTKLEIK 242

RESULT 3
US-07-946-421-26
Sequence 26, Application US/07946421
Patent No. 555864

GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Ketleborough, Catherine A.
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: Humanized and Chimeric Monoclonal
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Miller, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Boulevard, Suite 1400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946.421
FILING DATE: 06-NOV-1992
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP92/00480
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 911933892
FILING DATE: 06-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana

REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Merck 1430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-07-946-421-26

Query Match 90.8%; Score 502; DB 1; Length 128;
Best Local Similarity 94.2%; Pred. No. 7.5e-42;
Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPALMSASPEKRYTTTCSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPRFSG 63
DB 26 LTQSPALMSASPEKRYTMTCSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPRFSG 85

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106
DB 86 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 128

RESULT 4
US-07-634-278-58
Sequence 58, Application US/07634278
Patent No. 5530101

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: SCHNEIDER, William P.

APPLICANT: LANDOLFI, Nicholas F.

APPLICANT: COELINGH, Kathleen L.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend Kourile and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/634,278

FILING DATE: 19-DEC-1990

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-634-278-58

Query Match 90.6%; Score 501; DB 1; Length 106;
Best Local Similarity 93.2%; Pred. No. 7,6e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPRFSG 63
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPRFSG 63

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106
DB 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106
DB 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106

RESULT 5

US-08-477-728-58
Sequence 58, Application US/08477728
Patent No. 5585089

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: SCHNEIDER, William P.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,728

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-002600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-477-728-58

Query Match 90.6%; Score 501; DB 1; Length 106;
Best Local Similarity 93.2%; Pred. No. 7,6e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPRFSG 63
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYWYQQRGSSPRLLIYDTSNLASGVPRFSG 63

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106
DB 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106
DB 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106
DB 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106

QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106
DB 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIK 106

RESULT 6

US-08-474-040-58
Sequence 58, Application US/08474040
Patent No. 5693761

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung

APPLICANT: QUEEN, Cary L.

APPLICANT: CO, Man Sung


```
ADDRESSER: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-58

Query Match          90.6%; Score 501; DB 2; Length 106;
Best Local Similarity 93.2%; Pred. No. 7,6e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASGPERVTTTCSASSSVSYMYTQOKPGSSPRLIYDTSNLSAGVVRFSG 63
DB 4 LTGSPAIMSASGPERVTTTCSASSSVSYMYTQOKPGSSPRLIYDTSNLSAGVVRFSG 63
QY 64 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 106
DB 64 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 106

RESULT 9
US-07-634-278-31
Sequence 31, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
```

```
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-31

Query Match          90.6%; Score 501; DB 1; Length 128;
Best Local Similarity 93.2%; Pred. No. 9,5e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTGSPAIMSASGPERVTTTCSASSSVSYMYTQOKPGSSPRLIYDTSNLSAGVVRFSG 63
DB 26 LTGSPAIMSASGPERVTTTCSASSSVSYMYTQOKPGSSPRLIYDTSNLSAGVVRFSG 85
QY 64 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 106
DB 86 SSGGTSYSLTISRMEADATYTCOOMSSNPLTFGSGTGLBLK 128

RESULT 10
US-08-477-728-31
Sequence 31, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
```

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-728-31

Query Match 90.6%; Score 501; DB 1; Length 128;
Best Local Similarity 93.2%; Pred. No. 9.5e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTOSPAIMASPEKVTTCSSASSVSVMYQOQKPGSSPRLITYDTSNLSAGVPVRFSG 63
DB 26 LTOSPAIMASPEKVTTCSSASSVSVMYQOQKPGSSPRLITYDTSNLSAGVPVRFSG 85

QY 64 SSGSTSYSLTISRMEADATYTCQOMSSNPLTFGSGTKLEK 106
DB 86 SSGSTSYSLTISRMEADATYTCQOMSTYPLTFGAGTKLEK 128

RESULT 11
US-08-474-040-31
Sequence 31, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: CORLINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-31

Query Match 90.6%; Score 501; DB 1; Length 128;
Best Local Similarity 93.2%; Pred. No. 9.5e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTOSPAIMASPEKVTTCSSASSVSVMYQOQKPGSSPRLITYDTSNLSAGVPVRFSG 63
DB 26 LTOSPAIMASPEKVTTCSSASSVSVMYQOQKPGSSPRLITYDTSNLSAGVPVRFSG 85

QY 64 SSGSTSYSLTISRMEADATYTCQOMSSNPLTFGSGTKLEK 106
DB 86 SSGSTSYSLTISRMEADATYTCQOMSTYPLTFGAGTKLEK 128

RESULT 12
US-08-487-200-31
Sequence 31, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: CORLINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-200-31

Query Match 90.6%; Score 501; DB 1; Length 128;
Best Local Similarity 93.2%; Pred. No. 9.5e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTGSPAIMSAPGKRVTTTCASASSVSMTYQOKPGSSPRLIYDTSNLASGVPRPSG 63
Db 26 LTGSPAIMSAPGKRVTTTCGSSSVSFMTYQOKPGSSPRLIYDTSNLASGVPRPSG 85

Qy 64 SGSGTYSILTISRMEADPAATYYCOQWSNPLTFGSGTKLELK 106
Db 86 SGSGTYSILTISRMEADPAATYYCOQWSNPLTFGAGTKLELK 128

RESULT 13
US-08-484-537-31
Sequence 31, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELING, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-537-31

Query Match 90.6%; Score 501; DB 2; Length 128;
Best Local Similarity 93.2%; Pred. No. 9.5e-42;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTGSPAIMSAPGKRVTTTCASASSVSMTYQOKPGSSPRLIYDTSNLASGVPRPSG 63
Db 26 LTGSPAIMSAPGKRVTTTCGSSSVSFMTYQOKPGSSPRLIYDTSNLASGVPRPSG 85

Qy 64 SGSGTYSILTISRMEADPAATYYCOQWSNPLTFGSGTKLELK 106
Db 86 SGSGTYSILTISRMEADPAATYYCOQWSNPLTFGAGTKLELK 128

RESULT 14
US-08-553-497A-26
Sequence 26, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBOUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSLOW, DETLEF
APPLICANT: ADAM, JADME
APPLICANT: MITDANS, FRANCESCA
APPLICANT: ROSELL, ELISABETH
APPLICANT: BLASCO, FRANCISCO
APPLICANT: PIULATS, JADME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANNIGAN, P. C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
US-08-553-497A-26

Query Match      90.2%; Score 499; DB 1; Length 242;
Best Local Similarity 91.5%; Pred. No. 3.2e-41;
Matches 97; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      1 DTELTPAISMASPERKVTTCSSASSSVSYMYTQOKPGSSPRLIYDTSNLSAGVPR 60
Db      137 DIELTQSPITMSASPERKVTMTCSASSSVSYMYTQOKTSSPRLIYDTSNLSAGVPR 196

Qy      61 FSGSGSGTSTSLTISRMEADATYYCOQMSNP-LTFSGGKLEIK 106
Db      197 FSGSGSGTSTSLTISRMEADATYYCOQMSNP-LTFGGTKLEIK 242
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RESULT 15
US-08-553-497A-24
; Sequence 24; Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSLOW, DETLEF
; APPLICANT: ADAM, JAUME
; APPLICANT: MITJANS, FRANCESCA
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PUJOLAS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLER, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD, SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 9410416.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
```

```

; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
US-08-553-497A-24

Query Match      89.7%; Score 496; DB 1; Length 246;
Best Local Similarity 90.7%; Pred. No. 6.3e-41;
Matches 98; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

Qy      1 DTELTPAISMASPERKVTTCSSASSSVSYMYTQOKPGSSPRLIYDTSNLSAGVPR 60
Db      139 DIELTQSPITMSASPERKVTMTCSASSSVSYMYTQOKPGSSPRLIYDTSNLSAGVPR 198

Qy      61 FSGSGSGTSTSLTISRMEADATYYCOQMSNP--LTFSGGKLEIK 106
Db      199 FSGSGSGTSTSLTISRMEADATYYCOQMSNP-LTFGGTKLEIK 246
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Search completed: November 21, 2005, 12:07:36
Job time : 41.37 secs

1 CURRENT FILING DATE: 1998-08-31
1 NUMBER OF SEQ ID NOS: 98
1 SOFTWARE: Patentin Ver. 2.0
1 SEQ ID NO 78
1 LENGTH: 107
1 TYPE: PRT
1 ORGANISM: Artificial Sequence
1 FEATURE:
1 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
1 OTHER INFORMATION: C1 region VL epitope 1
US-09-144-886-78

Query Match 94.8%; Score 524; DB 3; Length 107;
Best Local Similarity 95.3%; Pred. No. 2,7e-39;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DTBLTQSPAIMSAPGKRVTTTCASASSSVSYMYQOKPGSSPRLIYDTSNLAGVPR 60
Db 1 DIELTQSPAIMSAPGKRVTTTCASASSSVSYMYQOKPGSSPRLIYDTSNLAGVPR 60
Qy 61 FSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
Db 61 FSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGAGTKLELR 107

RESULT 3
US-09-144-886-90

1 Sequence 90, Application US/09144886
1 Patent No. US2002015114A1
1 GENERAL INFORMATION:
1 APPLICANT: Marks, James D
1 APPLICANT: Amersdorfer, Peter
1 TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
1 TITLE OF INVENTION: Botulinum Neurotoxins
1 FILE REFERENCE: 2500.117050
1 CURRENT APPLICATION NUMBER: US/09/144,886
1 CURRENT FILING DATE: 1998-08-31
1 NUMBER OF SEQ ID NOS: 98
1 SOFTWARE: Patentin Ver. 2.0
1 SEQ ID NO 90
1 LENGTH: 107
1 TYPE: PRT
1 ORGANISM: Artificial Sequence
1 FEATURE:
1 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
1 OTHER INFORMATION: 3F4 region VL epitope 2
US-09-144-886-90

Query Match 94.0%; Score 520; DB 3; Length 107;
Best Local Similarity 94.4%; Pred. No. 6,2e-39;
Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DTBLTQSPAIMSAPGKRVTTTCASASSSVSYMYQOKPGSSPRLIYDTSNLAGVPR 60
Db 1 DTELTPSPAIMSAPGKRVTTTCASASSSVSYMYQOKPGSSPRLIYDTSNLAGVPR 60
Qy 61 FSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
Db 61 FSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGAGTKLELR 107

RESULT 4
US-10-632-706-88

1 Sequence 88, Application US/10632706
1 Publication No. US20040175385A1
1 GENERAL INFORMATION:
1 APPLICANT: MARKS, JAMES D.
1 APPLICANT: AMERSDORFER, PETER
1 TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
1 TITLE OF INVENTION: NEUROTOXINS
1 FILE REFERENCE: 4077-895120US
1 CURRENT APPLICATION NUMBER: US/10/632,706
1 CURRENT FILING DATE: 2003-08-01

1 PRIOR APPLICATION NUMBER: US 60/400,721
1 PRIOR FILING DATE: 2002-08-01
1 PRIOR APPLICATION NUMBER: US 09/144,806
1 PRIOR FILING DATE: 1998-08-31
1 NUMBER OF SEQ ID NOS: 278
1 SOFTWARE: Patentin version 3.2
1 SEQ ID NO 88
1 LENGTH: 109
1 TYPE: PRT
1 ORGANISM: Artificial
1 FEATURE:
1 OTHER INFORMATION: single chain antibody
US-10-632-706-88

Query Match 93.7%; Score 518; DB 4; Length 109;
Best Local Similarity 94.5%; Pred. No. 9,5e-39;
Matches 103; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 DTBLTQSPAIMSAPGKRVTTTCASASSSV--SYMYQOKPGSSPRLIYDTSNLAGVPR 58
Db 1 DIELTQSPAIMSAPGKRVTTTCASASSSVSSYLGYQOKPGSSPRLIYDTSNLAGVPR 60
Qy 59 VRFSGSGGTSTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
Db 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 109

RESULT 5
US-10-632-706-75

1 Sequence 75, Application US/10632706
1 Publication No. US20040175385A1
1 GENERAL INFORMATION:
1 APPLICANT: MARKS, JAMES D.
1 APPLICANT: AMERSDORFER, PETER
1 TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
1 TITLE OF INVENTION: NEUROTOXINS
1 FILE REFERENCE: 4077-895120US
1 CURRENT APPLICATION NUMBER: US/10/632,706
1 CURRENT FILING DATE: 2003-08-01
1 PRIOR APPLICATION NUMBER: US 60/400,721
1 PRIOR FILING DATE: 2002-08-01
1 PRIOR APPLICATION NUMBER: US 09/144,806
1 PRIOR FILING DATE: 1998-08-31
1 NUMBER OF SEQ ID NOS: 278
1 SOFTWARE: Patentin version 3.2
1 SEQ ID NO 75
1 LENGTH: 107
1 TYPE: PRT
1 ORGANISM: Artificial
1 FEATURE:
1 OTHER INFORMATION: single chain antibody
US-10-632-706-75

Query Match 93.3%; Score 516; DB 4; Length 107;
Best Local Similarity 94.4%; Pred. No. 1,4e-38;
Matches 101; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DTBLTQSPAIMSAPGKRVTTTCASASSSVSYMYQOKPGSSPRLIYDTSNLAGVPR 60
Db 1 DIELTQSPAIMSAPGKRVTTTCASASSSVSYMYQOKPGSSPRLIYDTSNLAGVPR 60
Qy 61 FSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGSGTKLELR 107
Db 61 FSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFGAGTKLELR 107

RESULT 6
US-10-344-779-2

1 Sequence 2, Application US/10344779
1 Publication No. US20030211106A1
1 GENERAL INFORMATION:
1 APPLICANT: SWEET, RAYMOND W.
1 APPLICANT: TORNETTA, MARK A.

APPLICANT: TRUNER, ALEMESEGED
APPLICANT: WATTAM, TREVOR A.
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
FILE REFERENCE: G950033
CURRENT APPLICATION NUMBER: US/10/344,779
PRIOR FILING DATE: 2003-02-17
PRIOR APPLICATION NUMBER: PCT/US01/26161
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,524
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 60/230,639
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 129
TYPE: PRT
ORGANISM: Mus musculus
US-10-344-779-2

Query Match 93.3%; Score 516; DB 4; Length 129;
Best Local Similarity 96.2%; Pred. No. 1.7e-38;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSAPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63
Db 4 LTQSPAIMSAPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63

Qy 64 SSGSGTSYSLTISRMEADPAATYYCCQMSNPITFGSGTKLEIKR 107
Db 64 SSGSGTSYSLTISRMEADPAATYYCCQMSNPITFGSGTKLEIKR 107

RESULT 7
US-10-738-809-2

Sequence 2, Application US/10738809
Publication No. US20040171117A1
GENERAL INFORMATION:
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TORNETTA, MARK A.
APPLICANT: TRUNER, ALEMESEGED
APPLICANT: WATTAM, TREVOR A.
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
FILE REFERENCE: G950033
CURRENT APPLICATION NUMBER: US/10/738,809
PRIOR FILING DATE: 2003-12-17
PRIOR APPLICATION NUMBER: US/10/344,779
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/US01/26161
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,524
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 60/230,639
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 129
TYPE: PRT
ORGANISM: Mus musculus
US-10-738-809-2

Query Match 93.3%; Score 516; DB 4; Length 129;
Best Local Similarity 96.2%; Pred. No. 1.7e-38;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTQSPAIMSAPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63
Db 4 LTQSPAIMSAPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPRFSG 63

Qy 64 SSGSGTSYSLTISRMEADPAATYYCCQMSNPITFGSGTKLEIKR 107

Db 64 SSGSGTSYSLTISRMEADPAATYYCCQMSNPITFGSGTKLEIKR 107

RESULT 8
US-10-895-135-46
Sequence 46, Application US/10895135
Publication No. US20050123549A1
GENERAL INFORMATION:
APPLICANT: Immunogen, Inc.
APPLICANT: PAYNE, Gillian
APPLICANT: CHUN, Philip
APPLICANT: TAYARS, Daniel
TITLE OF INVENTION: A C6 ANTIGEN-SPECIFIC CYTOTOXIC CONJUGATE AND METHODS OF USING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: A8621
CURRENT APPLICATION NUMBER: US/10/895,135
PRIOR FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: 60/488,447
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
US-10-895-135-46

Query Match 93.1%; Score 515; DB 5; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.7e-36;
Matches 98; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DTBLTQSPAIMSAPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPR 60
Db 1 DTBLTQSPAIMSAPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPR 60

Qy 61 FSSGSGTSYSLTISRMEADPAATYYCCQMSNPITFGSGTKLEIKR 107
Db 61 FSSGSGTSYSLTISRMEADPAATYYCCQMSNPITFGSGTKLEIKR 107

RESULT 9
US-09-144-886-75
Sequence 75, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 75
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: C15 region VL epitope 1
US-09-144-886-75

Query Match 92.9%; Score 514; DB 3; Length 107;
Best Local Similarity 92.5%; Pred. No. 2.1e-36;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DTBLTQSPAIMSAPGKVTTCSSASSSVSYMYWYQKPGSSPRLIYDTSNLASGVPR 60
Db 1 DTBLTQSPAIMSAPGKVTTCSSASSSVSHMYWYQKPGSSPRLIYDTSNLASGVPR 60

Qy 61 FSSGSGTSYSLTISRMEADPAATYYCCQMSNPITFGSGTKLEIKR 107

Db 61 FSGSGGTSYSLTISRMEADSAITYYCOQMSYPTFGSGTKLEIKR 107

RESULT 10
US-10-632-706-72
Sequence 72, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 72
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody
US-10-632-706-72

Query Match 91.5%; Score 506; DB 4; Length 107;
Best Local Similarity 91.6%; Pred. No. 1.1e-37;
Matches 98; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 DTELTPAISMASPEKXTTTCASASSSVYMTWYQKPPSSPRLIYDTSNLSAGVPVR 60
DB 1 DTELTPAISMASPEKXTTTCASASSSVYMTWYQKPPSSPRLIYDTSNLSAGVPVR 60
QY 61 FSGSGGTSYSLTISRMEADSAITYYCOQMSYPTFGSGTKLEIKR 107
DB 61 FSGSGGTSYSLTISRMEADSAITYYCOQMSYPTFGSGTKLEIKR 107

RESULT 11
US-10-468-370-643
Sequence 643, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Carr, Francis J.
APPLICANT: Jones, Tim
APPLICANT: Carter, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
APPLICANT: Hanlon, Marian
APPLICANT: Mackins, John
APPLICANT: Baker, Matthew
APPLICANT: May, Jeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REFERENCE: MER-118
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: BP 01103955.9
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: BP 01108291.4
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: PCT/EP02/01690
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 643
LENGTH: 106

TYPE: PRT
ORGANISM: Mus Musculus
US-10-468-370-643

Query Match 90.8%; Score 502; DB 4; Length 106;
Best Local Similarity 94.2%; Pred. No. 2.5e-37;
Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTOSPAISMASPEKXTTTCASASSSVYMTWYQKPPSSPRLIYDTSNLSAGVPVRFSG 63
DB 4 LTOSPAISMASPEKXTTTCASASSSVYMTWYQKPPSSPRLIYDTSNLSAGVPVRFSG 63
QY 64 SSGSGTSYSLTISRMEADSAITYYCOQMSYPTFGSGTKLEIKR 106
DB 64 SSGSGTSYSLTISRMEADSAITYYCOQMSYPTFGSGTKLEIKR 106

RESULT 12
US-10-468-528-2
Sequence 2, Application US/10468528
Publication No. US20040096442A1
GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
TITLE OF INVENTION: MODIFIED ANTI-BGFR ANTIBODIES WITH
TITLE OF INVENTION: REDUCED IMMUNOGENICITY
FILE REFERENCE: MER-116
CURRENT APPLICATION NUMBER: US/10/468,528
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: BP 01103954.2
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: PCT/EP02/01687
PRIOR FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antibody fragment
US-10-468-528-2

Query Match 90.8%; Score 502; DB 4; Length 106;
Best Local Similarity 94.2%; Pred. No. 2.5e-37;
Matches 97; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTOSPAISMASPEKXTTTCASASSSVYMTWYQKPPSSPRLIYDTSNLSAGVPVRFSG 63
DB 4 LTOSPAISMASPEKXTTTCASASSSVYMTWYQKPPSSPRLIYDTSNLSAGVPVRFSG 63
QY 64 SSGSGTSYSLTISRMEADSAITYYCOQMSYPTFGSGTKLEIKR 106
DB 64 SSGSGTSYSLTISRMEADSAITYYCOQMSYPTFGSGTKLEIKR 106

RESULT 13
US-10-389-155-17
Sequence 17, Application US/10389155
Publication No. US20030229208A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
APPLICANT: Co, Man Sung
APPLICANT: Schneider, William P.
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Coalingh, Kathleen L.
APPLICANT: Selick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,155
FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-389-155-17

Query Match 90.6%; Score 501; DB 4; Length 106;
Best Local Similarity 93.2%; Pred. No. 3,1e-37;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLLIYDTSNLTASGVPRFSG 63
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLLIYDTSNLTASGVPRFSG 63

QY 64 SSGSGTSLTISRMEADATYYCCQWSSNPITFGSGTKLEIK 106
DB 64 SSGSGTSLTISRMEADATYYCCQWSTYPLTFAGTKLEIK 106

RESULT 14
US-10-389-417-17
Sequence 17, Application US/10389417
Publication No. US20040049014A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
Co. Man Sung
Schneider, William P.
Landolfi, Nicholas F.
Coeligh, Kathleen L.
Selick, Harold B.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/389,417
FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/325,000
FILING DATE: 01-JUN-1999
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 08/484,537
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-389-417-17

Query Match 90.6%; Score 501; DB 4; Length 106;
Best Local Similarity 93.2%; Pred. No. 3,1e-37;
Matches 96; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLLIYDTSNLTASGVPRFSG 63
DB 4 LTQSPAINASPGKVTTCSSASSSVSYMYTQOKRGSSPRLLIYDTSNLTASGVPRFSG 63

QY 64 SSGSGTSLTISRMEADATYYCCQWSSNPITFGSGTKLEIK 106
DB 64 SSGSGTSLTISRMEADATYYCCQWSTYPLTFAGTKLEIK 106

RESULT 15
US-10-452-357-58
Sequence 58, Application US/10452357
Publication No. US20040058414A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary
Co. Man Sung
Schneider, William
Landolfi, Nicholas
Coeligh, Kathleen
Selick, Harold
TITLE OF INVENTION: Improved Humanized Immunoglobulins
FILE REFERENCE: 05882,0078,CNUS01
CURRENT APPLICATION NUMBER: US/10/452,357
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: 09/718,993
PRIOR FILING DATE: 2000-11-22

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? PRIOR APPLICATION NUMBER: 09/487,200
? PRIOR FILING DATE: 1995-06-07
? PRIOR APPLICATION NUMBER: 07/634,278
? PRIOR FILING DATE: 1990-12-19
? PRIOR APPLICATION NUMBER: 07/590,275
? PRIOR FILING DATE: 1990-09-28
? PRIOR APPLICATION NUMBER: 07/310,252
? PRIOR FILING DATE: 1989-02-13
? PRIOR APPLICATION NUMBER: 07/290,975
? PRIOR FILING DATE: 1988-12-28
? NUMBER OF SEQ ID NOS: 113
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 58
? LENGTH: 106
? TYPE: PR1
? ORGANISM: Artificial
? FEATURES:
? OTHER INFORMATION: murine m1k-1 beta 1 light chain antibody
? US-10-452-357-58

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Query Match	90.6%	Score 501	DB 4	Length 106
Best Local Similarity	93.2%	Pred. NO. 3.1e-37		
Matches 96	Conservative 4	Mismatches 3	Indels 0	Gaps 0

QY	DB
64	4
SGSGTSTSLTISRMBADATYYCOOMSSNPLTFGSGTKLEK	LTPSPALMSASPGKATVITTCASASSSYMMWYCOOKPSSSRLLIYDPSNLASGVPFRSG
106	63
SGSGTSTSLTISRMBADATYYCOOMSTVPLFGAATKLEK	LTPSPALMSASPGKATVITTCGSSSYVFMWYCOORPSSSRLLIYDPSNLASGVPFRSG
106	63

Search completed: November 21, 2005, 12:33:34
Job time : 133.476 secs

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: November 21, 2005, 12:04:27 ; Search time 1.95971 Seconds
(without alignments)
61.686 Million cell updates/sec

Title: US-10-632-706-87
Perfect score: 553
Sequence: 1 DTELQSPALMSASGPKVKT.....QQWSSNPLTFSGGTLELR 107

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	447	80.8	248 1	US-10-512-184-36 Sequence 36, Appl
2	447	80.8	615 1	US-10-512-184-50 Sequence 50, Appl
3	435	78.7	106 7	US-11-174-186-1 Sequence 1, Appl
4	427	77.2	106 7	US-11-174-186-1 Sequence 8, Appl
5	426	77.0	213 7	US-11-172-320-4 Sequence 4, Appl
6	424	76.7	213 7	US-11-174-186-42 Sequence 42, Appl
7	419	75.8	106 7	US-11-174-186-9 Sequence 9, Appl
8	416	75.2	213 7	US-11-172-320-8 Sequence 8, Appl
9	409	74.0	106 7	US-11-174-186-7 Sequence 7, Appl
10	409	74.0	106 7	US-11-174-186-16 Sequence 16, Appl
11	407	73.6	106 7	US-11-174-186-15 Sequence 15, Appl
12	394	71.2	106 7	US-11-174-186-10 Sequence 10, Appl
13	394	71.2	106 7	US-11-174-186-14 Sequence 14, Appl
14	392	70.9	106 7	US-11-174-186-12 Sequence 12, Appl
15	392	70.9	106 7	US-11-174-186-13 Sequence 13, Appl
16	388	70.2	106 7	US-11-174-186-11 Sequence 11, Appl
17	377.5	68.3	128 1	US-10-721-763-31 Sequence 31, Appl
18	375	67.8	106 7	US-11-174-186-5 Sequence 5, Appl
19	370.5	67.0	110 1	US-10-648-816-5 Sequence 5, Appl
20	369.5	66.8	129 1	US-10-721-763-19 Sequence 19, Appl
21	368.5	66.6	110 1	US-10-648-816-1 Sequence 1, Appl
22	366.5	66.3	543 1	US-10-495-664-3 Sequence 3, Appl
23	365.5	66.1	131 1	US-10-721-763-27 Sequence 27, Appl
24	363.5	65.7	129 1	US-10-721-763-23 Sequence 23, Appl
25	360.5	65.2	110 1	US-10-648-816-2 Sequence 2, Appl

26	360.5	65.2	110 1	US-10-648-816-3 Sequence 3, Appl
27	360.5	65.2	110 1	US-10-648-816-4 Sequence 4, Appl
28	360.5	65.2	110 1	US-10-648-816-6 Sequence 6, Appl
29	360.5	65.2	110 1	US-10-648-816-7 Sequence 7, Appl
30	360.5	65.2	110 1	US-10-648-816-8 Sequence 8, Appl
31	349.5	63.2	111 7	US-11-077-978-1 Sequence 31, Appl
32	342.5	61.9	259 1	US-10-512-184-31 Sequence 68, Appl
33	342.5	61.9	329 1	US-10-512-184-58 Sequence 29, Appl
34	340.5	61.6	263 1	US-10-512-184-29 Sequence 47, Appl
35	337.5	61.0	126 1	US-10-839-799-47 Sequence 65, Appl
36	337.5	61.0	126 1	US-10-839-799-65 Sequence 85, Appl
37	337.5	61.0	236 7	US-11-144-248-48 Sequence 35, Appl
38	335.5	60.8	126 1	US-10-839-799-85 Sequence 3, Appl
39	335.5	60.7	127 1	US-10-721-763-35 Sequence 43, Appl
40	334	60.4	106 7	US-11-174-186-3 Sequence 53, Appl
41	333.5	60.3	126 1	US-10-839-799-53 Sequence 52, Appl
42	333.5	60.3	126 7	US-11-144-248-52 Sequence 33, Appl
43	333.5	60.3	259 1	US-10-512-184-33 Sequence 70, Appl
44	333.5	60.3	329 1	US-10-512-184-70
45	333.5	60.3		

ALIGNMENTS

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RESULT 1
US-10-512-184-36
Sequence 36, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Praunhofer Geseellschaft zur F"orderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant plant disease
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv S52 with
OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match      80.8%; Score 447; DB 1; Length 248;
Best Local Similarity 81.3%; Pred. No. 8.9e-23;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DTELQSPALMSASGPKVKTTCSSASSSVYMYWTQOKGSSPRLIYDTNMLASGVPR 60
DB 141 DTVLQSPVINSASGPKVKTTCSSASSSVYMYWTQOKGSSPRLIYDTNMLASGVPR 200
QY 61 FSGSSGTSYSLTISRMEADATYTCQWSSNPLTFSGGTLELR 107
DB 201 FSGSSGTSYSLTISRMEADATYTCQWSSNPLTFSGGTLELR 247

RESULT 2
US-10-512-184-50
Sequence 50, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Geseellschaft zur F"orderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184

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/ CURRENT FILING DATE: 2004-10-22
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 615
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: fusion protein
/ OTHER INFORMATION: comprising the leader peptide - chitinase - linker
US-10-512-184-50

Query Match      80.8%; Score 447; DB 1; Length 615;
Best Local Similarity 81.3%; Pred. No. 1,8e-22;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

Cy 1 DTBLTSPAIMSASPGKRYTTTCSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPVRFSG 60
Db 482 DIVLFGSPVIMSASPGKRYTTTCSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPVRFSG 541
Cy 61 SSGSGTSLTISRMEADATYTCQWSSNPLTFGSGTKLEIKR 107
Db 542 SSGSGTSLTISRMEADATYTCQWSSNPLTFGAGTKLEIKR 588

RESULT 3
US-11-174-186-1
/ Sequence 1, Application US/11174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 1
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: KS VK mouse
US-11-174-186-1

Query Match      78.7%; Score 435; DB 7; Length 106;
Best Local Similarity 83.5%; Pred. No. 2,6e-22;
Matches 86; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

Cy 4 LTGSPAIMSASPGKRYTTTCSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPVRFSG 63
Db 4 LTGSPAIMSASPGKRYTTTCSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPVRFSG 63
Cy 64 SSGGTSLTISRMEADATYTCQWSSNPLTFGSGTKLEIK 106
Db 64 SSGGTSLTISRMEADATYTCQWSSNPLTFGSGTKLEIK 106

RESULT 4
US-11-174-186-8
/ Sequence 8, Application US/11174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
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/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: Patent version 3.3
/ SEQ ID NO 8
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: VK7 light chain
US-11-174-186-8

Query Match      77.2%; Score 427; DB 7; Length 106;
Best Local Similarity 81.6%; Pred. No. 8e-22;
Matches 84; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Cy 4 LTGSPAIMSASPGKRYTTTCSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPVRFSG 63
Db 4 LTGSPAIMSASPGKRYTTTCSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPVRFSG 63
Cy 64 SSGGTSLTISRMEADATYTCQWSSNPLTFGSGTKLEIK 106
Db 64 SSGGTSLTISRMEADATYTCQWSSNPLTFGSGTKLEIK 106

RESULT 5
US-11-172-320-4
/ Sequence 4, Application US/11172320
/ Publication No. US20050244413A1
/ GENERAL INFORMATION:
/ APPLICANT: Adolf, Guenther
/ APPLICANT: Baum, Anke
/ APPLICANT: Heider, Karl-Heinz
/ TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
/ TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunocjugates and
/ FILE REFERENCE: 1/1383
/ CURRENT APPLICATION NUMBER: US/11/172,320
/ CURRENT FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: US/10/645,215
/ PRIOR FILING DATE: 2003-08-21
/ PRIOR APPLICATION NUMBER: EP 02 018 686.2
/ PRIOR FILING DATE: August 21, 2002
/ PRIOR APPLICATION NUMBER: US 60/405,956
/ PRIOR FILING DATE: August 26, 2002
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: Patent Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain
US-11-172-320-4

Query Match      77.0%; Score 426; DB 7; Length 213;
Best Local Similarity 75.0%; Pred. No. 1,6e-21;
Matches 78; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Cy 4 LTGSPAIMSASPGKRYTTTCSASSSVSYMYWYQKPGSSPRLIYDTSNLSAGVPVRFSG 63
Db 4 LTGSPATLSLSPKRYTTTCSASSSVSYMYWYQKPGQAPRLIYDTSNLSAGVPVRFSG 63
Cy 64 SSGGTSLTISRMEADATYTCQWSSNPLTFGSGTKLEIKR 107
Db 64 SSGGTSLTISRMEADATYTCQWSSNPLTFGSGTKLEIKR 107

RESULT 6
US-11-174-186-42
/ Sequence 42, Application US/11174186
```



```
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ PRIOR FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 42
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: light chain
US-11-174-186-42
```

```
Query Match 76.7%; Score 424; DB 7; Length 213;
Best Local Similarity 79.8%; Pred. No. 2,1e-21;
Matches 83; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
```

```
QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPVRFSG 63
DB 4 LTQSPATLSLSPGRVTLTCSASSSVSYMLWYQOKPGSSPKWIPDTSNLSAGFPARFSG 63
```

```
QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIKR 107
DB 64 SSGSTSYSLTISRMEADATYYCHQRSQVPTFGSGTKLEIKR 107
```

```
RESULT 7
US-11-174-186-9
/ Sequence 9, Application US/11/174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ PRIOR FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 9
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: VK8 light chain
US-11-174-186-9
```

```
Query Match 75.8%; Score 419; DB 7; Length 106;
Best Local Similarity 79.6%; Pred. No. 2,5e-21;
Matches 82; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
```

```
QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPVRFSG 63
DB 4 LTQSPATLSLSPGRVTLTCSASSSVSYMLWYQOKPGSSPKWIPDTSNLSAGFPARFSG 63
```

```
QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIKR 106
DB 64 SSGSTSYSLTISRMEADATYYCHQRSQVPTFGSGTKLEIKR 106
```

```
RESULT 8
US-11-172-320-8
```

```
/ Sequence 8, Application US/11/172320
/ Publication No. US20050244413A1
/ GENERAL INFORMATION:
/ APPLICANT: Adolf, Guenther
/ APPLICANT: Baum, Anke
/ APPLICANT: Heider, Karl-Heinz
/ TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
/ TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunoconjugates and
/ FILE REFERENCE: 1/1383
/ CURRENT APPLICATION NUMBER: US/11/172,320
/ PRIOR FILING DATE: 2005-06-30
/ PRIOR APPLICATION NUMBER: US/10/645,215
/ PRIOR FILING DATE: 2003-08-21
/ PRIOR APPLICATION NUMBER: EP 02 018 686.2
/ PRIOR FILING DATE: August 21, 2002
/ PRIOR APPLICATION NUMBER: US 60/405,956
/ PRIOR FILING DATE: August 26, 2002
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 213
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Humanised Antibody B17A 8 light chain
US-11-172-320-8
```

```
Query Match 75.2%; Score 416; DB 7; Length 213;
Best Local Similarity 73.1%; Pred. No. 4,5e-21;
Matches 76; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
```

```
QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPVRFSG 63
DB 4 LTQSPATLSLSPGRATLSCASSSINYIWLQOKPGAPRILLYDTSNLSAGVPARFSG 63
```

```
QY 64 SSGSTSYSLTISRMEADATYYCOQWSSNPLTFGSGTKLEIKR 107
DB 64 SSGSTFTLTLSLPEDEFAVYCLQWSSNPLTFGSGTKLEIKR 107
```

```
RESULT 9
US-11-174-186-7
/ Sequence 7, Application US/11/174186
/ Publication No. US20050244418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xingyi
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ FILE REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ PRIOR FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 7
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: VK6 light chain
US-11-174-186-7
```

```
Query Match 74.0%; Score 409; DB 7; Length 106;
Best Local Similarity 74.8%; Pred. No. 1e-20;
Matches 77; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
```

```
QY 4 LTQSPAIMSASPGKVTTCSSASSSVSYMYWYQOKPGSSPRLIYDTSNLSAGVPVRFSG 63
DB 4 LTQSPATLSLSPGRVTLTCSASSSVSYMLWYQOKPGAPRILLYDTSNLSAGIPARFSG 63
```

```
Qy      64 SSGTSYSLTISRMEADATYYCQWSSNPLTFPGSGTKLEK 106
      |||||:||||:|||||:|||||:|
Db      64 SSGSDTYLTLTSSLEPEDFAVYYCHQRSQPYPTFGGGTKLEIK 106
```

```

RESULT 10
US-11-174-186-16
: Sequence 16, Application US/11/174186
: Publication No. US20050244418A1
: GENERAL INFORMATION:
: APPLICANT: Gillies, Stephen
: APPLICANT: Lo, Kin-Ming
: APPLICANT: Qian, Xiang
: TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
: FILE REFERENCE: LEX-019
: CURRENT APPLICATION NUMBER: US/11/174,186
: CURRENT FILING DATE: 2005-07-01
: PRIOR APPLICATION NUMBER: US 60/288,564
: PRIOR FILING DATE: 2001-05-03
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 16
: LENGTH: 106
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: KS VK mouse
US-11-174-186-16

```

[illegible]

```

RESULT 11
US-11-174-186-15
/ Sequence 15, Application US/11/174186
/ Publication No. US2005024418A1
/ GENERAL INFORMATION:
/ APPLICANT: Gillies, Stephen,
/ APPLICANT: Lo, Kin-Ming
/ APPLICANT: Qian, Xiang
/ TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
/ PIR REFERENCE: LEX-019
/ CURRENT APPLICATION NUMBER: US/11/174,186
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US 60/288,564
/ PRIOR FILING DATE: 2001-05-03
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 15
/ LENGTH: 106
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURES:
/ OTHER INFORMATION: KS de-immunized VKS
US-11-174-186-15

```

Query Match	73.6%	Score 407;	DB 7;	Length 106;
Best Local Similarity	74.8%	Pred. M. 1.4e-20;		
Matches	77;	Conservative 16;	Indels 0;	Gaps 0;
Qy	4	LTGSPALMSAGPGEKVTTCSSASSSVSYMYWYQKPGSSPRLLIYDTSTNLASGVVRPFG	63	
Qb	4	LTGSPALMSAVPQGGATITTCSSASSSVSTMLWYQKPGSSPKRWIYDTSTNLASGVFPARFG	63	

QY 64 SGGSTSYLTISRMEADAATYYCQWSSNPLTFPGSGTKLEK 106
||| | : ||| | | | | | | | | | | | | | |
Db 64 SGGSTSYLTINSLEADAATYYCHORSGYPTFGGGTKVELK 106

```

RESULT: 12
US-11-174-186-10
; Sequence 10, Application US/11/174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; PIR REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: KS VK veneered
US-11-174-186-10

```

	Query Match	Similarity	71.2%	Score 394	DB 7	Length 106
Best Local			71.8%	Pred. No. 8.7e-20		
Matches	74	Conservative	11	Mismatches	18	Indels 0, Gaps 0
QY	4	LTGSPALMASPGKAKVTTCGSSASSVSVMYTYOQKPGSSPLLIIYDTSNLASGVPRVRS	63			
DB	4	LTGSPALMASPGKRAITTCGSSASSVSVMYTYOQKPGPPPMWTFDDISNLASGPAFSPG	63			
QY	64	SGSGTSTSLITSRMEADDAATYYTCQWSSNPLTFGSGTKLEK	106			
DB	64	SGSGTSTSLITSLNSLEADDAATYYCHQSGSGVYTTGGGKIVIK	106			

```

RESULT 13
US-11-174-186-14
; Sequence 14, Application US/11/74186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; PIR REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VK4
US-11-174-186-14

```

```
Query Match          71.2%; Score 394; DB 7; Length 106;
Best Local Similarity 71.8%; Pred. No. 8.7e-20;
Matches      74; Conservative    11; Mismatches    18; Indels     0; Gaps     0;
```

Db 4 LTQSPALAVSPQGRATITCSASSSVSYMLWYQKPGQPKPWIFDTSNLSAGFPRFSG 63
 QY 64 SSGSTSYSLTISRMEADATYYCQWSSNPLTFGSGTKLEK 106
 Db 64 SSGSTSYTLTINSLEADATYYCHQRSQGYPTFGGKTKEIK 106

RESULT 14
 US-11-174-186-12
 ; Sequence 12, Application US/11174186
 ; Publication No. US20050244418A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gillies, Stephen
 ; APPLICANT: Lo, Kin-Ming
 ; APPLICANT: Qian, Xiang
 ; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
 ; FILE REFERENCE: LEX-019
 ; CURRENT FILING DATE: 2005-07-01
 ; PRIOR FILING DATE: 2001-05-03
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 12
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: KS de-immunized VK2
 US-11-174-186-12

Query Match 70.9%; Score 392; DB 7; Length 106;
 Best Local Similarity 71.8%; Pred. No. 1.2e-19;
 Matches 74; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTQSPALAVSPQGRATITCSASSSVSYMLWYQKPGQPKPWIFDTSNLSAGFPRFSG 63
 Db 4 LTQSPALAVSPQGRATITCSASSSVSYMLWYQKPGQPKPWIFDTSNLSAGFPRFSG 63
 QY 64 SSGSTSYSLTISRMEADATYYCQWSSNPLTFGSGTKLEK 106
 Db 64 SSGSTSYTLTINSLEADATYYCHQRSQGYPTFGGKTKEIK 106

RESULT 15
 US-11-174-186-13
 ; Sequence 13, Application US/11174186
 ; Publication No. US20050244418A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gillies, Stephen
 ; APPLICANT: Lo, Kin-Ming
 ; APPLICANT: Qian, Xiang
 ; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
 ; FILE REFERENCE: LEX-019
 ; CURRENT FILING DATE: 2005-07-01
 ; PRIOR FILING DATE: 2001-05-03
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 13
 ; LENGTH: 106
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: KS-deimmunized VK3
 US-11-174-186-13

Query Match 70.9%; Score 392; DB 7; Length 106;
 Best Local Similarity 71.8%; Pred. No. 1.2e-19;
 Matches 74; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 4 LTQSPALAVSPQGRATITCSASSSVSYMLWYQKPGQPKPWIFDTSNLSAGFPRFSG 63

Db 4 LTQSPALAVSPQGRATITCSASSSVSYMLWYQKPGQPKPWIFDTSNLSAGFPRFSG 63
 QY 64 SSGSTSYSLTISRMEADATYYCQWSSNPLTFGSGTKLEK 106
 Db 64 SSGSTSYTLTINSLEADATYYCHQRSQGYPTFGGKTKEIK 106

Search completed: November 21, 2005, 12:33:50
 Job time : 2.05971 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 145.932 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-88

Perfect score: 559
Sequence: 1 DIETQSPALMSAPGKVT.....QWSSNPLRTGSGTKELKR 109

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Geneseq_21:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003s:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	559	100.0	109	8	ADR38686	Adt38686 Mouse lig
2	518	92.7	107	8	ADR38685	Adt38685 Mouse lig
3	492	88.0	107	8	ADR38673	Adt38673 Mouse lig
4	491	87.8	107	9	ADM86126	Adm86126 Novel cyt
5	491	87.8	210	8	ADU86565	Adu86565 Immunoglo
6	491	87.8	210	8	ADU86571	Adu86571 Immunoglo
7	490	87.7	110	5	AAR21305	Aar21305 Murine VL
8	489	87.5	129	5	ABR75616	Abt75616 Anti-RANK
9	486	86.9	107	8	ADR38670	Adt38670 Mouse lig
10	482	86.2	244	2	ADR79867	Aar79867 Anti-EGFR
11	481	86.0	108	8	ADT74993	Adt74993 Light cha
12	481	86.0	109	8	ADR38691	Adt38691 Mouse lig
13	481	86.0	242	2	AAR79870	Aar79870 Anti-EGFR
14	481	86.0	242	2	AAR79871	Aar79871 Anti-EGFR
15	479	85.7	110	2	AAR21306	Aar21306 Murine VL
16	478	85.5	122	2	AAR25958	Aar25958 ICM-1 in
17	477	85.3	110	2	AAR21304	Aar21304 Murine VL
18	476	85.2	106	4	AAB69673	Aab69673 Murine ml
19	476	85.2	106	8	ADO47720	Ado47720 Mouse mlk
20	476	85.2	110	2	AAR21287	Aar21287 Murine VL
21	476	85.2	128	4	AAB69655	Aab69655 Murine ml
22	476	85.2	128	8	ADO47747	Ado47747 Mouse mlk
23	475	85.0	106	5	ABG32682	Abg32682 Murine an
24	475	85.0	106	5	AAE27810	Aae27810 Mouse 425

25	475	85.0	128	2	AAR27050	Aar27050 VL425 ant
26	475	85.0	242	2	AAR79872	Aar79872 Anti-EGFR
27	473	84.6	106	5	AAU72834	Aau72834 Anti-NG2
28	473	84.6	107	4	ADM80852	Adm80852 Anti-CD3
29	472	84.4	246	2	AAR79869	Aar79869 Anti-EGFR
30	471.5	84.3	108	9	ADM86127	Adm86127 Novel cyt
31	471.5	84.3	214	8	ADU86519	Adu86519 Immunoglo
32	471	84.3	108	2	AAR21293	Aar21293 Murine VL
33	471	84.3	110	2	ADT75125	Adt75125 Light cha
34	471	84.3	110	8	ADT75054	Adt75054 Light cha
35	471	84.3	110	8	ADT75053	Adt75053 Light cha
36	470	84.1	106	8	ADU16879	Adu16879 Murine an
37	470	84.1	109	8	ADH59678	Adh59678 cPAM4 VK
38	470	84.1	109	8	ADH59707	Adh59707 Chimeric
39	469	83.9	106	9	ADV66151	Adv66151 CD3-speci
40	469	83.9	106	9	ADZ64982	Adz64982 Non-deimm
41	469	83.9	106	9	ADZ83490	Adz83490 Non-deimm
42	469	83.9	108	5	AAE22196	Aae22196 CD3-speci
43	469	83.9	110	2	AAR21307	Aar21307 Murine VL
44	469	83.9	128	4	AAE65521	Aae65521 Mouse ant
45	469	83.9	240	9	ADV14577	Adv14577 VL(CD3)-V

ALIGNMENTS

RESULT 1
ID ADR38686 standard; peptide; 109 AA.

AC ADR38686;

DT 02-DEC-2004 (first entry)

DE Mouse light chain variable region scFv seqid 88.

XX antibody; antibody; botulinum neurotoxin type A; BoNT/A;

XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;

XX light chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PT 01-AUG-2002; 2002US-0400721P.

PS (REGC) UNIV CALIFORNIA.

PT Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

XX useful for diagnosing botulism or for treating pathologies associated

XX with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 88; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

XX to an epitope specifically bound by an antibody expressed by a specific

XX clone where (I) binds to and neutralises botulinum neurotoxin type A

XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope

XX specifically bound by an antibody expressed by a clone chosen from clone

XX S25, C39, C39, 1C6, 3D12, B4, 1F3, huc25, A1, Ar2, WRI (V), WRI (V), 3-1,

XX 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum

XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)

XX comprising BoNT/A neutralising epitope having an epitope that is

PT useful for diagnosing botulism or for treating pathologies associated
 with botulinum neurotoxin poisoning.

Example 1; SEQ ID NO 75; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and IN61, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having a clone as mentioned in (I) specifically bound by an antibody expressed by clones as mentioned in (I), producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contracting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinum single antibodies in surplus. (I) is useful for diagnosing the botulinum or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of a mouse light chain variable fragment anti-botulinum toxin scFv.

Sequence 107 AA;

Query Match 88.0%; Score 492; DB 8; Length 107;
 Best Local Similarity 90.8%; Pred. No. 1.1e-29;
 Matches 99; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 DIELTQSPAINASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLAAGVP 60
 DB 1 DIELTQSPAINASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLAAGVP 58
 QY 61 VRFSGSGGTSISLTISRMEADATYYCQNSNPILTFGSGTKLELR 109
 DB 59 VRFSGSGGTSISLTISRMEADATYYCQNSNPILTFGSGTKLELR 107

RESULT 4

ID ADW86126
 ID ADW86126 standard; protein; 107 AA.

AC ADW86126;

DT 21-APR-2005 (first entry)

DE Novel cytotoxic conjugate-related mouse aY1 protein region SeqID46.

XX cytotoxic; immunosuppressive; cytostatic; immunosuppressive; virucide;
 XX apoptosis stimulation; cancer; ovary tumor; uterine cervix tumor;
 KW endometrial carcinoma; breast tumor; pancreas tumor; CA6 glycotope;
 KW autoimmune disease; graft rejection; viral infection; DS6;
 KW antibody engineering; aY1.

OS Mus musculus.

PN WO2005009369-A2.

PD 03-FEB-2005.

PF 21-JUL-2004; 2004WO-US023340.

PR 21-JUL-2003; 2003US-0488447P.

PA (IMMUNO-) IMMUNOGEN INC.

PI Payne G, Chun P, Tavares DJ;

DR WPI; 2005-142544/15.

PT Cytotoxic conjugate useful for treating cancer, autoimmune diseases, and
 graft rejections or viral infections, comprises cell binding agent and
 cytotoxic agent.

Example 12; SEQ ID NO 46; 179pp; English.

This invention relates to a novel cytotoxic conjugate which comprises a cell binding agent and a cytotoxic agent, where the cell binding agent binds to CA6 glycotope. Preferably, the cell binding agent is the murine anti-CA6 monoclonal antibody DS6 or their epitope-binding fragments or a humanized version of the same. The cytotoxic agent is chosen from maytansinoid compounds, taxoid compounds, CC-1065 compounds, dolastatin compounds, daunorubicin compounds or doxorubicin compounds. The invention may be useful for the production of compounds with a cytostatic, immunosuppressive or virucide activity acting as stimulators of apoptosis. The invention is useful for inhibiting growth of a cell expressing CA6 glycotope and may be used for treating a subject having a cancer (for example serous ovarian carcinoma, endometrial ovarian carcinoma, neoplasm of the uterine cervix, neoplasm of the endometrium, neoplasm of the vulva, breast carcinoma, pancreatic tumor or tumor of the urothelium), in which CA6 glycotope is expressed or overexpressed. In addition, the invention may be useful for treating autoimmune diseases, graft rejections or viral infections. The present sequence is that of a region of the mouse aY1 protein which was used to demonstrate homology with a region of the mouse DS6 antibody light chain protein during the exemplification of the invention.

Sequence 107 AA;

Query Match 87.8%; Score 491; DB 9; Length 107;
 Best Local Similarity 88.1%; Pred. No. 1.3e-29;
 Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

QY 1 DIELTQSPAINASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLAAGVP 60
 DB 1 DIELTQSPAINASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLLIYDTSNLAAGVP 58
 QY 61 VRFSGSGGTSISLTISRMEADATYYCQNSNPILTFGSGTKLELR 109
 DB 59 VRFSGSGGTSISLTISRMEADATYYCQNSNPILTFGSGTKLELR 107

RESULT 5

ID ADW86565
 ID ADW86565 standard; protein; 210 AA.

AC ADW86565;

DT 10-FEB-2005 (first entry)

DE Immunoglobulin variable domain protein SeqID 54.

XX antiinflammatory; antibacterial; virucide; cytostatic; antiproliferative;
 KW antidiabetic; vasotrophic; vaccine; protein purification; protein folding;
 KW diagnosis; inflammation; immune disorder; allergic hypersensitivity;
 KW infection; autoimmune disease; asthma; psoriasis;
 KW insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
 KW systemic lupus erythematosus; myasthenia gravis; hematological disease;
 KW neoplasm; immunoglobulin; variable region.

OS Homo sapiens.

PN WO2004101790-A1.

PD 25-NOV-2004.

PF 14-MAY-2004; 2004WO-GB002102.

XX 14-MAY-2003; 2003US-0470340P.
PR 17-MAR-2004; 2004US-0554021P.
XX
PA (DOMA-) DOMANTIS LTD.
XX
PI Jespers LS, Jones PC, Famm KHJ, Winter GP,
XX WPI, 2004-821888/81.
DR
XX
XX Recovering a polypeptide that unfolds reversibly from a repertoire of
PT polypeptides for treating e.g., cancer, by unfolding a portion of the
PT displayed polypeptides and refolding a portion of the unfolded
PT polypeptides.
XX
PS Disclosure; SEQ ID NO 54; 222pp; English.
XX
CC The invention describes a method of recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that unfolds reversibly and
CC has a common selectable characteristic that distinguishes folded
CC polypeptides from unfolded or misfolded polypeptides. The method
CC comprises: providing a polypeptide display system comprising the
CC repertoire of displayed polypeptides; unfolding at least a portion of the
CC displayed polypeptides; refolding at least one polypeptide that unfolds
CC reversibly and has the selectable characteristic from the refolded
CC portion. The method is useful in recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that unfolds reversibly. The
CC library or repertoire is useful for selecting a polypeptide comprising an
CC antibody variable domain that unfolds reversibly or a polypeptide that
CC is useful in the manufacture of a medicament for diagnosing, treating or
CC preventing a disease or medical condition mediated by a cytokine,
CC cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
CC as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
CC viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
CC I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
CC tumor. This is the amino acid sequence of an immunoglobulin variable
CC region associated with the protein purification method of the invention.
XX
SQ Sequence 210 AA;
Query Match 87.8%; Score 491; DB 8; Length 210;
Best Local Similarity 88.1%; Pred. No. 2; e-29;
Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;
QY 1 DIELTOSPAIMASAPGKVTITTCRASSSVSSSYLYGWYQOKRSPRLIYDTSNLASGVP 60
DB 1 DIELTOSPAIMASAPGKVTITTCRASSSV--SYMYWYQOKRSPRLIYDTSNLASGVP 58
QY 61 VRFSGSGSGTSYSYLITISRMEDDAATYYCOQWMSNPITFGSGTKLEIKR 109
DB 59 VRFSGSGSGTSYSYLITISRMEDDAATYYCOQWSTYPLTFAGTKLEIKR 107
RESULT 6
ID ADU86571 standard; protein; 210 AA.
XX
XX ADU86571;
XX
DT 10-FEB-2005 (first entry)
XX
DE Immunoglobulin variable domain protein seqid 60.
XX
XX antiinflammatory; antibacterial; virucide; cytostatic; antiparasitic;
KM antidiabetic; vasotropic; vaccine; protein purification; protein folding;
KM diagnoses; inflammation; immune disorder; allergic hypersensitivity;
KM infection; autoimmune disease; asthma; psoriasis;
KM insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
KM systemic lupus erythematosus; myasthenia gravis; hematological disease;
KM neoplasm; immunoglobulin; variable region.

XX Homo sapiens.
OS
XX WO2004101790-A1.
FN
XX
XX 25-NOV-2004.
PD
XX
XX 14-MAY-2004; 2004MO-GB002102.
PF
XX
XX 14-MAY-2003; 2003US-0470340P.
PR 17-MAR-2004; 2004US-0554021P.
XX
PA (DOMA-) DOMANTIS LTD.
XX
PI Jespers LS, Jones PC, Famm KHJ, Winter GP;
XX WPI, 2004-821888/81.
DR
XX
XX Recovering a polypeptide that unfolds reversibly from a repertoire of
PT polypeptides for treating e.g., cancer, by unfolding a portion of the
PT displayed polypeptides and refolding a portion of the unfolded
PT polypeptides.
XX
PS Disclosure; SEQ ID NO 60; 222pp; English.
XX
CC The invention describes a method of recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that unfolds reversibly and
CC has a common selectable characteristic that distinguishes folded
CC polypeptides from unfolded or misfolded polypeptides. The method
CC comprises: providing a polypeptide display system comprising the
CC repertoire of displayed polypeptides; unfolding at least a portion of the
CC displayed polypeptides; refolding at least a portion of the unfolded
CC polypeptides; and recovering at least one polypeptide that unfolds
CC reversibly and has the selectable characteristic from the refolded
CC portion. The method is useful in recovering a polypeptide that unfolds
CC reversibly from a repertoire of polypeptides that unfolds reversibly. The
CC library or repertoire is useful for selecting a polypeptide comprising an
CC antibody variable domain that unfolds reversibly or a polypeptide that
CC refolds reversibly and comprising an antibody format. The polypeptide is
CC useful in the manufacture of a medicament for diagnosing, treating or
CC preventing a disease or medical condition mediated by a cytokine,
CC cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
CC as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
CC viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
CC I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
CC tumor. This is the amino acid sequence of an immunoglobulin variable
CC region associated with the protein purification method of the invention.
XX
SQ Sequence 210 AA;
Query Match 87.8%; Score 491; DB 8; Length 210;
Best Local Similarity 88.1%; Pred. No. 2; e-29;
Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;
QY 1 DIELTOSPAIMASAPGKVTITTCRASSSVSSSYLYGWYQOKRSPRLIYDTSNLASGVP 60
DB 1 DIELTOSPAIMASAPGKVTITTCRASSSV--SYMYWYQOKRSPRLIYDTSNLASGVP 58
QY 61 VRFSGSGSGTSYSYLITISRMEDDAATYYCOQWMSNPITFGSGTKLEIKR 109
DB 59 VRFSGSGSGTSYSYLITISRMEDDAATYYCOQWSTYPLTFAGTKLEIKR 107
RESULT 7
ID AAR21305 standard; protein; 110 AA.
XX
XX AAR21305;
XX
DT 21-MAY-1992 (first entry)
XX
DE Murine VL kappa group IV/VI chain c specific for phox.

XX	Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
KW	g93; binding; adsorption; gene VIII; diverse repertoire;
KW	specific binding pairs; replicable genetic display package.
XX	
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FM	Binding-site 24..35
FT	/label= CDR1
FT	Binding-site 51..57
FT	/label= CDR2
FT	Binding-site 90..98
FT	/label= CDR3
FT	/note= " D-X-G-X-X motif "
XX	
FN	W09201047-A.
PD	23-JAN-1992.
PE	10-JUL-1990; 90GB-00015198.
PR	10-JUL-1990; 90GB-00015198.
PR	19-OCT-1990; 90GB-00022845.
PR	12-NOV-1990; 90GB-00024503.
PR	06-MAR-1991; 91GB-00004744.
PR	15-MAY-1991; 91GB-00010549.
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA	(MEDI-) MED RES COUNCIL.
P1	Mccafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
P1	Jackson RH, Holliger KP, Marks JD;
DR	WPI. 1992-056862/07.
PT	Producing members of specific binding pairs - by expression in
PT	recombinant host cells with a secreting replicable genetic display
PT	package.
PS	Example 22; Fig 24; 20pp; English.
CC	The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
CC	Fv library. The library produces a diverse repertoire of antibody
CC	fragments specific for 2-phenyl-5-oxazolone (phox). It was prepd. using
CC	cDNA generated from mRNA from mice immunised with phox coupled to chicked
CC	serum albumin. The VH and VL kappa sequences were separately amplified by
CC	PCR (AAQ23374-84) and ligated into fdCAT? (AAQ23463) for expression on
CC	the phage surface as fusions with gene III. The resulting library of 8
CC	clones was diverse; 23 hapten binding clones were sequenced revealing 8
CC	VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
CC	; AAR21286-92). Most clones were VH-B combinations so a further
CC	hierarchical library was prepd. by "crossing" VH-B with the VK
CC	repertoire. The resulting library was screened for haptan binding and 24
CC	clones sequenced. 14 new partners (AAR21293-308) for VH-B were
CC	identified. Nearly all the VK genes were "ox-like"; only F, (from the
CC	original library) and h, p, q, and r (from the hierarchical library) were
CC	"t". The Kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest
CC	values found. This suggests that phage bearing scFv fragments having weak
CC	affinit-ies can be selected with antigen, probably due to the avidity of
CC	the multiple antibody heads on the phage. The different combinations
CC	could also be isolated on a basis of antigen affinity. See also AAR21260-
CC	307, 309-311; AAR22450, 565-581
XX	
SO	Sequence 110 AA;
Query Match	87.7%; Score 490; DB 2; Length 110;
Best Local Similarity	89.0%; Pred. No. 1,6e-29;
Matches 97; Conservative	4; Mismatches 8; Indels 0; Gaps 0

1 DIETLOSFAIMASPGERKYTCRASSVSSTYAGWQQPSSPLLTYDTSNLASGVP 60

Db	1	DIELTQSGALINASBGEKVMTTCASSSVSDSYLWVQKSGASPCLMTYTSNLASGP	60
Qy	61	VRFSGSGSGTSYSLTISMEAEADATYYCOQMSNPITFGSTKYLEKR	109
Db	61	ARFGSGSGTSYSLTISMEAEADATYYCOQMSNPITFGSTKYLEKR	109
RESULT 8			
ID	ABB75616	ABB75616 standard; protein, 129 AA.	
XX	XX	ABB75616;	
DT	10-JUN-2002	(first entry)	
XX	XX		
DE	XX	Anti-RANK ligand mAb 19H22 light chain variable region.	
XX	XX		
KM	KM	RANK ligand; RANK-L; monoclonal antibody; mAb; 19H22; antibody;	
KM	KM	complementarity determining region; CDR; rheumatoid arthritis;	
KM	KM	osteoporosis; bone cancer; metastasis; osteolysis; osteoarthritis;	
KM	KM	psoriasis; inflammatory bowel disease; multiple sclerosis; diabetes;	
KM	KM	cytotoxic; antirheumatic; antiinflammatory; osteopathic; antidiabetic;	
KM	KM	antirheumatic; immunosuppressive; antipsoriatic; neuroprotective;	
XX	XX	light chain; VL; mouse.	
XX	XX		
OS	OS	Mus musculus.	
XX	XX		
PH	PH	Key	Location/Qualifiers
FT	FT	Region	24..33
		/label= CDR1	
FT	FT	/note= "complementarity determining region 1"	
FT	FT	Region	49..55
		/label= CDR2	
FT	FT	/note= "complementarity determining region 2"	
FT	FT	Region	88..96
		/label= CDR3	
FT	FT	/note= "complementarity determining region 3"	
XX	XX		
PN	PN	WO200215846-AZ.	
XX	XX		
PD	PD	28-FEB-2002.	
XX	XX		
PF	PF	21-AUG-2001; 2001WO-US026161.	
XX	XX		
PR	PR	21-AUG-2000; 2000US-0226524P.	
XX	XX		
PR	PR	07-SEP-2000; 2000US-0230639P.	
XX	XX		
PA	PA	(SMIK) SMITHKLINE BEECHAM CORP.	
XX	XX	(SMIK) SMITHKLINE BEECHAM PLC.	
XX	XX		
PI	PI	Sweet RW, Tornetta MA, Truneh A, Wattam TA;	
XX	XX		
DR	DR	WPI; 2002-242022/29.	
XX	XX	N-PSDB; ABL53530.	
PT	PT		
XX	XX	A mouse monoclonal antibody 19H22 for treating or preventing osteopenic	
XX	XX	disease including rheumatoid arthritis and osteoporosis.	
XX	XX		
PS	PS	Claim 6; Page 7; 45pp; English.	
XX	XX		
CC	CC	The present sequence is that of the light chain variable region of	
CC	CC	claimed anti-human RANK ligand (RANK-L) murine monoclonal antibody (mAb)	
CC	CC	19H22 (isotype IgG2b/kappa). The mAb is produced by hybridoma cells	
CC	CC	obtained by immunising CB6 f1 mice with human RANK-L protein, and fusing	
CC	CC	spleen cells with X63-Ag8.653 myeloma cells. 19H22 mAb is specific for	
CC	CC	human RANK-L, having a binding affinity characterised by a dissociation	
CC	CC	constant of about 10 power -10 M. RANK-L is a member of the tumour	
CC	CC	necrosis factor family of proteins and a key regulator of the immune	
CC	CC	system, bone development and homeostasis. The invention provides altered	
CC	CC	chimeric and humanised 19H22 antibodies, including Fab or F(ab')2	
CC	CC	fragments, antibodies comprising the light and heavy chain variable	
CC	CC	regions of 19H22, and antibodies comprising the complementarity	
CC	CC	determining regions of 19H22. These are used in methods for the	

CC diagnosis, treatment and prevention of osteopenic diseases, including
 CC rheumatoid arthritis, osteoporosis, metastatic and primary bone cancer,
 CC wear debris induced osteolysis or osteoarthritis, and immune diseases
 CC including psoriasis, insulin dependent diabetes, inflammatory bowel
 CC disease or multiple sclerosis. Methods are also provided for the
 CC recombinant production of the antibodies, using isolated nucleic acids
 CC and transfected host (preferably mammalian) host cells, and a method of
 CC diagnosing conditions associated with Th1 T-cell activity or osteoclast
 CC development and activation, in particular those listed above

XX Sequence 129 AA;
 SQ

Query Match 87.5%; Score 489; DB 5; Length 129;
 Best Local Similarity 90.7%; Pred. No. 2,2e-29;
 Matches 98; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 2 IEITGSPAIMSASPEKVTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVP 61
 DB 2 IVLTGSPAIMSASPEKVTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVP 59
 QY 62 RFSGSGSGTSTSLTISRMEADATYCCQWMSNPLTFGSGTKLELR 109
 DB 60 RFSGSGSGTSTSLTISRMEADATYCCQWMSNPLTFGSGTKLELR 107

RESULT 9
 ADR38670
 ID ADR38670 standard; peptide; 107 AA.
 AC ADR38670;
 XX
 DT 02-DEC-2004 (first entry)
 XX

DE Mouse light chain variable region scFv seqid 72.
 XX

XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KM light chain variable region; single chain antibody; scFv.
 XX

OS Mus sp.
 XX

XX US2004175385-A1.
 PN
 PD 09-SEP-2004.
 XX

PF 01-AUG-2003; 2003US-00632706.
 XX

PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX

PA (REGC) UNIV CALIFORNIA.
 PI
 PI Marks JD, Amerdorter P;
 PI
 PI WPI; 2004-652009/63.
 DR

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX

XX Example 1; SEQ ID NO 72; 110pp; English.
 PS

CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, I6, J012, B4, I63, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and IWC1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)

CC / producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse light chain variable fragment anti-botulinum toxin
 CC scFv.

XX Sequence 107 AA;
 SQ

Query Match 86.9%; Score 486; DB 8; Length 107;
 Best Local Similarity 89.0%; Pred. No. 3,1e-29;
 Matches 97; Conservative 2; Mismatches 8; Indels 2; Gaps 1;

QY 1 DIEITGSPAIMSASPEKVTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVP 60
 DB 1 DIEITGSPAIMSASPEKVTTCRASSSVSSYLGMVQOKPGSSPRLIYDTSNLASGVP 58
 QY 61 VRFGSGSGTSTSLTISRMEADATYCCQWMSNPLTFGSGTKLELR 109
 DB 59 IRFGSGSGTSTSLTISRMEADATYCCQWMSNPLTFGSGTKLELR 107

RESULT 10
 AAR79867
 ID AAR79867 standard; protein; 244 AA.
 AC AAR79867;
 XX
 DT 02-JUL-1996 (first entry)
 XX

DE Anti-EGFR single chain antibody (Clone 1b D 2).
 XX

XX Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
 KM tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
 KM phage antibody library.
 XX

OS Mus musculus.
 XX

XX WO9525167-A1.
 PN
 PD 21-SEP-1995.
 XX

PF 16-MAR-1995; 95WO-EP000978.
 XX

PR 17-MAR-1994; 94EP-00104160.
 PR 02-DEC-1994; 94EP-00118970.
 XX

PA (MERE) MERCK PATENT GMBH.
 PI
 PI Kettleborough AC, Bendig MM, Ansell KH, Guesow D, Adan J;
 PI Mcljans F, Roseell E, Blasco F, Pluats J;
 PI
 PI WPI; 1995-336972/43.
 DR

XX Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
 PT from phage-antibody libraries, useful for diagnosis and therapy of
 PT tumours.
 XX

PS Claim 4; Page 60-61; 93pp; English.
 XX

CC Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
 CC antibodies constructed from anti-EGFR antibody fragments can be used for

diagnosis of tumours and assessment of tumour growth in vitro and in vivo. They may also be used in a pharmaceutical composition for the therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and fragments are derived from mice but are humanised so as to cause minimum reaction against them. They are produced using the phage antibody library. They are produced using the phage antibody library. (see AA104011-704026 and AA179858-R79873)

Sequence 244 AA;

Query Match 86.2%; Score 482; DB 2; Length 244;
Best Local Similarity 89.1%; Pred. No. 1.3e-26;
Matches 98; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 1 DIETQSPALMSAPGKGVTTTCRASSSVSSYLGMVQOKGSSPRLLIYDTSNLAGVP 60
DB 137 DIETQSPALMSAPGKGVTTTCRASSSV--SYMYVQOKGSSPRLLIYDTSNLAGVP 194

QY 61 VRFSGSGSTSYSLTIISMEAEADATYYCQOMSSNP--LTFGSGTKLEIK 108
DB 195 VRFSGSGSTSYSLTIISMEAEADATYYCQOMSSYPPMYTFGGGTLEIK 244

RESULT 11
ADT74993
ID ADT74993 standard; protein; 108 AA.

AC ADT74993;

DT 13-JAN-2005 (first entry)

DE Light chain murine anti-hL-SIGN scFv antibody protein A2UC Seq 39.

XX autoimmune disease; antibody; antigen presenting cell; APC;
KM diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hL-SIGN.

OS Mus sp.

PM WO2004091543-A2.

PD 28-OCT-2004.

PF 04-MAR-2004; 2004WO-US006570.

PR 04-MAR-2003; 2003US-0451816P.

PR 15-DEC-2003; 2003US-0523500P.

PR 28-FEB-2004; 2004US-0548385P.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Kretz-Rommel A, Dakappagari N;

DR WPI; 2004-758274/74.

PT Treating an autoimmune disease comprises providing an
PT antibody/antigen construct containing an autoantigen linked to an
PT antibody to a receptor of an antigen presenting cell and administering
PT the construct to a subject.

Example 9; Fig 8; 71pp; English.

XX This invention relates to the novel treatment of an autoimmune disease
CC that utilizes an antibody/ autoantigen construct. Specifically, it refers
CC to a peptide autoantigen that is linked to an antibody raised against an
CC antigen presenting cell (APC) receptor. The present invention describes a
CC method for treating diabetes mellitus by inducing an immune tolerance to
CC an autoantigen, which can be chosen from glutamic acid decarboxylase
CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC from each thereof or beta cell antigens that are linked to an APC
CC receptor antibody. In particular, the antibody recognises a receptor
CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC others, which is expressed on the surface of the APC. The antibody/

CC autoantigen construct then works to interfere with the interaction
CC between the APC and immune cells such as autoreactive T cells, and hence
CC inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC anti-diabetic and immunosuppressive activities and can be used in the
CC development of vaccines. Note that the single chain antibodies (scFvs)
CC used in this specification contain both variable light and heavy chain
CC regions connected by a linker, their short length makes these antibody
CC fragments particularly suitable for antigen linkage, and the capacity for
CC binding to the receptor is preserved. This polypeptide sequence is a
CC light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the
CC invention.

Sequence 108 AA;

Query Match 86.0%; Score 481; DB 8; Length 108;
Best Local Similarity 90.6%; Pred. No. 7.4e-29;
Matches 96; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 4 LTQSPALMSAPGKGVTTTCRASSSVSSYLGMVQOKGSSPRLLIYDTSNLAGVP 63
DB 4 LTQSPALMSAPGKGVTTTCRASSSV--SYMYVQOKGSSPRLLIYDTSNLAGVP 61

QY 64 SSGSGSTSYSLTIISMEAEADATYYCQOMSSNP-LTFGSGTKLEIK 109
DB 62 SSGSGSTSYSLTIISMEAEADATYYCQOMSSYPPMYTFGGGTLEIK 107

RESULT 12
ADR38691
ID ADR38691 standard; peptide; 109 AA.

AC ADR38691;

DT 02-DEC-2004 (first entry)

DE Mouse light chain variable region scFv seqid 93.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KW light chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marks JD, Amersdorfer P;

DR WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.

Example 1; SEQ ID NO 93; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 26.5513 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-88

Perfect score: 559
Sequence: 1 DIETLOSPAIMSAPGKVT.....QWSSNPLTFGGSTKLELR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	463	82.8	107 2	PC4405 Ig kappa chain V r
2	462	82.6	130 2	A32513 Ig kappa chain pre
3	456	81.6	107 2	A42848 Ig light chain V r
4	455	81.4	120 2	S66536 Ig light chain V r
5	455	81.4	130 2	B32456 Ig kappa chain pre
6	453	81.0	130 2	S04573 Ig kappa chain pre
7	452	80.9	107 2	A30562 Ig kappa chain V r
8	452	80.9	113 2	S03410 Ig kappa chain pre
9	451	80.7	107 2	B30562 Ig kappa chain V r
10	450	80.5	130 1	JL0079 Ig kappa chain pre
11	450	80.5	235 2	S25058 Ig kappa chain - m
12	446	79.8	103 2	S29591 Ig kappa chain V r
13	446	79.8	123 2	S05269 Ig kappa chain pre
14	445	79.6	108 2	S29581 Ig kappa chain V r
15	444.5	79.5	108 2	S38720 Ig light chain V r
16	444	79.4	106 2	PS0071 Ig kappa chain V r
17	443	79.2	108 2	PS0069 Ig kappa chain V r
18	442	79.1	104 2	B49049 Ig kappa chain V r
19	441	78.9	107 2	PD0011 Ig kappa chain V r
20	441	78.9	140 2	PI0013 Ig kappa chain pre
21	440	78.7	109 2	PT0405 Ig light chain V r
22	439.5	78.6	108 2	G30560 Ig kappa chain V r
23	439	78.5	108 2	PL0278 Ig kappa chain V r
24	438	78.4	124 2	S05267 Ig kappa chain pre
25	436	78.0	107 2	S11119 Ig kappa chain V r
26	435	77.8	106 2	PL0082 Ig kappa chain V r
27	435	77.8	106 2	B54378 Ig light chain V r
28	435	77.8	108 2	PL0277 Ig kappa chain V r
29	435	77.8	108 2	PL0276 Ig kappa chain V r

30	435	77.8	109 2	S13699 Ig kappa chain V r
31	435	77.8	109 2	PT0404 Ig light chain V r
32	434	77.6	107 2	S11118 Ig kappa chain V r
33	428	76.6	107 2	S11121 Ig kappa chain V r
34	426	76.2	107 2	PT0406 Ig kappa chain V r
35	426	76.2	108 2	S11125 Ig kappa chain pre
36	424	75.8	132 2	S05268 Ig kappa chain pre
37	422	75.5	106 2	PS0070 Ig kappa chain V r
38	422	75.5	106 2	G27867 Ig kappa chain V r
39	421	75.3	105 2	S26338 Ig kappa chain V r
40	421	75.3	106 2	S29583 Ig kappa chain V r
41	421	75.3	107 2	S11117 Ig kappa chain V r
42	420	75.1	100 2	S29590 Ig kappa chain V r
43	420	75.1	129 1	KVMS7B Ig kappa chain pre
44	418	74.8	97 2	S26341 Ig light chain V r
45	418	74.8	102 2	S29582 Ig kappa chain V r

ALIGNMENTS

RESULT 1

PC4405 Ig kappa chain V region (F3, anti-AFP) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004

C/Accession: PC4405

R/Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996

A/Title: Generation of a phage display library of the immunoglobulin repertoire from hum

A/Reference number: PC4405

A/Accession: PC4405

A/Residues: 1-107 <DEN>

A/Cross-references: UNIPROT:Q8K1F0; UNIPARC:UPI000017677B

A/Experimental source: spleen cell

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F16-89/Domain: immunoglobulin homology <IMM>

Query Match	82.8%	Score 463;	DB 2;	Length 107;
Best Local Similarity	82.6%	Pred. No. 3.4e-32;		
Matches	90;	Conservative	6;	Mismatches 11; Indels 2; Gaps 1;
QY	1 DIETLOSPAIMSAPGKVTTCRASSVSISYIGWYQKGGSPRLIYDTSNLSAGVP 60			
DB	1 DIETLOSPAIMSAPGKVTTCSSSSI--SYHWYQKGGTSPKRWIYDTSKLASVP 58			
QY	61 VRFSGSGSTSYSLTIISMEADATYYCQWSSNPLTFGGSTKLELR 109			
DB	59 ARFSGSGSTSYSLTIISMEADATYYCQWRDNPFTFGGKLELR 107			

RESULT 2

A32513 Ig kappa chain precursor V region (MRU22) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C/Accession: A32513

R/Koffler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.R.; Noonan, D.J.; Duchosal, M.A.; I

J. Clin. Invest. 82, 852-860, 1988

A/Title: Immunoglobulin kappa light chain variable region gene complex organization and ;

A/Reference number: A94689; MUID:8831394; PMID:3138286

A/Accession: A32513

A/Molecule type: DNA

A/Cross-references: UNIPARC:UPI0000114D9C; GB:M20834; NID:9196943; PIDD:AAA3846.1; PIDD: ;

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F138-113/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 462; DB 2; Length 130;

Best Local Similarity 85.0%; Pred. No. 5.1e-32;

Matches 91; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 61
 DB 24 IVLQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 83

QY 62 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 108
 DB 84 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 130

RESULT 3
 Ig light chain V region - mouse (fragment)
 A:Accession: A42848
 A:Residues: 1-107 <FE>
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Cross-references: UNIPARC:UPI0000115334; EMBL:M90690
 A:Note: sequence extracted from NCBI backbone (NCBI:109958, NCBI:109959)
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: Immunoglobulin homology <IM>
 F:16-89/Domain: Immunoglobulin homology <IM>

Query Match 81.6%; Score 456; DB 2; Length 107;
 Best Local Similarity 83.3%; Pred. No. 1,38-31;
 Matches 90; Conservative 8; Mismatches 8; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 61
 DB 2 IVLQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 59

QY 62 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 109
 DB 60 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 107

RESULT 4
 Ig light chain V region - mouse (fragment)
 A:Accession: S66536
 A:Residues: 1-107 <FE>
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Cross-references: UNIPARC:UPI0000113780; EMBL:X88903; NID:8895870; PIDD:CAA6135.1; PI
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 F:16-91/Domain: Immunoglobulin homology <IM>

Query Match 81.4%; Score 455; DB 2; Length 120;
 Best Local Similarity 80.7%; Pred. No. 1,88-31;
 Matches 88; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 DIETQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 60
 DB 1 IELTQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 60

QY 61 VRFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 109
 DB 61 ARFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 109

RESULT 5
 Ig kappa chain precursor V region - mouse
 A:Accession: B32456
 A:Residues: 1-130 <DOM>
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Cross-references: UNIPARC:UPI0000114889; GB:J04610; NID:9556313; PIDD:AAA50296.1; PID:5
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:38-113/Domain: Immunoglobulin homology <IM>

Query Match 81.4%; Score 455; DB 2; Length 130;
 Best Local Similarity 84.8%; Pred. No. 28-31;
 Matches 89; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 IETQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 63
 DB 26 IETQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 85

QY 64 SGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 108
 DB 86 SGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 130

RESULT 6
 Ig kappa chain precursor V region (MRL-histone 7L) - mouse (fragment)
 A:Accession: S04573
 A:Residues: 1-130 <KOP>
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Cross-references: UNIPARC:UPI0000115DF8; EMBL:X14620; NID:952031; PIDD:CAA32773.1; PID:
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F:38-113/Domain: Immunoglobulin homology <IM>

Query Match 81.0%; Score 453; DB 2; Length 130;
 Best Local Similarity 83.2%; Pred. No. 2,98-31;
 Matches 89; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 IELTQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 61
 DB 24 IVLQSPAIMSAPGKRYTTTCRASSSVSSYLGMWYQOKPGSSPRLIYDTSNLASGVP 83

QY 62 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 108
 DB 84 RFGSGSGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELK 130

RESULT 7
 Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse
 A:Accession: A30662
 A:Residues: 1-130 <DOM>
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Cross-references: UNIPARC:UPI0000115DF8; EMBL:X14620; NID:952031; PIDD:CAA32773.1; PID:
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-130/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
 F:38-113/Domain: Immunoglobulin homology <IM>

J. Siskender, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A>Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
C:Reference number: A30562; MUID:89110066; PMID:2464031
A:Accession: A30562
A>Status: preliminary
Molecule type: mRNA
A:Residues: 1-107 <SIK>
A:Cross-references: UNIPARC:UPI00001767B0
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMV>

Query Match 80.9%; Score 452; DB 2; Length 107;
Best Local Similarity 83.5%; Pred. No. 2,9e-31;
Matches 90; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 2 IELTSPALMSAPGKVTTCRASSSVSSSYLGWYOOKPSSPLLIYDTSNLASGVV 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2 IVLTSPALMSAPGKVTTCSSHSSV--SYMHWIOOKSGTSPRWIYDTSKLASCYPV 59
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DY 62 RPSGGSGSTYSILTIISMEADATYYCCQOWSNPLTFGSCTKLELR 109
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
60 RPSGGSGSTYSILTIISMEADATYYCCQOWSNPLYFGGTKEIKR 107
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
S03410
Ig kappa chain precursor V region (ABE8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S03410
R:Seising, E.; Vosr, J.; Scorb, U.
Nucleic Acids Res. 12, 4229-4246, 1984
A>Title: Immunoglobulin gene 'remnant' DNA - implications for antibody gene recombination
A:Reference number: S03410; MUID:84221356; PMID:6328416
A:Accession: S03410
A:Molecule type: DNA
A:Residues: 1-113 <SEL>
A:Cross-references: UNIPARC:UPI00001767B; EMBL:X00651
A>Note: this sequence was determined from the nonfunctional differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-6/Domain: signal sequence (fragment) #status predicted <SIG>
F:7-113/Product: Ig kappa chain V region ABE8 #status predicted <MAT>
F:22-97/Domain: immunoglobulin homology <IMV>

Query Match 80.9%; Score 452; DB 2; Length 113;
Best Local Similarity 83.5%; Pred. No. 3e-31;
Matches 91; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

QY 1 DIELTSPALMSAPGKVTTCRASSSVSSSYLGWYOOKPSSPLLIYDTSNLASGVV 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 7 ELVLTPALMSAPGKVTTCSSHSSVSSSYLVYIOOKSGSSPRGLWIYSINLASGVV 66
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 VRPSGGSGSTYSILTIISMEADATYYCCQOWSNPLTFGSCTKLELR 109
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 67 ARPSGGSGSTYSILTIISMEADATYYCCQOWST--LTFGAGTKLEIKR 113
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30562
R:Siskender, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A>Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site
A:Reference number: A30562; MUID:89110066; PMID:2464031
A:Accession: B30562
A>Status: preliminary

```

A:Molecule type: mRNA
A:Residues: 1-107 <SIR>
A:Cross-references: UNIPARC:UPI00001767BA
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:16-89/Domain: Immunoglobulin homology <IMM>

Query Match      80.7%; Score 451; DB 2; Length 107;
Best Local Similarity 82.4%; Pred. No. 3.5e-31;
Matches 89; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 2 IELTOSPAIMASPEKEVTTTCRASSSVSSTLVGMVQKRGSSPRLIYDTSNLASGVP 61
DB 2 IVLTPSPAIMSAPGEKVTMTCSASSV--SYMHVYQKSGTSPKRWYDTSKLASGVP 59
62 RPSGSGSGTSYSLTISRMEAEADATYYCCQWSSNPFTPSGTGLKLR 109
60 RPSGSGSGTSYSLTISRMEAEADATYYCCQWSSNPFTPSGTGLKLR 107

RESULT 10
JL0079
1g kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence revision 09-Aug-1996 #text_change 16-Jul-1999
C:Accession: JL0079; A49044; B49044
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, J.
Mol. Immunol. 25, 859-865, 1988
A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-react
A:Reference number: JL0076; MUID:89096973; PMID:3211160
A:Accession: JL0079
A:Molecule type: mRNA
A:Residues: 1-130 <KAA>
A:Cross-references: UNIPARC:UPI000017371F; GB:M27792; NID:9197159
A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6
A>Note: The authors translated the codon TTC for residue 8 as Pro and TTC for residue 10
A>Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation
R:Milstein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A>Title: Non-random features of the repertoire expressed by the members of one V kappa ge
A:Reference number: A49044; MUID:92289826; PMID:1601044
A:Accession: A49044
A:Molecule type: DNA
A:Residues: 1-25 <MTL>
A:Cross-references: UNIPARC:UPI000011760C; GB:S37663; NID:9250214; PIDN:AB22331.1; PID:G
A>Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBI:P.106809)
A:Accession: B49044
A:Molecule type: DNA
A:Residues: 114-116 <MTL2>
A:Cross-references: UNIPARC:UPI000011EB85; GB:S37664; NID:9250215; PIDN:AB22332.1; PID:G
A:Experimental source: BALB/c germ-line
A>Note: sequence extracted from NCBI backbone; partial nucleotide sequences of 13 addit
C:Genetics:
A:Gene: V(kappa)Ox1
A:Antons: 1/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lat
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MNT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:45-109/Disulfide bonds: #status predicted

Query Match      80.5%; Score 450; DB 1; Length 130;
Best Local Similarity 83.3%; Pred. No. 5.1e-31;
Matches 90; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

QY 2 IELTOSPAIMASPEKEVTTTCRASSSVSSTLVGMVQKRGSSPRLIYDTSNLASGVP 61
DB 2 IVLTPSPAIMSAPGEKVTMTCSASSV--SYMHVYQKSGTSPKRWYDTSKLASGVP 61
24 IVLTPSPAIMSAPGEKVTMTCSASSV--SYMHVYQKSGTSPKRWYDTSKLASGVP 61

```

```

Oy      62 RFGSGSGSTSYSLTISRMEADATYYCOQWSSNPLTFSGGKLELR 109
      |||||
Db      82 RFGSGSGSGSYSLTISRMEADATYYCOQWSSNPLTFAGTKLEKR 129
      |||||

```

```

RESULT 11
S25058
Ig kappa chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C/Accession: S25058
R/Fischer, R.; Voas, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A/Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A/Reference number: S25057
A/Accession: S25058
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-235 <P18>
A/Cross-references: UNIPARC:UP10000116096; EMBL:X67211, NID:G54828; PIDN:CAA7650.1, PILIT
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology <IMV>
J38-111/Domains: Immunoglobulin homology <IMV>

```

Query Match	80.5%	Score 450	DB 2	length 235
Best Local	84.3%	Pred. No. 9.2e-31		
Matches 91	Conservative 4	Mismatches 11	Indels 2	Gaps 1

QY 2 IELTQSPAINMSASGEKVTITTCASSSVSSSYGKQKQKQSSPRLLIYDTSMLAGVAV 61
Db 24 IVLTSQAINMSASGEKVTITTCASSSVSR--MQWQKQSGTSPKKNITDTSMLAGVGR 81
QY 62 RFGSGSGSTYSLTLSMEAEADATYYCOOMSSNPLTFSGTGLKLR 109
Db 82 RFGSGSGSTYSLTLSMEAEADATYYCOOMSSNPLTFSGTGLKLR 129

```

RESULT 12
829591
IG kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S29591
R/Kavaler, J.
submitted to the EMBL Data Library, April 1991
A/Accession: S29591
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-103 <KAV>
A/Cross-references: UNIPARC:UPI0000115F57; EMBL:X59094; NID:G52227; PIDN:CAA41820.1; PIIID:
C/Superfamily: Immunoglobulin V region, immunoglobulin homology
C/Keywords: heterocyclamer; immunoglobulin
C/15-88/Domain: immunoglobulin homology <IMM>

```

	Query Match	79.8%	Score 446;	DB 2;	Length 103;
	Best Local Similarity	84.8%;	Pred. No. 8.8e-31;		
	Matches	89;	Conservative	4; Mismatches	10; Indels 2; Gaps 1,
Oy	2	IELTOSPAINASPGKEVTTTCRASSSVSSSYLGWQOKPQSAPLTIYDTNSLASGVPV	61		
	:				
Dd	1	IVLTQSPAINASPGKRVMTCSASSV--SYMHWQQSGTSPPRMVIYDTSKLASGVPA	58		
	:				
Oy	62	RFSGGSGSTSYSLTISRMEADDAITYYCQMSSNPLTGSGTKLE	106		
	:				
Dd	59	RFSGGSGSTSYSLTISIRMEADDAITYYCQMSSNPLTGAGTKLE	103		
	:				

RESULT 13
505269
IG kappa chain precursor V-J region (38C13-V4) - mouse (Fragment)
C1Species: Mus musculus (house mouse)
C1Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C1Accession: 505269; J00064; 503847

R. Levy, S.
submitted to the EMBL Data Library, February 1989
;Reference number: S05267

Query Match	79.8%	Score 446;	DB 2;	Length 123;
Best Local Similarity	79.8%	Pred. No. 1e-30;		
Matches 87; Conservative	7;	Mismatches 15;	Indels 0;	Gaps

QY _ DIELTOSPATMSKSPBKAYTTTCRASSVSSXILGYWYOOKPGSPPLLIDYDNTSLASGVP 6
:
:
Db 14 EIVLTDSPTTMAASPGEKITITTSABSSISBNTLHHYOOKPGSPPLLIYRTSNLASGVP 73

RESULT 14
529581
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 21-Jan-2000
C/Accession: S29581, S26477, S29589, B33730, S26476
R/Kavaler, J.
submitted to the EMBL Data Library, April 1991
A/Reference number: S26459
A/Accession: S29581
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <KAV>
A/Cross-references: UNIPARC:UPI00001150BD, EMBL:X59096; NID:g52219; PIDN:CAA41822.1; PID
A/Accession: S26477
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-106 <KA2>
A/Cross-references: UNIPARC:UPI0000115F5D, EMBL:X59103; NID:g52213; PIDN:CAA41829.1; PID
A/Accession: S29589
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 2-104 <KA3>
A/Cross-references: UNIPARC:UPI0000115F55, EMBL:X59092; NID:g52223; PIDN:CAA41818.1; PID
R/Lavler, A.M., Kearney, J.F., Kuehl, M., Geathart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A/Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, ungly
A/Reference number: A33730, MUID:89367325, PMID:2505260
A/Accession: B33730
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-96 <LAW>
A/Cross-references: UNIPARC:UPI0000114B56, GB:M25998; NID:g197113; PIDN:AAA38913.1; PID:g
A/Note: the authors translated the codon ATT for residue 2 as Ala
C/Keywords: heterotetramer, immunoglobulin
J16-91/Domain: immunoglobulin homology <IMM>

Query Match 79.6%; Score 445; DB 2; Length 108;
 Best Local Similarity 81.5%; Pred. No. 1,1e-30;
 Matches 88; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSYLGMWYQOKPGSSPRLIYDTSNLAGVP 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 EIVLTQSPALMASPGKVTTCRASSSVSYLGMWYQOKPGSSPRLIYDTSNLAGVP 60
 DB 1 EIVLTQSPALMASPGKVTTCRASSSVSYLGMWYQOKPGSSPRLIYDTSNLAGVP 60
 QY 61 VRFSGSGGTSTLTISRMEADDAATYYCQWSSNPPLTFGAGTKLEK 108
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 61 VRFSGSGGTSTLTISRMEADDAATYYCQWSSNPPLTFGAGTKLEK 108
 DB 61 VRFSGSGGTSTLTISRMEADDAATYYCQWSSNPPLTFGAGTKLEK 108

RESULT 15

S38720
 Ig light chain V region - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 C/Accession: S38720
 R/Cimanis, A.Y.
 Submitted to the EMBL Data Library, November 1993
 A/Reference number: S38713
 A/Accession: S38720
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-108 <CIW>
 A/Cross-references: UNIPARC:UPI0000117544; EMBL:X76023; NID:g416104; PIDN:CAA53610.1; PI
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: immunoglobulin
 P.16-89/Domain: immunoglobulin homology <IMM>

Query Match 79.5%; Score 444.5; DB 2; Length 108;
 Best Local Similarity 82.7%; Pred. No. 1.2e-30;
 Matches 91; Conservative 7; Mismatches 9; Indels 3; Gaps 2;
 QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSYLGMWYQOKPGSSPRLIYDTSNLAGVP 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 EIVLTQSPALMASPGKVTTCRASSSVSYLGMWYQOKPGSSPRLIYDTSNLAGVP 60
 DB 1 EIVLTQSPALMASPGKVTTCRASSSVSYLGMWYQOKPGSSPRLIYDTSNLAGVP 60
 QY 61 VRFSGSGGTSTLTISRMEADDAATYYCQWSSNPPLTFGAGTKLEK 109
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 59 LRFSGSGGTSTLTISRMEADDAATYYCQWSSNPPLTFGAGTKLEK 108
 DB 59 LRFSGSGGTSTLTISRMEADDAATYYCQWSSNPPLTFGAGTKLEK 108

Search completed: November 21, 2005, 12:22:13
 Job time : 27.5513 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 161.304 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-88
Perfect score: 559
Sequence: 1 DIELOSPAINSPASPEKVT.....QOWSSNPLTFGSGTKLEIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	474	84.8	106	Q9U410_MOUSE
2	468	83.7	114	Q8K1F1_MOUSE
3	463.5	82.9	131	Q811C3_MOUSE
4	461	82.5	108	KV6K_MOUSE
5	460	82.5	112	Q8K1F2_MOUSE
6	450	80.5	235	Q58BV6_MOUSE
7	447	80.0	235	Q5XFY8_MOUSE
8	445	79.6	107	KV6F_MOUSE
9	440	78.7	107	KV6I_MOUSE
10	439	78.5	107	KV6H_MOUSE
11	439	78.5	112	Q8K1F3_MOUSE
12	438	78.4	107	KV6G_MOUSE
13	438	78.4	107	KV6J_MOUSE
14	438	78.4	237	Q569Y8_MOUSE
15	433	77.5	112	Q8K1F0_MOUSE
16	431	77.1	134	Q8VDD0_MOUSE
17	420	75.1	129	KV4A_MOUSE
18	408	73.0	109	Q9UL78_HUMAN
19	401.5	71.8	97	Q9JL76_MOUSE
20	399.5	71.5	101	Q9JL78_MOUSE
21	397	71.0	129	KV3I_HUMAN
22	395	70.7	107	KV6B_MOUSE
23	394	70.5	107	KV6C_MOUSE
24	394	70.5	129	KV3K_HUMAN
25	393	70.3	109	KV3D_HUMAN
26	391	69.9	107	KV6D_MOUSE
27	390	69.8	107	KV6E_MOUSE
28	390	69.8	109	KV3B_HUMAN
29	389	69.6	109	KV3E_HUMAN
30	387	69.2	107	KV6A_MOUSE
31	383.5	68.6	236	Q6P1I8_HUMAN

32	382.5	68.4	235	2	Q6P1I7_HUMAN	Q6P1I7_homo sapien
33	380	68.0	235	2	Q6GMV9_HUMAN	Q6GMV9_homo sapien
34	379	67.8	109	2	Q9UL86_HUMAN	Q9UL86_homo sapien
35	376	67.3	109	1	KV3F_HUMAN	P01624_homo sapien
36	375	67.1	235	2	Q6PJF2_HUMAN	Q6PJF2_homo sapien
37	373	66.7	107	2	Q6PSA9_HUMAN	Q6PSA9_homo sapien
38	371.5	66.5	108	2	Q9UL77_HUMAN	Q9UL77_homo sapien
39	371.5	66.5	244	2	Q6SZC8_HUMAN	Q6SZC8_homo sapien
40	370.5	66.3	108	2	Q9UL70_HUMAN	Q9UL70_homo sapien
41	369.5	66.1	236	2	Q6P1T5_HUMAN	Q6P1T5_homo sapien
42	368.5	65.9	128	1	KV3A_HUMAN	P06311_homo sapien
43	368	65.8	108	1	KV3L_HUMAN	P01594_homo sapien
44	367.5	65.7	108	1	KV3B_HUMAN	Q9UL79_homo sapien
45	367.5	65.7	108	2	Q9UL79_HUMAN	

ALIGNMENTS

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RESULT 1
Q9U410_MOUSE                                PRT; 106 AA.
ID Q9U410_MOUSE PRELIMINARY;
AC Q9U410;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 25, Last sequence update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30
DE immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12567627;
RA Song X.T., Peng Z.Q., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,
  Huang H.L., Guan X.H.;
RT "Cloning and sequence analysis of the light chain variable region
RT gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
RT japonicum."
RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
  18:257-259(2000).
RL EMBL; AF207620; AAF19434.1; -, Genomic DNA.
DR HSSP; P01679; 2FBJ.
DR SMR; Q9U410; 4-106.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
FT 1
FT 106
SQ SEQUENCE 106 AA; 11478 MW; F20F5444JBAE63B CRC64;

Query Match      84.8%; Score 474; DB 2; Length 106;
Best local Similarity 90.5%; Pred. No. 1,1e-38;
Matches 95; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 4 LNOSPAINSPASPEKVTTCRASSSVSXSLCMYQOKPSSPRLLIYDTSNLASGVPRF 63
DB 4 LQSPAINSPASPEKVTTCASSSV--SYVWYLOKPESSRRLIYDTSNLASGVPRF 61
QY 64 SSGSGSTSYSLTISRMEADATYYCOQWSNPPLTFGSGTKLEIK 108
DB 62 SSGSGSTSYSLTISRMEADATYYCOQWTSYPTFGSGTKLEIK 106

RESULT 2
Q8K1F1_MOUSE                                PRT; 114 AA.
ID Q8K1F1_MOUSE PRELIMINARY;
AC Q8K1F1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

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DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-VIPase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAIB/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Terrynek T., Avrameas S.;
RT "Two murine natural polyclonal antibodies are encoded by
RT nonmutated germ-line genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA Tillingham D.M., Jon N.T., Hill R.J., Marion T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZW)F1 mice."
RL J. Exp. Med. 176:761-779(1992).
DR EMBL/ AF516284; AAM64202.1; -; Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PH1058; PH1058.
DR HSBP; P01837; 25C8.
DR SMR; Q8K1F1; 2-114.
DR Ensembl; ENSMUSG0000059896; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 114 AA; 12163 MW; 8BD9833DBF3BFD1 CRC64;
SQ
Query Match 83.7%; Score 468; DB 2; Length 114;
Best Local Similarity 85.3%; Pred. No. 4.8e-38;
Matches 93; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
QY 1 DIETOSPAINASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 60
DB 1 DIVLTQSPALMSASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 60
QY 61 VRPFGSGSGTSYSLTISRMEADATYYCCQWSSNP-LTFSGGTLELKR 109
DB 61 ARPFGSGSGTSYSLTISRMEADATYYCCQWSSNP-LTFSGGTLELKR 109
RESULT 3
Q81C3 MOUSE PRELIMINARY; PRT; 131 AA.
AC Q81C3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Immunoglobulin gamma-3 kappa chain precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MRL-Moj-1Dpr; TISSUE=Spleen;
RX MEDLINE=93156722; PubMed=8429833; DOI=10.1016/0161-5890(93)90089-T;
RA Takahashi S., Itoh U., Nose M., Ono M., Yamamoto T., Kyogoku M.;
RT "Cloning and cDNA sequence analysis of nephritic genetic monoclonal
RT antibodies derived from an MRL-lpr lupus mouse."

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RL Moj. Immunol. 30:177-182(1993).
DR EMBL; D14629; BAA03482.1; -; mRNA.
DR HSBP; P01679; 2FBJ.
DR SMR; Q81C3; 23-131.
DR Ensembl; ENSMUSG0000059987; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT SIGNAL 1
FT SIGNAL 22
FT CHAIN 23 >131 Potential.
FT NON_TER 131 Immunoglobulin gamma-3 kappa chain.
FT SEQUENCE 131 AA; 14083 MW; 5E83659546682E CRC64;
SQ
Query Match 82.9%; Score 463.5; DB 2; Length 131;
Best Local Similarity 86.1%; Pred. No. 1.6e-37;
Matches 93; Conservative 6; Mismatches 8; Indels 1; Gaps 1;
QY 2 IELTOSPAINASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 61
DB 24 IVLTQSPALMSASPGKRVTTTCRASSSVSSSYLGWYQOKGSSPRLIYDTSNLASGVP 83
QY 62 RFPSSGSGTSYSLTISRMEADATYYCCQWSSNP-LTFSGGTLELKR 108
DB 84 RFPSSGSGTSYSLTISRMEADATYYCCQWSSNP-LTFSGGTLELKR 131
RESULT 4
KV6K MOUSE STANDARD; PRT; 108 AA.
AC P04945;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-JI region NO2-6.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Matham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazoline and its early diversification."
RL Nature 304:320-324(1983).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X00746; AAA38691.1; -; mRNA.
DR HSBP; Q91W12; 1AY1.
DR SMR; P04945; 1-108.
DR Ensembl; ENSMUSG0000062686; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KV Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1
FT REGION 23
FT REGION 33 Framework-1.
FT REGION 34 Framework-2.
FT REGION 48 Framework-2.
FT REGION 49 Complementarity-determining-2.
FT REGION 55 Complementarity-determining-2.
FT REGION 56 Framework-3.
FT REGION 88 Complementarity-determining-3.
FT REGION 98 Framework-4.
FT REGION 99 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 108 108

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SQ SEQUENCE 108 AA; 11713 MW; DABF235CD9680AC6 CRC64;
 Query Match 82.5%; Score 461; DB 1; Length 108;
 Best Local Similarity 86.2%; Pred. No. 2.2e-37;
 Matches 94; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

QY 2 IELTQSPAIMSAPGKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 61
 DB 2 IELTQSPAIMSAPGKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 59

QY 62 RPSGSGSGTSYSLTISRMEADAAATYYCOQWSSNP-LTPSGGTLEIKR 108
 DB 60 RPSGSGSGTSYSLTISRMEADAAATYYCOQWSSNP-LTPSGGTLEIKR 108

RESULT 5
 Q8K1F2_MOUSE PRELIMINARY; PRT; 112 AA.
 ID Q8K1F2_MOUSE PRELIMINARY; PRT; 112 AA.
 AC Q8K1F2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BAUB/c; TISSUE=Hypermunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polypeptide autoantibodies are encoded by
 nomenclated germ-line genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 DR EMBL; AF516283; AA64201.1; -; Genomic_DNA.
 DR PIR; H33932; H33932.
 DR HSRP; P01837; 25C8.
 DR SMR; Q8K1F2; 2-112.
 DR Ensembl; ENSMUSG0000064150; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 112
 SQ SEQUENCE 112 AA; 11953 MW; 4716B87FADB543BD CRC64;

Query Match 82.5%; Score 461; DB 2; Length 112;
 Best Local Similarity 85.3%; Pred. No. 2.3e-37;
 Matches 93; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 1 DIELTQSPAIMSAPGKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 60
 DB 1 DIELTQSPAIMSAPGKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 58

QY 61 RPSGSGSGTSYSLTISRMEADAAATYYCOQWSSNP-LTPSGGTLEIKR 109
 DB 59 RPSGSGSGTSYSLTISRMEADAAATYYCOQWSSNP-LTPSGGTLEIKR 107

RESULT 6
 Q58BV6_MOUSE PRELIMINARY; PRT; 235 AA.
 ID Q58BV6_MOUSE PRELIMINARY; PRT; 235 AA.
 AC Q58BV6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Igk-C protein.
 GN Name=Igk-C;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,
 RA Buterfield Y.S., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC091738; AA91738.1; -; mRNA.
 DR SMR; Q58BV6; 23-235.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; C1-sect; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 235 AA; 25719 MW; BEA84ABD2576252 CRC64;

Query Match 80.5%; Score 450; DB 2; Length 235;
 Best Local Similarity 82.4%; Pred. No. 6.7e-36;
 Matches 89; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSAPGKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 61
 DB 24 IELTQSPAIMSAPGKVTTCRASSSVSSYLGMVQKPGSSPRLIYDTSNLSAGVP 81

QY 62 RPSGSGSGTSYSLTISRMEADAAATYYCOQWSSNP-LTPSGGTLEIKR 109
 DB 82 RPSGSGSGTSYSLTISRMEADAAATYYCOQWSSNP-LTPSGGTLEIKR 129

RESULT 7
 Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
 ID Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
 AC Q5XFY8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchen L., Marusina K., Farmer A.A., Rubin J.A., Gunaratne P.H.,
RA Stadelman M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Tothyluk S., Carinot P., Prange C.,
RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heaton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blesbey R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.B.,
RA Schnerch A., Schein J.R., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Director MGC Project;
RX Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC084683; AA84683.1; -; mRNA.
DR SMR; Q5XY8; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25835 MW; 828B9ED277FDC667 CRC64;

Query Match 80.0%; Score 447; DB 2; Length 235;
Best Local Similarity 81.5%; Pred. No. 1.3e-35;
Matches 88; Conservative 8; Mismatches 10; Indels 2; Gaps 1;

QY 2 IELTSPAINASASGKVTTCRASSSVSSYLGMVYOOKPSPRLTYDTSNLASGVV 61
DQ 24 IVLSGSPALISGFGKVTTCRASSSV--NYMMYQOKSPSSKRPVATYSKLASGVV 81
QY 62 RFSSGSGTSYSLTISRMEADAAATYTCQWBSNPLTFGSGTKLELR 109
DQ 82 RFSSGSGTSYSLTISRMEADAAATYTCQWBSNPLTFGAGTKLELR 129

RESULT 8
KV6F MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig kappa chain V-VI region NQ2-17.4.1.
MS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstien C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenylloxazolone and its early diversification."
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; K00735; AAA3680.1; -; mRNA.
DR HSSP; P01679; 2PBJ.
DR SMR; P04940; 1-107.
DR Ensembl; ENSMUSG0000062047; Mus musculus.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hydrionema; Immunoglobulin domain; Immunoglobulin V region.
RN REGION 1 23
FT REGION 1 23 Complementarity-determining-1.
FT REGION 2 34 Complementarity-determining-2.
FT REGION 3 48 Complementarity-determining-3.
FT REGION 4 55 Complementarity-determining-4.
FT REGION 5 87 Complementarity-determining-5.
FT REGION 6 96 Complementarity-determining-6.
FT REGION 7 106 Complementarity-determining-7.
FT REGION 8 107 By similarity.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11561 MW; 6F694284BCFA68B6 CRC64;

Query Match 79.6%; Score 445; DB 1; Length 107;
Best Local Similarity 81.5%; Pred. No. 8e-36;
Matches 88; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

QY 2 IELTSPAINASASGKVTTCRASSSVSSYLGMVYOOKPSPRLTYDTSNLASGVV 61
DQ 2 IVLTSPAINASASGKVTTCRASSSV--SYMMYQOKSGTSKRPVATYSKLASGVV 59
QY 62 RFSSGSGTSYSLTISRMEADAAATYTCQWBSNPLTFGSGTKLELR 109
DQ 60 RFSSGSGTSYSLTISRMEADAAATYTCQWBSNPLTFGAGTKLELR 107

RESULT 9
KV6I MOUSE STANDARD; PRT; 107 AA.
AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig kappa chain V-VI region NQ6-8.3.1.
MS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstien C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
phenylloxazolone and its early diversification."
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.

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CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL, K00740; AAA38685.1; -; mRNA.

DR HSSP, P01679; 2PBJ.

DR SMR, P04943; 1-107.

DR Ensembl, ENSMUSG00000062047; Mus musculus.

DR InterPro, IPR007110; Ig-like.

DR SMART, SM00406; IGV; 1.

DR PROSITE, PS50835; IG_LIKE; 1.

DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.

FT REGION 1 23 Framework-1.

FT REGION 24 33 Complementarity-determining-1.

FT REGION 34 48 Framework-2.

FT REGION 49 55 Complementarity-determining-2.

FT REGION 56 87 Framework-3.

FT REGION 88 96 Complementarity-determining-3.

FT REGION 97 106 Framework-4.

FT DISULFID 23 87 By similarity.

FT NON TER 107 107

SEQUENCE 107 AA; 11573 MW; 6F694824ECFC08E6 CRC64;

Query Match 78.7%; Score 440; DB 1; Length 107;

Best Local Similarity 80.6%; Pred. No. 2.5e-35;

Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 2 IELTSPAIMSASPEKVTITTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVV 61
DB 2 IYLTQSPAIMSASPEKVTITTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVV 59
QY 62 RPSGSGSGTSLTISRMEDATATYCCQMSNPLTFGSGTKLELR 109
DB 60 RPSGSGSATSLTITSMQABDATTYCCQMSNPLTFGAGTKLELR 107

RESULT 10

ID KV6H MOUSE STANDARD; PRT; 107 AA.

AC P04942;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Ig kappa chain V-VI region N05-61.1.2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

NP NUCLEOTIDE SEQUENCE.

RA MEDLINE=83271467; PubMed=6877353;

RA Kaartinen M., Griffiths G.M., Markham A.F., Mjellein C.;

RT "mRNA sequences define an unusually restricted Igg response to 2-

RT phenylloxazalone and its early diversification.";

RT Nature 304:320-324(1993).

CC 1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL, K00739; AAA38684.1; -; mRNA.

DR HSSP, P01679; 2PBJ.

DR SMR, P04942; 1-107.

DR Ensembl, ENSMUSG00000062047; Mus musculus.

DR InterPro, IPR007110; Ig-like.

DR InterPro, IPR003596; Ig_V.

DR SMART, SM00406; IGV; 1.

DR PROSITE, PS50835; IG_LIKE; 1.

DR Hybridoma; Immunoglobulin domain; Immunoglobulin V region.

FT REGION 1 23 Framework-1.

FT REGION 24 33 Complementarity-determining-1.

FT REGION 34 48 Framework-2.

FT REGION 49 55 Complementarity-determining-2.

FT REGION 56 87 Framework-3.

FT REGION 88 96 Complementarity-determining-3.

FT REGION 97 106 Framework-4.

FT DISULFID 23 87 By similarity.

FT NON TER 107 107

SEQUENCE 107 AA; 11605 MW; CA6C4284ECFCB550 CRC64;

Query Match 78.5%; Score 439; DB 1; Length 107;

Best Local Similarity 80.6%; Pred. No. 3.1e-35;

Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

QY 2 IELTSPAIMSASPEKVTITTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVV 61
DB 2 IYLTQSPAIMSASPEKVTITTCRASSSVSSYLGWYQOKPSSPRLIYDTSNLASGVV 59
QY 62 RPSGSGSGTSLTISRMEDATATYCCQMSNPLTFGSGTKLELR 109
DB 60 RPSGSGSATSLTITSMQABDATTYCCQMSNPLTFGAGTKLELR 107

RESULT 11

ID Q8K1F3 MOUSE PRELIMINARY; PRT; 112 AA.

AC Q8K1F3;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Anti-VIPase light chain variable region (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

NP NUCLEOTIDE SEQUENCE.

RA STRAIN=BALB/c; TISSUE=Hyperimmunized spleen;

RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;

RT "Two murine natural polyclonal autoantibodies are encoded by

RT nonmutated germ-line genes.";

RT Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).

CC 1- FUNCTION: Anti-VIPase light chain variable region (Fragment).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL, AF516282; AA064200.1; -; Genomic_DNA.

DR PIR, A33933; A33933.

DR PIR, P01085; P01085.

DR HSSP, P01837; 25C8.

DR SMR, Q8K1F3; 2-112.

DR Ensembl, ENSMUSG00000063156; Mus musculus.

DR InterPro, IPR007110; Ig-like.

DR SMART, SM00406; IGV; 1.

DR PROSITE, PS50835; IG_LIKE; 1.

FT NON TER 1 1

FT NON TER 112 112

SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;

Query Match 78.5%; Score 439; DB 2; Length 112;
Best Local Similarity 81.7%; Pred. No. 3.3e-35;
Matches 89; Conservative 5; Mismatches 13; Indels 2; Gaps 1;

Qy 1 DIELTOSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
Db 1 DILVLTOSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 58
Qy 61 VRFGSGSGTSTSLTISRMEADATYTCOOMSSNPLTFGSGTKLEKR 109
Db 59 ARFGSGSGTSTSLTISRMEADATYTCOOMSSNPLTFGSGTKLEKR 107

RESULT 12
KV6G_MOUSE STANDARD; PRT; 107 AA.
ID KV6G_MOUSE
AC P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
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CC -----
CC EMBL; K00737; AAA38682.1; -; mRNA.
CC HSSP; Q91W12; IAY1.
CC SMR; P04941; 1-103.
CC Ensembl; ENSMUSG0000062047; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11557 MW; 72488DA9EF354934 CRC64;

Query Match 78.4%; Score 438; DB 1; Length 107;
Best Local Similarity 80.6%; Pred. No. 3.9e-35;
Matches 87; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 61
Db 2 ILVLTOSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 59
Qy 62 RFGSGSGTSTSLTISRMEADATYTCOOMSSNPLTFGSGTKLEKR 109
Db 60 RFGSGSGTSTSLTISRMEADATYTCOOMSSNPLTFGSGTKLEKR 107

RESULT 13
KV6J_MOUSE STANDARD; PRT; 107 AA.
ID KV6J_MOUSE
AC P04944;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NQ5-78.2.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-phenylloxazolone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
CC -----
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CC -----
CC EMBL; K00744; AAA38689.1; -; mRNA.
CC HSSP; Q91W12; IAY1.
CC SMR; P04944; 1-106.
CC Ensembl; ENSMUSG0000062047; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 33 Complementarity-determining-1.
FT REGION 34 48 Framework-2.
FT REGION 49 55 Complementarity-determining-2.
FT REGION 56 87 Framework-3.
FT REGION 88 96 Complementarity-determining-3.
FT REGION 97 106 Framework-4.
FT DISULFID 23 87 By similarity.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11613 MW; A38290781F3C30D3 CRC64;

Query Match 78.4%; Score 438; DB 1; Length 107;
Best Local Similarity 80.6%; Pred. No. 3.9e-35;
Matches 87; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

Qy 2 IELTOSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 61
Db 2 ILVLTOSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 59
Qy 62 RFGSGSGTSTSLTISRMEADATYTCOOMSSNPLTFGSGTKLEKR 109
Db 60 RFGSGSGTSTSLTISRMEADATYTCOOMSSNPLTFGSGTKLEKR 107

RESULT 14
Q569Y8_MOUSE PRELIMINARY; PRT; 237 AA.
ID Q569Y8_MOUSE
AC Q569Y8;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Igg-C protease.
GN Name=Igg-C;
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RP NCBI_TaxID=10090;
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klusner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carroll P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullik S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (Apr-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC092251; AA092251.1; -, mRNA.
 DR SMR, Q66978; 23-237.
 DR InterPro: IPR003599; 19.
 DR InterPro: IPR007110; 19-11ke.
 DR InterPro: IPR003597; 19-11.
 DR InterPro: IPR003006; 19-MHC.
 DR InterPro: IPR003596; 19-V.
 DR Pfam, PF07654; Cl-sect. 1.
 DR SMART, SM00409; 19; 2.
 DR SMART, SM00407; IG1; 1.
 DR SMART, SM00406; IG1; 1.
 DR PROSITE, PS50835; IG LIKE; 2.
 DR PROSITE, PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 237 AA; 25978 MW; A88596AA47FFB932 CRC64;
 Query Match 78.4%; Score 438; DB 2; Length 237;
 Best Local Similarity 78.0%; Pred. No. 1e-34;
 Matches 85; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
 QY 1 DIELTGSPAINASPGKVTTCRASSSVSSSYLGWYQKGGSPRLIYDTSNLASGVP 60
 DB 23 EIVLTGSPALMAASPGKVTTCRASSSVSSSIDSSNLHMYQKGGSPKAWIYGTSNLASGVP 82
 QY 61 VPFSGSGSTSYSLTISRMEADATYTCQOWSNPLTFGSGTKLELR 109
 DB 83 PPFSGSGSTSYSLTISRMEADATYTCQOWSNPLTFGSGTKLELR 131
 RESULT 15
 O8K1FO_MOUSE PRELIMINARY; PRT; 112 AA.
 AC O8K1FO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Anti-Virapase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=BL6/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RX PubMed=2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 DR EMBL, AF516285; AA064203.1; -, Genomic DNA.
 DR PIR, A33933; A33933.
 DR PIR, PC4405; PC4405.
 DR HSSP, P01837; 10R0.
 DR SMR, O8K1FO; 3-112.
 DR EMBL, ENSMUSG0000062047; Mus musculus.
 DR InterPro: IPR007110; 19-11ke.
 DR InterPro: IPR003596; 19-V.
 DR SMART, SM00406; IG1; 1.
 DR PROSITE, PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT 112
 SQ SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;
 Query Match 77.5%; Score 433; DB 2; Length 112;
 Best Local Similarity 81.1%; Pred. No. 1.3e-34;
 Matches 86; Conservative 4; Mismatches 14; Indels 2; Gaps 1;
 QY 4 LTGSPAINASPGKVTTCRASSSVSSSYLGWYQKGGSPRLIYDTSNLASGVP 63
 DB 4 LTGSPAINASPGKVTTCRASSSV--SYHMYQKGGSPKRWIYDTSKLASGVP 61
 QY 64 SGSGSGSTSYSLTISRMEADATYTCQOWSNPLTFGSGTKLELR 109
 DB 62 SGSGSGSTSYSLTISRMEADATYTCQOWSNPLTFGSGTKLELR 107

Search completed: November 21, 2005, 12:04:06
 Job time : 162.304 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 / Search time 41.1245 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-88

Perfect score: 559
Sequence: 1 DIELTQSPAIMSASGPKVKT.....QOWSSNPLTFGSGTKELIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgnt2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgnt2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgnt2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgnt2_6/ptodata/1/1aa/BCTMS_COMB.pep:*
5: /cgnt2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgnt2_6/ptodata/1/1aa/backfilled.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	484	86.6	110	2	US-09-726-219A-237
2	484	86.6	110	2	US-09-196-522-237
3	482	86.2	244	1	US-08-553-497A-20
4	481	86.0	110	2	US-09-726-219A-255
5	481	86.0	110	2	US-09-196-522-255
6	481	86.0	242	1	US-08-553-497A-26
7	481	86.0	242	1	US-08-553-497A-28
8	476	85.2	106	1	US-07-634-278-58
9	476	85.2	106	1	US-08-474-040-58
10	476	85.2	106	1	US-08-474-040-58
11	476	85.2	106	1	US-08-487-200-58
12	476	85.2	106	2	US-08-484-537-58
13	476	85.2	128	1	US-07-634-278-31
14	476	85.2	128	1	US-08-477-728-31
15	476	85.2	128	1	US-08-474-040-31
16	476	85.2	128	1	US-08-487-200-31
17	476	85.2	128	1	US-08-484-537-31
18	475	85.0	128	1	US-07-946-421-26
19	472	84.4	246	1	US-08-553-497A-24
20	471	84.3	108	2	US-09-726-219A-243
21	471	84.3	108	2	US-09-196-522-243
22	470	84.1	110	2	US-09-726-219A-256
23	470	84.1	108	2	US-09-196-522-256
24	469	83.9	108	2	US-09-948-004-28
25	469	83.9	107	2	US-09-948-004-18
26	468	83.7	107	1	US-08-211-202-3
27	468	83.7	110	2	US-09-726-219A-254

28	468	83.7	110	2	US-09-196-522-254	Sequence 254, App
29	468	83.7	246	1	US-08-469-486-57	Sequence 57, App
30	468	83.7	246	1	US-08-469-658-57	Sequence 57, App
31	467	83.5	108	2	US-09-726-219A-251	Sequence 251, App
32	467	83.5	108	2	US-09-196-522-251	Sequence 251, App
33	466	83.4	110	2	US-09-726-219A-250	Sequence 250, App
34	466	83.4	110	2	US-09-196-522-250	Sequence 250, App
35	464	83.0	244	1	US-08-553-497A-22	Sequence 22, App
36	463.5	82.9	108	2	US-09-232-290-2	Sequence 2, App
37	463	82.8	255	2	US-09-553-498-8	Sequence 8, App
38	463	82.8	255	2	US-09-618-869-8	Sequence 8, App
39	462	82.6	215	6	US-09-310-3	Sequence 9, App
40	461	82.5	108	2	US-09-171-945-9	Sequence 9, App
41	461	82.5	108	2	US-09-910-059-9	Sequence 9, App
42	460	82.3	105	2	US-09-091-071-1	Sequence 1, App
43	460	82.3	108	2	US-09-726-219A-253	Sequence 253, App
44	460	82.3	108	2	US-09-196-522-253	Sequence 253, App
45	460	82.3	110	2	US-09-726-219A-257	Sequence 257, App

ALIGNMENTS

RESULT 1
US-09-726-219A-237
Sequence 237, Application US/09726219A
Patent No. 6806079
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Medical Research Council
APPLICANT: McAfferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Jackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT FILING DATE: US/09/726,219A
CURRENT APPLICATION NUMBER: US-09-726-219A
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 237
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone

US-09-726-219A-237

Query Match 86.6%; Score 484; DB 2; Length 110;
Best Local Similarity 86.2%; Pred. No. 7.3e-39;
Matches 94; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLASGVP 60
DB 1 DIELTOSPAIMASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLASGVP 60

QY 61 VRFGSGSGTSTYSLTISRMEADATYYCCQWSSNPLTFSGTLEIKR 109
DB 61 ARFGSGSGTSTYSLTISRMEADATYYCCQYSGVPLTFGAGTLEIKR 109

RESULT 2
US-09-196-522-237
Sequence 237, Application US/09196522
Patent No. 6916605

GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Giffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonet, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-0004
CURRENT APPLICATION NUMBER: US/09/196,522
CURRENT FILING DATE: 1998-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patent version 3.1
SEQ ID NO 237
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-237

Query Match 86.6%; Score 484; DB 2; Length 110;
Best Local Similarity 86.2%; Pred. No. 7.3e-39;
Matches 94; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 DIELTOSPAIMASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLASGVP 60
DB 1 DIELTOSPAIMASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLASGVP 60

DB 1 DIELTOSPAIMASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLASGVP 60

QY 61 VRFGSGSGTSTYSLTISRMEADATYYCCQWSSNPLTFSGTLEIKR 109
DB 61 ARFGSGSGTSTYSLTISRMEADATYYCCQYSGVPLTFGAGTLEIKR 109

RESULT 3
US-08-553-497A-20
Sequence 20, Application US/08553497A
Patent No. 5844093

GENERAL INFORMATION:
APPLICANT: KETTERBROUGH, C. A.
APPLICANT: BRIDG, MARY M.
APPLICANT: ANSEL, KEITH H.
APPLICANT: GUSOW, DETLEF
APPLICANT: ADAM, JADME
APPLICANT: MITJANS, FRANSESC
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILATS, JADME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HANLEY-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-20

Query Match 86.2%; Score 482; DB 1; Length 244;
Best Local Similarity 89.1%; Pred. No. 2.8e-38;
Matches 98; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 1 DIELTOSPAIMASPGKVTTCRASSSVSSYLGMVQOKPGSPRLIYDTSNLASGVP 60
DB 137 DIELTOSPAIMASPGKVTTCRASSSV--SYMVYQOKPGSPRLIYDTSNLASGVP 194
QY 61 VRFGSGSGTSTYSLTISRMEADATYYCCQWSSNPLTFSGTLEIKR 108

Db 195 VRFSGSGGTSTYSLTISRMEADATYYCQQRSSYPMTFTGGTKLEIK 244

RESULT 4
US-09-726-219A-255
; Sequence 255, Application US/09726219A

; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Grifflths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 255
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-255

Query Match 86.0%; Score 481; DB 2; Length 110;
Best Local Similarity 87.2%; Pred. No. 1,4e-38;
Matches 95; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSISYLGWYQOKPGSSPRLIYDTSNLASGVP 60
DB 1 DIELTQSPAIMSASPGKVTTCRASSSVSISYLGWYQOKPGSSPRLIYDTSNLASGVP 60
QY 61 VRFSGSGGTSTYSLTISRMEADATYYCQQRSSYPMTFTGGTKLEIK 109
DB 61 VRFSGSGGTSTYSLTISRMEADATYYCQQRSSYPMTFTGGTKLEIK 109

RESULT 5
US-09-196-522-255
; Sequence 255, Application US/09196522
; Patent No. 6916605

; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Grifflths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 255
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-255

Query Match 86.0%; Score 481; DB 2; Length 110;
Best Local Similarity 87.2%; Pred. No. 1,4e-38;
Matches 95; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSISYLGWYQOKPGSSPRLIYDTSNLASGVP 60
DB 1 DIELTQSPAIMSASPGKVTTCRASSSVSISYLGWYQOKPGSSPRLIYDTSNLASGVP 60
QY 61 VRFSGSGGTSTYSLTISRMEADATYYCQQRSSYPMTFTGGTKLEIK 109
DB 61 VRFSGSGGTSTYSLTISRMEADATYYCQQRSSYPMTFTGGTKLEIK 109

RESULT 6
US-08-553-497A-26
; Sequence 26, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTERBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSLOW, DETLEF
; APPLICANT: ADAM, JAUME
; APPLICANT: MITTANS, FRANSISC
; APPLICANT: ROSELL, ELISABET

APPLICANT: BLASCO, FRANCESC
APPLICANT: PITLATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-26

Query Match 86.0%; Score 481; DB 1; Length 242;
Best Local Similarity 88.9%; Pred. No. 3.5e-38;
Matches 96; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 1 DIETLOSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLASGVP 60
DB 137 DIETLOSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLASGVP 194

QY 61 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGTKLEIK 108
DB 195 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGTKLEIK 242

RESULT 7
US-08-553-497A-28
Sequence 28, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTLERBROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSOW, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESC
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PITLATS, JAUME
TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR

TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZEILANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD, SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-28

Query Match 86.0%; Score 481; DB 1; Length 242;
Best Local Similarity 88.9%; Pred. No. 3.5e-38;
Matches 96; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 1 DIETLOSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLASGVP 60
DB 137 DIETLOSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPSSPRLIYDTSNLASGVP 194

QY 61 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGTKLEIK 108
DB 195 VRFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGTKLEIK 242

RESULT 8
US-07-634-278-58
Sequence 58, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHREIBER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COBLINGH, Kathleen L.
APPLICANT: SELICK, Harold B.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-634-278-58

Query Match 85.2%; Score 476; DB 1; Length 106;
Best Local Similarity 88.8%; Pred. No. 4e-38;
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 IELTSPAIMSAPPEKVTTCRASSSVSYLGWYQKPGSSPRLIYDTSNLASGVV 61
DB 2 IYLTSPAIMSAPPEKVTTCRASSSVSYLGWYQKPGSSPRLIYDTSNLASGVV 59
QY 62 RPSGSGSTSYSLTISRMEADPAATYYCOQMSNPLTSGSKLEIK 108
DB 60 RPSGSGSTSYSLTISRMEADPAATYYCOQMSNPLTSGSKLEIK 106

RESULT 9
US-08-477-728-58
Sequence 58, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728

FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-728-58

Query Match 85.2%; Score 476; DB 1; Length 106;
Best Local Similarity 88.8%; Pred. No. 4e-38;
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 IELTSPAIMSAPPEKVTTCRASSSVSYLGWYQKPGSSPRLIYDTSNLASGVV 61
DB 2 IYLTSPAIMSAPPEKVTTCRASSSVSYLGWYQKPGSSPRLIYDTSNLASGVV 59
QY 62 RPSGSGSTSYSLTISRMEADPAATYYCOQMSNPLTSGSKLEIK 108
DB 60 RPSGSGSTSYSLTISRMEADPAATYYCOQMSNPLTSGSKLEIK 106

RESULT 10
US-08-474-040-58
Sequence 58, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas P.
APPLICANT: COELINGH, Kathleen L.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-040-58

Query Match 85.2%; Score 476; DB 1; Length 106;
Best Local Similarity 88.8%; Pred. No. 48-38; Indels 2; Gaps 1;
Matches 95; Conservative 3; Mismatches 7;

QY 2 IELTQSPAINASAPGKVTTCRASSSVSSSYLGWYQOKFGSSPRLIYDTSNLASGVV 61
DB 2 IVLTQSPAINASAPGKVTTCRASSSVSSSYLGWYQOKFGSSPRLIYDTSNLASGVV 59

QY 62 RFGSGSGTSTSLTISRMEADAATYYCQWMSNPITFGSGTLEK 108
DB 60 RFGSGSGTSTSLTISRMEADAATYYCQWMSNPITFGSGTLEK 106

RESULT 11
US-08-487-200-58
Sequence 58, Application US/08487200
Patent No. 5693762
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,200
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-200-58

Query Match 85.2%; Score 476; DB 1; Length 106;
Best Local Similarity 88.8%; Pred. No. 48-38; Indels 2; Gaps 1;
Matches 95; Conservative 3; Mismatches 7;

QY 2 IELTQSPAINASAPGKVTTCRASSSVSSSYLGWYQOKFGSSPRLIYDTSNLASGVV 61
DB 2 IVLTQSPAINASAPGKVTTCRASSSVSSSYLGWYQOKFGSSPRLIYDTSNLASGVV 59

QY 62 RFGSGSGTSTSLTISRMEADAATYYCQWMSNPITFGSGTLEK 108
DB 60 RFGSGSGTSTSLTISRMEADAATYYCQWMSNPITFGSGTLEK 106

RESULT 12
US-08-484-537-58
Sequence 58, Application US/08484537
Patent No. 6180370
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knoutie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE: 13-FEB-1989
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-537-58

Query Match      85.2%; Score 476; DB 2; Length 106;
Best Local Similarity 88.8%; Pred. No. 4e-38;
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 2 IELTSPAIMSASPGKVTTCRASSVSSYLGMYYOQKPGSSPRLIYDTSNLASGVV 61
Db 2 IVLTQSPAIMSASPGKVTMTCSGSSVSFMY--WYQORPGSSPRLIYDTSNLASGVV 59
62 RFGSGSGTSYSLTISRMEADATYYCOQWSNPLTFGSGTKLEK 108
60 RFGSGSGTSYSLTISRMEADATYYCOQWSYPLTFGAGTKLEK 106

RESULT 13
US-07-634-278-31
Sequence 31, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas P.
APPLICANT: SELICK, Harold B.
APPLICANT: SELICK, Harold B.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223

```

```

REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-31

Query Match      85.2%; Score 476; DB 1; Length 128;
Best Local Similarity 88.8%; Pred. No. 5e-38;
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 2 IELTSPAIMSASPGKVTTCRASSVSSYLGMYYOQKPGSSPRLIYDTSNLASGVV 61
Db 24 IVLTQSPAIMSASPGKVTMTCSGSSVSFMY--WYQORPGSSPRLIYDTSNLASGVV 81
62 RFGSGSGTSYSLTISRMEADATYYCOQWSNPLTFGSGTKLEK 108
82 RFGSGSGTSYSLTISRMEADATYYCOQWSYPLTFGAGTKLEK 128

RESULT 14
US-08-477-728-31
Sequence 31, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold B.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids

```

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-728-31

Query Match 85.2%; Score 476; DB 1; Length 128;
Best Local Similarity 88.8%; Pred. No. 5e-38;
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 2 IELTQSPAIMSASPGKVTTCRASSSVSSYLGMWQKPGSSPRLLIYDTNLSAGVPV 61
DB 24 IVLTQSPAIMSASPGKVTTCRASSSVSSYLGMWQKPGSSPRLLIYDTNLSAGVPV 81
QY 62 RFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGGTKLELK 108
DB 82 RFSGSGSGTSTSLTISRMEADATYYCOQWSTYPLTFGAGTKLELK 128

RESULT 15

US-08-474-040-31
Sequence 31, Application US/08474040
Patent No. 5693761
GENERAL INFORMATION:
APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,040
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-040-31

Query Match 85.2%; Score 476; DB 1; Length 128;
Best Local Similarity 88.8%; Pred. No. 5e-38;
Matches 95; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSASPGKVTTCRASSSVSSYLGMWQKPGSSPRLLIYDTNLSAGVPV 61
DB 24 IVLTQSPAIMSASPGKVTTCRASSSVSSYLGMWQKPGSSPRLLIYDTNLSAGVPV 81
QY 62 RFSGSGSGTSTSLTISRMEADATYYCOQWSSNPLTFSGGTKLELK 108
DB 82 RFSGSGSGTSTSLTISRMEADATYYCOQWSTYPLTFGAGTKLELK 128

Search completed: November 21, 2005, 12:07:36
Job time : 41.1245 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: November 21, 2005, 11:50:51 / Search time 134.952 Seconds
(without alignments)
337.478 Million cell updates/sec

Title: US-10-632-706-88
Perfect score: 559
Sequence: 1 DIETLOSPAINASGPKERTV.....QQWSSNPLTFGSGTKLEKLR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	100.0	109	4	US-10-632-706-88 Sequence 88, App1
2	518	92.7	107	4	US-10-632-706-87 Sequence 87, App1
3	518	92.7	109	3	US-09-144-886-91 Sequence 91, App1
4	500	89.4	107	3	US-09-144-886-78 Sequence 78, App1
5	494	88.4	107	3	US-09-144-886-75 Sequence 75, App1
6	492	88.0	107	4	US-10-632-706-75 Sequence 75, App1
7	491	87.8	107	5	US-10-895-135-46 Sequence 46, App1
8	489	87.5	129	4	US-10-344-779-2 Sequence 2, App1
9	489	87.5	129	4	US-10-738-809-2 Sequence 2, App1
10	486	86.9	107	4	US-10-632-706-72 Sequence 72, App1
11	485	86.9	107	3	US-09-144-886-90 Sequence 90, App1
12	484	86.6	110	4	US-10-803-653-237 Sequence 237, App
13	484	86.6	110	4	US-10-803-653-237 Sequence 237, App
14	481	86.0	109	3	US-09-144-886-96 Sequence 96, App1
15	481	86.0	109	4	US-10-632-706-93 Sequence 93, App1
16	481	86.0	110	4	US-10-803-622-255 Sequence 255, App
17	481	86.0	110	4	US-10-803-653-255 Sequence 255, App
18	476	85.2	106	4	US-10-389-155-17 Sequence 17, App1
19	476	85.2	106	4	US-10-389-417-17 Sequence 17, App1
20	476	85.2	106	4	US-10-452-357-58 Sequence 58, App1
21	476	85.2	106	4	US-10-452-357-58 Sequence 58, App1
22	475	85.0	106	4	US-10-468-370-643 Sequence 643, App1
23	475	85.0	106	4	US-10-468-370-643 Sequence 643, App1
24	473	84.6	106	4	US-10-239-656-18 Sequence 18, App1
25	471	84.3	108	5	US-10-895-135-47 Sequence 47, App1
26	471	84.3	108	4	US-10-803-622-243 Sequence 243, App
27	471	84.3	108	4	US-10-803-653-243 Sequence 243, App

28	470	84.1	109	4	US-10-461-878-12 Sequence 12, App1
29	470	84.1	109	5	US-10-461-878-12 Sequence 12, App1
30	470	84.1	110	4	US-10-803-622-256 Sequence 256, App
31	470	84.1	110	4	US-10-803-693-256 Sequence 256, App
32	470	84.1	128	4	US-10-389-195-44 Sequence 44, App1
33	470	84.1	128	4	US-10-389-417-44 Sequence 44, App1
34	469	83.9	105	5	US-10-966-406-72 Sequence 72, App1
35	469	83.9	108	3	US-09-948-004-78 Sequence 28, App1
36	469	83.9	108	3	US-10-672-932-28 Sequence 28, App1
37	469	83.9	128	3	US-09-772-103-6 Sequence 6, App1
38	469	83.9	243	5	US-10-966-406-2 Sequence 2, App1
39	469	83.9	492	4	US-10-362-591-2 Sequence 59, App1
40	469	83.9	492	4	US-10-682-845-59 Sequence 61, App1
41	469	83.9	492	4	US-10-682-845-61 Sequence 61, App1
42	469	83.9	492	4	US-10-682-845-63 Sequence 63, App1
43	469	83.9	492	4	US-10-682-845-65 Sequence 65, App1
44	469	83.9	492	4	US-10-682-845-67 Sequence 67, App1
45	469	83.9	492	4	US-10-682-845-69 Sequence 69, App1

ALIGNMENTS

RESULT 1
US-10-632-706-88
; Sequence 88, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: single chain antibody
US-10-632-706-88
Query Match 100.0%; Score 559; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e-40;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIETLOSPAINASGPKERTVTCRASSVS4SLGMVCOOKPSSPRLIYDTSNLASGVP 60
DB 1 DIETLOSPAINASGPKERTVTCRASSVS3SLGMVCOOKPSSPRLIYDTSNLASGVP 60
QY 61 VAFSSGSGTSTSLTISRMKEDATYYCOQWSSNPLTFGSGTKLEKLR 109
DB 61 VAFSSGSGTSTSLTISRMKEDATYYCOQWSSNPLTFGSGTKLEKLR 109
RESULT 2
US-10-632-706-87
; Sequence 87, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01

;/ CURRENT FILING DATE: 2003-08-01
;/ PRIOR APPLICATION NUMBER: US 60/400,721
;/ PRIOR FILING DATE: 2002-08-01
;/ PRIOR APPLICATION NUMBER: US 09/144,806
;/ PRIOR FILING DATE: 1998-08-31
;/ NUMBER OF SEQ ID NOS: 278
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 87
;/ LENGTH: 107
;/ TYPE: PRT
;/ ORGANISM: Artificial
;/ FEATURE:
;/ OTHER INFORMATION: single chain antibody
US-10-632-706-87

Query Match 92.7%; Score 518; DB 4; Length 107;
Best Local Similarity 94.5%; Pred. No. 1,1e-36;
Matches 103; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 DIELTOSPAIMASPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASPGKVTTCRASSSV--SYMWTQOKPGSPRLIYDTSNLSAGVP 58

QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 109
DB 59 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 107

RESULT 3
US-09-144-886-91
;/ Sequence 91, Application US/09144886
;/ Patent No. US20020155114A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Marks, James D
;/ APPLICANT: Amersdorfer, Peter
;/ TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
;/ TITLE OF INVENTION: Botulinum Neurotoxins
;/ FILE REFERENCE: 2500.117USO
;/ CURRENT APPLICATION NUMBER: US/09/144,886
;/ CURRENT FILING DATE: 1998-08-31
;/ NUMBER OF SEQ ID NOS: 98
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 91
;/ LENGTH: 109
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURES:
;/ OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
;/ OTHER INFORMATION: 3H4 region VL epitope 2
US-09-144-886-91

Query Match 92.7%; Score 518; DB 3; Length 109;
Best Local Similarity 93.6%; Pred. No. 1,1e-36;
Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIELTOSPAIMASPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60

QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 109
DB 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 109

RESULT 4
US-09-144-886-78
;/ Sequence 78, Application US/09144886
;/ Patent No. US20020155114A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Marks, James D
;/ APPLICANT: Amersdorfer, Peter
;/ TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
;/ TITLE OF INVENTION: Botulinum Neurotoxins

;/ FILE REFERENCE: 2500.117USO
;/ CURRENT APPLICATION NUMBER: US/09/144,886
;/ CURRENT FILING DATE: 1998-08-31
;/ NUMBER OF SEQ ID NOS: 98
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 78
;/ LENGTH: 107
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
;/ OTHER INFORMATION: C15 region VL epitope 1
US-09-144-886-78

Query Match 89.4%; Score 500; DB 3; Length 107;
Best Local Similarity 91.7%; Pred. No. 3,7e-35;
Matches 100; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 1 DIELTOSPAIMASPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASPGKVTTCRASSSV--SYMWTQOKPGSPRLIYDTSNLSAGVP 58

QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 109
DB 59 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 107

RESULT 5
US-09-144-886-75
;/ Sequence 75, Application US/09144886
;/ Patent No. US20020155114A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Marks, James D
;/ APPLICANT: Amersdorfer, Peter
;/ TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
;/ TITLE OF INVENTION: Botulinum Neurotoxins
;/ FILE REFERENCE: 2500.117USO
;/ CURRENT APPLICATION NUMBER: US/09/144,886
;/ CURRENT FILING DATE: 1998-08-31
;/ NUMBER OF SEQ ID NOS: 98
;/ SOFTWARE: PatentIn Ver. 2.0
;/ SEQ ID NO 75
;/ LENGTH: 107
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURES:
;/ OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
;/ OTHER INFORMATION: C15 region VL epitope 1
US-09-144-886-75

Query Match 88.4%; Score 494; DB 3; Length 107;
Best Local Similarity 89.9%; Pred. No. 1,2e-34;
Matches 98; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY 1 DIELTOSPAIMASPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 60
DB 1 DIELTOSPAIMASPGKVTTCRASSSVSSSYLGWYQOKPGSPRLIYDTSNLSAGVP 58

QY 61 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 109
DB 59 VRFGSGSGTSTSLTISRMEADATYYCCQWSSNPLTFGSGTKLEIKR 107

RESULT 6
US-10-632-706-75
;/ Sequence 75, Application US/10632706
;/ Publication No. US20040175385A1
;/ GENERAL INFORMATION:
;/ APPLICANT: MARKS, JAMES D.
;/ APPLICANT: AMERSDORFER, PETER
;/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;/ TITLE OF INVENTION: NEUROTOXINS
;/ FILE REFERENCE: 407T-895120US

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CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 75
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody
US-10-632-706-75

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Query Match      88.0%; Score 492; DB 4; Length 107;
Best Local Similarity 90.8%; Pred. No. 1,8e-34;
Matches 99; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

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Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60
Db 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 58

```

```

Qy 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELR 109
Db 59 VRFSGSGGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELR 107

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```

RESULT 7
US-10-895-135-46
Sequence 46, Application US/10895135
Publication No. US20050123549A1
GENERAL INFORMATION:
APPLICANT: Immunogen, Inc.
APPLICANT: PAYNE, Gillian
APPLICANT: CHUN, Philip
APPLICANT: TAVARES, Daniel
TITLE OF INVENTION: A CA6 ANTIGEN-SPECIFIC CYTOTOXIC CONJUGATE AND METHODS OF USING
FILE REFERENCE: A8621
CURRENT APPLICATION NUMBER: US/10/895,135
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: 60/488,447
PRIOR FILING DATE: 2003-07-21
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 46
LENGTH: 107
TYPE: PRT
ORGANISM: Mus musculus
US-10-895-135-46

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```

Query Match      87.8%; Score 491; DB 5; Length 107;
Best Local Similarity 88.1%; Pred. No. 2.1e-34;
Matches 96; Conservative 7; Mismatches 4; Indels 2; Gaps 1;

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Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 60
Db 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 58

```

```

Qy 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELR 109
Db 59 VRFSGSGGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELR 107

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RESULT 8
US-10-344-779-2
Sequence 2, Application US/10344779
Publication No. US20030211106A1
GENERAL INFORMATION:
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TORNETTA, MARK A.

```

```

APPLICANT: TRINER, ALEMEGED
APPLICANT: WATTAM, TREVOR A.
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
FILE REFERENCE: GP50033
CURRENT APPLICATION NUMBER: US/10/344,779
CURRENT FILING DATE: 2003-02-17
PRIOR APPLICATION NUMBER: PCT/US01/26161
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,524
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 60/230,639
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 129
TYPE: PRT
ORGANISM: Mus musculus
US-10-344-779-2

```

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Query Match      87.5%; Score 489; DB 4; Length 129;
Best Local Similarity 90.7%; Pred. No. 3.8e-34;
Matches 98; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

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Qy 2 IELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 61
Db 2 IELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 59

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Qy 62 RPSGSGGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELR 109
Db 60 RPSGSGGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELR 107

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RESULT 9
US-10-738-809-2
Sequence 2, Application US/10738809
Publication No. US2004017117A1
GENERAL INFORMATION:
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TORNETTA, MARK A.
APPLICANT: TRINER, ALEMEGED
APPLICANT: WATTAM, TREVOR A.
TITLE OF INVENTION: ANTI-RANK LIGAND MONOCLONAL ANTIBODIES
TITLE OF INVENTION: USEFUL IN TREATMENT OF RANK LIGAND MEDIATED DISORDERS
FILE REFERENCE: GP50033
CURRENT APPLICATION NUMBER: US/10/738,809
CURRENT FILING DATE: 2003-12-17
PRIOR APPLICATION NUMBER: US/10/344,779
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: PCT/US01/26161
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,524
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 60/230,639
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 129
TYPE: PRT
ORGANISM: Mus musculus
US-10-738-809-2

```

```

Query Match      87.5%; Score 489; DB 4; Length 129;
Best Local Similarity 90.7%; Pred. No. 3.8e-34;
Matches 98; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

```

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Qy 2 IELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 61
Db 2 IELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLSAGVP 59

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Qy 62 RPSGSGGTSTSLTISRMEADATYYCOQWSNPLTFGSGTKLELR 109

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Sequence 237, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803,653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 237
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scfv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-237

Query Match      86.6%; Score 484; DB 4; Length 110;
Best Local Similarity 86.2%; Pred. No. 8.7e-34;
Matches 94; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIELTSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
DB 1 DIELTSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60

QY 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSSNPITFGSGTKVELR 109
DB 61 AAFSGSGGTSTSLTISRMEADATYYCOQWSSNPITFGSGTKVELR 109

RESULT 14
US-09-144-886-96
Sequence 96, Application US/09144886
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117USO
```

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CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 96
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: 1H6 region VL epitope 3
US-09-144-886-96

Query Match      86.0%; Score 481; DB 3; Length 109;
Best Local Similarity 86.2%; Pred. No. 1.6e-33;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
DB 1 DIELTSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60

QY 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSSNPITFGSGTKVELR 109
DB 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSSNPITFGSGTKVELR 109

RESULT 15
US-10-632-706-93
Sequence 93, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 93
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody
US-10-632-706-93

Query Match      86.0%; Score 481; DB 4; Length 109;
Best Local Similarity 86.2%; Pred. No. 1.6e-33;
Matches 94; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIELTSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
DB 1 DIELTSPAIMSASPEKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60

QY 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSSNPITFGSGTKVELR 109
DB 61 VRFSGSGGTSTSLTISRMEADATYYCOQWSSNPITFGSGTKVELR 109

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Job time : 134.952 secs
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OM protein - protein search, using sw model

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61.686 Million cell updates/sec

Title: US-10-632-706-88

Perfect score: 559
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	427	76.4	248 1	US-10-512-184-36 Sequence 36, Appl
2	427	76.4	615 1	US-10-512-184-50 Sequence 50, Appl
3	414	74.1	106 7	US-11-174-186-1 Sequence 1, Appl
4	406	72.6	106 7	US-11-174-186-1 Sequence 8, Appl
5	406	72.6	213 7	US-11-174-186-42 Sequence 42, Appl
6	405	72.5	213 7	US-11-172-320-4 Sequence 4, Appl
7	401	71.7	106 7	US-11-174-186-9 Sequence 9, Appl
8	398.5	71.3	131 1	US-10-721-763-27 Sequence 37, Appl
9	395.5	70.8	128 1	US-10-721-763-31 Sequence 31, Appl
10	395	70.7	213 7	US-11-172-320-8 Sequence 8, Appl
11	391	69.9	106 7	US-11-174-186-7 Sequence 7, Appl
12	389	69.6	106 7	US-11-174-186-16 Sequence 16, Appl
13	387.5	69.3	129 1	US-10-721-763-19 Sequence 19, Appl
14	386	69.1	106 7	US-11-174-186-15 Sequence 15, Appl
15	381.5	68.2	129 1	US-10-721-763-23 Sequence 23, Appl
16	376.5	67.4	110 1	US-10-648-816-3 Sequence 2, Appl
17	376.5	67.4	110 1	US-10-648-816-3 Sequence 3, Appl
18	376.5	67.4	110 1	US-10-648-816-6 Sequence 4, Appl
19	376.5	67.4	110 1	US-10-648-816-6 Sequence 6, Appl
20	376.5	67.4	110 1	US-10-648-816-7 Sequence 7, Appl
21	376.5	67.4	110 1	US-10-648-816-8 Sequence 8, Appl
22	375.5	67.2	110 1	US-10-648-816-5 Sequence 5, Appl
23	375.5	67.2	543 1	US-10-495-664-3 Sequence 3, Appl
24	373.5	66.8	110 1	US-10-648-816-1 Sequence 1, Appl
25	373	66.7	106 7	US-11-174-186-10 Sequence 10, Appl

26	373	66.7	106 7	US-11-174-186-14 Sequence 14, Appl
27	372	66.5	106 7	US-11-174-186-11 Sequence 11, Appl
28	372	66.5	106 7	US-11-174-186-12 Sequence 12, Appl
29	371	66.4	106 7	US-11-174-186-13 Sequence 13, Appl
30	361.5	64.7	236 7	US-11-144-248-48 Sequence 48, Appl
31	359	64.2	106 7	US-11-174-186-5 Sequence 5, Appl
32	357.5	64.0	111 7	US-11-077-978-1 Sequence 1, Appl
33	357.5	64.0	236 7	US-11-144-248-42 Sequence 52, Appl
34	356.5	63.8	107 7	US-11-144-248-14 Sequence 14, Appl
35	354.5	63.4	259 1	US-10-512-184-31 Sequence 31, Appl
36	354.5	63.4	259 1	US-10-512-184-29 Sequence 29, Appl
37	354.5	63.4	329 1	US-10-512-184-68 Sequence 68, Appl
38	351	62.8	96 7	US-11-144-248-38 Sequence 38, Appl
39	349.5	62.5	126 1	US-10-839-799-47 Sequence 47, Appl
40	349.5	62.5	126 1	US-10-839-799-65 Sequence 65, Appl
41	349.5	62.5	127 1	US-10-721-763-35 Sequence 35, Appl
42	348.5	62.3	126 1	US-10-839-799-85 Sequence 85, Appl
43	345.5	61.8	126 1	US-10-839-799-43 Sequence 43, Appl
44	345.5	61.8	126 1	US-10-839-799-53 Sequence 53, Appl
45	345.5	61.8	259 1	US-10-512-184-33 Sequence 33, Appl

ALIGNMENTS

```
RESULT 1
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies and fusions mediated plant disease
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cFv S22 with
; OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match      76.4%; Score 427; DB 1; Length 248;
Best Local Similarity 78.9%; Pred. No. 2,5e-19;
Matches 86; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

QY 1 DIELOSPPAIMSASGKRVKTCRASVSYSYLGWYQOKPSSPRLIYDTSNLASGVP 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 141 DVLVQSPVIMASGKRVKTCRASVS--NYITWYQKSTSKRMKFDISKALASGVP 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 VRFSSGSGTSTSLTISRMEDADATYTCQWSSNPLTFGSGTKELKLR 109
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 199 VRFSSGSGTSTSLTISRMEDADATYTCQWSSNPLTFGSGTKELKLR 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 2
US-10-512-184-50
; Sequence 50, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
```

```

; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
; OTHER INFORMATION: completing the leader peptide - chitinase - linker
; OTHER INFORMATION: - scfv S2 - cmyc/H186.
US-10-512-184-50

Query Match          76.4%; Score 427; DB 1; Length 615;
Best Local Similarity 78.9%; Pred. No. 4.6e-19;
Matches 86; Conservative 7; Mismatches 14; Indels 2; Gaps 1;

QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 482 DIVLFGSPVIMASASPGKVTTCRASSSV--NYIWMYQOKSGSPKWIIFDTSNLASGVP 539
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VRFSGSGSGTSYSYLTISSMEADATYYCQOMSNPLTFGSGTKLEIK 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 540 VRFSGSGSGTSYSYLTISSMEADATYYCQOMSNPLTFGAGTKLEIKR 588
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
US-11-174-186-1
; Sequence 1, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VK mouse
US-11-174-186-1

Query Match          74.1%; Score 414; DB 7; Length 106;
Best Local Similarity 79.4%; Pred. No. 7.4e-19;
Matches 85; Conservative 4; Mismatches 16; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 IELTQSPAIMSASPGKVTTCRASSSV--SYMLMYQOKPGSSPKWIFDTSNLASGFP 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 RFGSGSGTSYSYLTISSMEADATYYCQOMSNPLTFGSGTKLEIK 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 RFGSGSGTSYSYLTISSMEADATYYCHQSGYPTFGGTKLEIK 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
US-11-174-186-8
; Sequence 8, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
```

```

; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VK7 light chain
US-11-174-186-8

Query Match          72.6%; Score 406; DB 7; Length 106;
Best Local Similarity 77.6%; Pred. No. 2.1e-18;
Matches 83; Conservative 5; Mismatches 17; Indels 2; Gaps 1;

QY 2 IELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 IELTQSPAIMSASPGKVTTCRASSSV--SYMLMYQOKPGSSPKWIFDTSNLASGFP 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 RFGSGSGTSYSYLTISSMEADATYYCQOMSNPLTFGSGTKLEIK 108
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 60 RFGSGSGTSYSYLTISSMEADATYYCHQSGYPTFGGTKLEIK 106
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
US-11-174-186-42
; Sequence 42, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: light chain
US-11-174-186-42

Query Match          72.6%; Score 406; DB 7; Length 213;
Best Local Similarity 75.2%; Pred. No. 3.3e-18;
Matches 82; Conservative 7; Mismatches 18; Indels 2; Gaps 1;

QY 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EIVLTQSPATLSASPGKVTTCRASSSV--SYMLMYQOKPGSSPKWIFDTSNLASGFP 59
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VRFSGSGSGTSYSYLTISSMEADATYYCQOMSNPLTFGSGTKLEIK 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 59 ARFSGSGSGTSYSYLTISSMEADATYYCHQSGYPTFGGTKLEIKR 107
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
US-11-172-320-4
; Sequence 4, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Helinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
```

```
;; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
;; FILE REFERENCE: 1/1383
;; CURRENT APPLICATION NUMBER: US/11/172,320
;; PRIOR FILING DATE: 2005-06-30
;; PRIOR APPLICATION NUMBER: US/10/645,215
;; PRIOR FILING DATE: 2003-08-21
;; PRIOR APPLICATION NUMBER: EP 02 018 686.2
;; PRIOR FILING DATE: August 21, 2002
;; PRIOR APPLICATION NUMBER: US 60/405,956
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 213
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; OTHER INFORMATION: Humanised Murine Antibody Biwa 4 Light Chain
US-11-172-320-4
```

```
Query Match 72.5%; Score 405; DB 7; Length 213;
Best Local Similarity 70.6%; Pred. No. 3.8e-18;
Matches 77; Conservative 13; Mismatches 17; Indels 2; Gaps 1;
```

```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLAGVP 60
Db 1 EIVLTQSPATLSLSPGERATLSCASASSI--NYIYWOQKPGQARRLIYDTSNLAGVP 58
```

```
Qy 61 VRFGSGSGTSTSLTISRMKADATYYCOQWSSNPLTFGGGTKLEIKR 109
Db 59 ARFSGSGGTDFLTITSLLEPEDFAVYYCLOWSSNPLTFGGGTKVEIKR 107
```

```
RESULT 7
US-11-174-186-9
;; Sequence 9, Application US/11174186
;; Publication No. US20050244418A1
;; GENERAL INFORMATION:
;; APPLICANT: Gliles, Stephen
;; APPLICANT: Lo, Kin-Ming
;; APPLICANT: Qian, Xiang
;; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
;; FILE REFERENCE: LEX-019
;; CURRENT APPLICATION NUMBER: US/11/174,186
;; PRIOR FILING DATE: 2005-07-01
;; PRIOR APPLICATION NUMBER: US 60/288,564
;; PRIOR FILING DATE: 2001-05-03
;; NUMBER OF SEQ ID NOS: 42
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 9
;; LENGTH: 106
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: VK8 light chain
US-11-174-186-9
```

```
Query Match 71.7%; Score 401; DB 7; Length 106;
Best Local Similarity 75.0%; Pred. No. 4e-18;
Matches 81; Conservative 7; Mismatches 18; Indels 2; Gaps 1;
```

```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLAGVP 60
Db 1 EIVLTQSPATLSLSPGERATLSCASASSI--SYMLTYQKPGSSPKPWTFDTSNLAGSP 58
```

```
Qy 61 VRFGSGSGTSTSLTISRMKADATYYCOQWSSNPLTFGGGTKLEIK 108
Db 59 ARFSGSGGTSTSLTISRMKADATYYCQWSSNPLTFGGGTKLEIK 106
```

```
RESULT 8
US-10-721-763-27
```

```
;; Sequence 27, Application US/10721763
;; Publication No. US20050249729A1
;; GENERAL INFORMATION:
;; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
;; FILE REFERENCE: PH-1573-PCT
;; CURRENT APPLICATION NUMBER: US/10/721,763
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: JP2001-150213
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: JP2001-243040
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: JP2001-314489
;; PRIOR FILING DATE: 2001-10-11
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 27
;; LENGTH: 131
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-721-763-27
```

```
Query Match 71.3%; Score 398.5; DB 1; Length 131;
Best Local Similarity 69.1%; Pred. No. 6.3e-18;
Matches 76; Conservative 14; Mismatches 19; Indels 1; Gaps 1;
```

```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLAGVP 60
Db 21 EIVLTQSPATLSLSPGERATLSCASQSV--SYLAWYQKPGQARRLIYDASNATGIP 80
```

```
Qy 61 VRFGSGSGTSTSLTISRMKADATYYCOQWSSNPLTFGGGTKLEIKR 109
Db 81 DRFGSGSGTDFLTITSLLEPEDFAVYYCQOYGSSPLTFGGGTKVEIKR 130
```

```
RESULT 9
US-10-721-763-31
;; Sequence 31, Application US/10721763
;; Publication No. US20050249729A1
;; GENERAL INFORMATION:
;; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
;; APPLICANT: KIRIN BEER TRAIL-R ANTIBODY
;; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
;; FILE REFERENCE: PH-1573-PCT
;; CURRENT APPLICATION NUMBER: US/10/721,763
;; PRIOR FILING DATE: 2003-11-26
;; PRIOR APPLICATION NUMBER: JP2001-150213
;; PRIOR FILING DATE: 2001-05-18
;; PRIOR APPLICATION NUMBER: JP2001-243040
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: JP2001-314489
;; PRIOR FILING DATE: 2001-10-11
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 31
;; LENGTH: 128
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-721-763-31
```

```
Query Match 70.8%; Score 395.5; DB 1; Length 128;
Best Local Similarity 69.7%; Pred. No. 9.2e-18;
Matches 76; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
```

```
Qy 1 DIELTQSPAIMSASPGKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLAGVP 60
Db 21 EIVLTQSPATLSLSPGERATLSCASQSV--SYLAWYQKPGQARRLIYDASNATGIP 79
```

```
Qy 61 VRFGSGSGTSTSLTISRMKADATYYCOQWSSNPLTFGGGTKLEIKR 109
Db 80 ARFSGSGGTDFLTITSLLEPEDFAVYYCQOQWSSNPLTFGGGTKVEIKR 128
```

```
RESULT 10
```

```
US-11-172-320-8
; Sequence 8, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Antibody BiMA 8 Light Chain
US-11-172-320-8

Query Match          70.7%; Score 395; DB 7; Length 213;
Best Local Similarity 68.8%; Pred. No. 1.4e-17;
Matches 75; Conservative 14; Mismatches 18; Indels 2; Gaps 1;

QY 1 DIELTOSPAIMASAPGERKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVLTOSPATLISAPGERATLSCASSSI--NYIWMYQOKPGQAPRLIYLTSTNLASGVP 58
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VRFGSGSGTYSYLTISRMEADAATYYCCQWMSNPILTFSGGTLEIKR 109
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 59 ARFGSGSGTDFTLTISLEPEDFAVYVYCCQWMSNPILTFGGGTVEIKR 107
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
US-11-174-186-7
; Sequence 7, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Vks 6 light chain
US-11-174-186-7

Query Match          69.9%; Score 391; DB 7; Length 106;
Best Local Similarity 70.4%; Pred. No. 1.4e-17;
Matches 76; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 DIELTOSPAIMASAPGERKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVLTOSPATLISAPGERVTLTCSASSSV--SYMLMYQOKPGQAPKLLIFDTSNLASGIP 58
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 61 VRFGSGSGTYSYLTISRMEADAATYYCCQWMSNPILTFSGGTLEIKR 108
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 59 ARFGSGSGTDFTLTISLEPEDFAVYVYCCQWMSNPILTFGGGTVEIKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-11-174-186-16
; Sequence 16, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VK mouse
US-11-174-186-16

Query Match          69.6%; Score 389; DB 7; Length 106;
Best Local Similarity 73.8%; Pred. No. 1.9e-17;
Matches 79; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 2 IELTOSPAIMASAPGERKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 61
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 2 IIVTOSPATLISAPGERVTLTCSASSSV--SYMLMYQKPGSSPXPWIFDTSNLASGFPs 59
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 RFSGSGSGTYSYLTISRMEADAATYYCCQWMSNPILTFSGGTLEIKR 108
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 60 RFSGSGSGTYSYLTISLEADAATYYCHORBGYPYTFGGGTLEIKR 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-721-763-19
; Sequence 19, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: ANTI TRAIL-R ANTIBODY
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCF
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19

Query Match          69.3%; Score 387.5; DB 1; Length 129;
Best Local Similarity 67.9%; Pred. No. 2.6e-17;
Matches 74; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 DIELTOSPAIMASAPGERKVTTCRASSSVSSSYLGWYQOKPGSSPRLIYDTSNLASGVP 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVLTOSPATLISAPGERVTLTCSASSSV--SYMLMYQOKPGQAPKLLIFDTSNLASGIP 58
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

DB 21 EIVLTQSPATLSLPGGERATLSCRASQSV-SFLAWYQKPGQAPRLLIYDASNRATGIP 79
QY 61 VRFGSGSGTSTSYLTISRMEADATYYCOQWSSNPLTFGSGTLELR 109
DB 80 ARFGSGSGTDFTLTISLSEPEDFAVYCCQQRSDWPLTFGSGTKVDIKR 128

RESULT 14
US-11-174-186-15

Sequence 15, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xing
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VKS
US-11-174-186-15

Query Match 69.1%; Score 386; DB 7; Length 106;
Best Local Similarity 71.0%; Pred. No. 2,7e-17;
Matches 76; Conservative 11; Mismatches 18; Indels 2; Gaps 1;

QY 2 IEIQTSPAIMSASPGKAVTTTCRASSSVSSYIGWYQKPGSSPRLIYDTSNLSGVF 61
DB 2 ILTQSPALIAVSPGGRATITCSASSV--SYLWYQKPGSSPKFWIYDTSNLSGVF 59
QY 62 RFGSGSGTSTSYLTISRMEADATYYCOQWSSNPLTFGSGTLELR 108
DB 60 RFGSGSGTSTSYLTISRMEADATYYCHQSGPYTFGSGTKVDIKR 106

RESULT 15
US-10-721-763-23

Sequence 23, Application US/10721763
Publication No. US20050249729A1
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
FILE REFERENCE: PH-1573-PCT
CURRENT APPLICATION NUMBER: US/10/721,763
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: JP2001-150213
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: JP2001-243040
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: JP2001-314489
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 129
TYPE: PRT
ORGANISM: Homo sapiens
US-10-721-763-23

Query Match 68.2%; Score 381.5; DB 1; Length 129;
Best Local Similarity 67.9%; Pred. No. 5.6e-17;
Matches 74; Conservative 13; Mismatches 21; Indels 1; Gaps 1;
QY 1 DIEIQTSPAIMSASPGKAVTTTCRASSSVSSYIGWYQKPGSSPRLIYDTSNLSGVF 60

DB 21 EIVLTQSPATLSLPGGERATLSCRASQSV-SFLAWYQKPGQAPRLLIYDASNRATGIP 79
QY 61 VRFGSGSGTSTSYLTISRMEADATYYCOQWSSNPLTFGSGTLELR 109
DB 80 ARFGSGSGTDFTLTISLSEPEDFAVYCCQQRSDWPLTFGSGTKVDIKR 128

Search completed: November 21, 2005, 12:33:50
Job time : 2.09634 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 145.932 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-89

Perfect score: 563
Sequence: 1 DSELTQSPPTWASGSEKIT.....QQSSIPRTFGGTYLTIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003s: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	563	100.0	109	8	ADR38687	Adx38687 Mouse I19
2	548	97.3	109	2	AAU79864	AAU79864 Anti-EGFR
3	541	96.1	110	2	AAU71297	AAU71297 Murine VL
4	541	96.1	315	4	AAU70843	AAU70843 SNV-env 1
5	540	95.9	110	2	AAU71289	AAU71289 Murine VL
6	537	95.4	110	2	AAU71295	AAU71295 Murine VL
7	535	95.0	110	2	AAU71288	AAU71288 Murine VL
8	532	94.5	110	2	AAU71298	AAU71298 Murine VL
9	530	94.1	297	2	AAU705363	AAU705363 HBV speci
10	528	93.8	109	2	AAU79162	AAU79162 Human IGE
11	526	93.4	256	5	AAU72866	AAU72866 PS-3 ring
12	525	93.4	503	5	AAU72874	AAU72874 JBI0xP5-2
13	525	93.3	109	8	ADR38693	ADR38693 Mouse I19
14	521	92.5	110	2	AAU71300	AAU71300 Murine VL
15	521	92.5	239	2	AAU71963	AAU71963 Mouse scF
16	518	92.0	110	2	AAU71289	AAU71289 Murine VL
17	518	92.0	240	8	ADR59121	ADR59121 Anti-K88
18	517	91.8	109	2	AAU72516	AAU72516 Thyroid h
19	514	91.3	137	9	AAU7084	AAU7084 Light cha
20	510	90.6	136	9	AAU7086	AAU7086 Light cha
21	508	90.2	110	2	AAU71296	AAU71296 Murine VL
22	508	90.2	136	9	AAU7090	AAU7090 Light cha
23	508	90.2	136	9	AAU7088	AAU7088 Light cha
24	508	90.2	138	9	AAU7082	AAU7082 Light cha

25	508	90.2	138	9	AAU7094	AAU7094 Light cha
26	507	90.1	245	2	AAU75783	AAU75783 Anti-T3 a
27	502	89.2	110	8	ADG25837	ADG25837 Anti-CD30
28	496	88.1	103	2	AAU705362	AAU705362 HBV speci
29	495	87.9	138	9	AAU7092	AAU7092 Light cha
30	494	87.7	109	8	AAU7098	AAU7098 Humanised
31	458	81.3	108	2	AAU70440	AAU70440 Anti-DNA
32	451	80.1	122	2	AAU75958	AAU75958 ICAV-1 in
33	450	79.9	109	8	ADR38686	ADR38686 Mouse I19
34	446	79.2	109	6	ABU63531	ABU63531 Anti-cucu
35	445	79.0	110	2	AAU71305	AAU71305 Murine VL
36	445	79.0	110	2	AAU71305	AAU71305 Murine VL
37	444	78.9	107	8	ADR38685	ADR38685 Mouse I19
38	444	78.9	242	6	ADR62132	ADR62132 Single ch
39	444	78.9	242	8	ADT91209	ADT91209 Single ch
40	443	78.7	108	3	AAU59306	AAU59306 DC8 Light
41	443	78.7	109	8	ADH59678	ADH59678 CPAM4 VR
42	443	78.7	109	8	ADH59707	ADH59707 Chimeric
43	443	78.7	951	3	AAU44993	AAU44993 DC8scFv-e
44	442	78.5	108	3	AAU97236	AAU97236 Variable
45	442	78.5	108	4	AAU82710	AAU82710 VEGF anta

ALIGNMENTS

RESULT 1
ADR38687
ID ADR38687 standard; peptide; 109 AA.
XX
AC ADR38687;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse light chain variable region scFv seqid 89.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KW light chain variable region; single chain antibody; scFv.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
XX WPI; 2004-652009/63.
XX
PS New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX
XX Example 1; SEQ ID NO 89; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (II) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC 325, C25, C39, I6, 3D12, B4, I63, huc25, Ar1, Ar2, WRI (V), WRI (T), 3-1,
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is

CC The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
 CC Fv library. The library produces a diverse repertoire of antibody
 CC fragments specific for 2-phenyl-5-oxazolone (phOx). It was prep. using
 CC cDNA generated from mRNA from mice immunised with phOx coupled to chick
 CC serum albumin. The VH and VL kappa sequences were separately amplified by
 CC PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
 CC the phage surface as fusions with gene III. The resulting library of
 CC clones was diverse; 23 hapten binding clones were sequenced revealing 8
 CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (A-G
 CC / AAR21286-92). Most clones were VH-B combinations so a further
 CC hierarchical library was prep. by "crossing" VH-B with the VK
 CC repertoire. The resulting library was screened for hapten binding and 24
 CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were
 CC identified. Nearly all the VK genes were "ox-like", only f, (from the
 CC original library) and h, p, q, and r (from the hierarchical library) were
 CC "1". The Kd of VH-B/VK-d for phOx-GABA was 10 nM, one of the highest
 CC values found. This suggests that phage bearing scFv fragments having weak
 CC affinity-ies can be selected with antigen, probably due to the avidity of
 CC the multiple antibody heads on the phage. The different combinations
 CC could also be isolated on a basis of antigen affinity. See also AAR21260-
 CC 307, 309-311, AAR22450, 565-581
 CC XX

SQ Sequence 110 AA;

Query Match 96.1%; Score 541; DB 2; Length 110;
 Best Local Similarity 96.3%; Pred. No. 5.5e-35;
 Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGSPKLLIYRTSNLASGVP 60
 DB 1 DIETLQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGSPKLLIYRTSNLASGVP 60

QY 61 AAFSGSGSGTYSLTITGTEADVAITYCQOQSSIPRTFGGSKLEIKR 109
 DB 61 AAFSGSGSGTYSLTITGTEADVAITYCQOQSSIPRTFGGSKLEIKR 109

RESULT 4
 AAB70843
 ID AAB70843 standard; protein; 315 AA.

AC AAB70843;

DT 11-SRP-2003 (revised)
 DT 25-JUN-2001 (first entry)

XX SNV-env leader/human 7B4-scFv fusion construct.

XX T lymphocyte; antibody; single chain variable antibody; scFv; human;
 KW cell-targeting vector; antiviral; cytostatic; immunostimulant; AIDS;
 KW gene therapy; immunization; diagnosis; T cell-associated disease; SCID;
 KW acquired immune deficiency syndrome; severe combined immune deficiency;
 KW T cell lymphoma; fusion construct.

OS Homo sapiens.
 OS Spleen necrosis virus.
 OS Chimeric.

XX Key Location/Qualifiers
 FT Protein 1..45
 FT /label= SNV-env_leader
 FT Protein 46..315
 FT /label= 7B4-scFv

XX DE19946142-A1.

XX 29-MAR-2001.

XX 27-SRP-1999; 99DE-01046142.

XX 27-SRP-1999; 99DE-01046142.

XX

PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRICH-INST.

XX Cichutek X, Engelsbaedter M;

XX MPI; 2001-246140/26.

DR N-P8DB; AAF61512.

XX Cell-targeting vector selective for T lymphocytes, useful in gene therapy
 PT e.g. acquired immune deficiency syndrome, encodes a single-chain
 PT variable antibody fragment.

PS Claim 1; Fig 4; 18pp; German.

XX This invention describes a novel cell-targeting vector (A) containing a
 CC DNA sequence (I) encoding a single-chain variable antibody fragment
 CC (scFv). The products of the invention have antiviral, cytostatic and
 CC immunostimulant activity and can be used in gene therapy, immunization
 CC and diagnosis particularly of T cell-associated diseases, specifically
 CC acquired immune deficiency syndrome (AIDS), severe combined immune
 CC deficiency (SCID) or T cell lymphoma. (A) target T cells, independently
 CC of the CD4 receptor, with high selectivity, 4-5 fold selectivity over
 CC human B cells, and 1000 fold selectivity over other human cells. A vector
 CC designated 7A5 encodes a 329 amino acid single-chain variable antibody
 CC fragment, fully defined in the specification. It was used to transform
 CC D17 (canine osteosarcoma cells susceptible to spleen necrosis virus
 CC (SNV)) cells, C8166 (human T lymphocyte) cells, and HeLa (human cervical
 CC carcinoma) cells. After 48 hours, the cells were stained with X-gal to
 CC determine transfection. The viral titer (infectious units/ml) was over
 CC 1 million for D17, 1 million for C8166 but less than 100 for HeLa,
 CC showing the high selectivity for human T cells. This sequence represents
 CC the SNV-env leader/human 7B4-scFv fusion construct used in the
 CC construction of novel cell targeting vectors described in the invention.
 CC (updated on 11-SRP-2003 to standardise OS field)

SQ Sequence 315 AA;

Query Match 96.1%; Score 541; DB 4; Length 315;
 Best Local Similarity 96.3%; Pred. No. 1.6e-34;
 Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGSPKLLIYRTSNLASGVP 60
 DB 184 DIETLQSPPTMAASPGSEKITTTCSSASSISISNYLHWYQORPGSPKLLIYRTSNLASGVP 243

QY 61 AAFSGSGSGTYSLTITGTEADVAITYCQOQSSIPRTFGGSKLEIKR 109
 DB 244 AAFSGSGSGTYSLTITGTEADVAITYCQOQSSIPRTFGGSKLEIKR 292

RESULT 5
 AAR21299
 ID AAR21299 standard; protein; 110 AA.

AC AAR21299;

DT 21-MAY-1992 (first entry)

XX Murine VL kappa group V chain n specifid for phOx.

KW Rd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; plus;
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers
 FT Binding-site 24..35
 FT /label= CDR1
 FT Binding-site 51..57
 FT /label= CDR2
 FT Binding-site 90..98
 FT /label= CDR3
 FT /note= "D-X-G-X-X motif "

```

XX PN W09201047-A.
XX PD 23-JAN-1992.
XX PF 10-JUL-1990; 90GB-00015198.
XX PR 10-JUL-1990; 90GB-00015198.
XX PR 19-OCT-1990; 90GB-00022845.
XX PR 12-NOV-1990; 90GB-00024503.
XX PR 06-MAR-1991; 91GB-00004744.
XX PR 15-MAY-1991; 91GB-00010549.
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PA (MEDI-) MED RES COUNCIL.
XX PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX PI Jackson RH, Holliger KP, Marks JD;
XX WPI; 1992-056862/07.
XX PT Producing members of specific binding pairs - by expression in
XX PT recombinant host cells with a secreting replicable genetic display
XX PT package.
XX PS Example 22; Fig 24; 209pp; English.
XX CC The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
XX CC Fv library. The library produces a diverse repertoire of antibody
XX CC fragments specific for 2-phenyl-5-oxazolone (phox). It was prep'd. using
XX CC cDNA generated from mRNA from mice immunised with phox coupled to chicked
XX CC serum albumin. The VH and VL kappa sequences were separately amplified by
XX CC PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
XX CC the phage surface as fusions with gene III. The resulting library of
XX CC clones was diverse; 23 hapten binding clones were sequenced revealing 8
XX CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
XX CC ; AAR21286-92). Most clones were VH-B combinations so a further
XX CC hierarchical library was prep'd. by "crossing" VH-B with the VK
XX CC repertoire. The resulting library was screened for hapten binding and 24
XX CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were
XX CC identified. Nearly all the VK genes were "ox-like"; only f, (from the
XX CC original library) and h, p, q, and r (from the hierarchical library) were
XX CC Vxox1 type genes. Of the 24 hierarchical clones, only one was of type
XX CC "n". The Kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest
XX CC values found. This suggests that phage bearing scfv fragments having weak
XX CC affinity-ies can be selected with antigen, probably due to the avidity of
XX CC the multiple antibody heads on the phage. The different combinations
XX CC could also be isolated on a basis of antigen affinity. See also AAR21260-
XX CC 307, 309-311; AAR22450, 565-581
XX S0 Sequence 110 AA;

Query Match 95.9%; Score 540; DB 2; Length 110;
Best Local Similarity 96.3%; Pred. No. 6.6e-35;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

DE Murine VL kappa group V chain J specific for phox.
XX CC Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
XX CC g3p; binding; adsorption; gene VIII; diverse repertoire;
XX CC specific binding pairs; replicable genetic display package.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FH Binding-site 24..35
XX FT /label= CDR1
XX FT Binding-site 51..57
XX FT /label= CDR2
XX FT Binding-site 90..98
XX FT /label= CDR3
XX FT /note= "D-X-G-X-X motif"
XX PN W09201047-A.
XX PD 23-JAN-1992.
XX PF 10-JUL-1990; 90GB-00015198.
XX PR 10-JUL-1990; 90GB-00015198.
XX PR 19-OCT-1990; 90GB-00022845.
XX PR 12-NOV-1990; 90GB-00024503.
XX PR 06-MAR-1991; 91GB-00004744.
XX PR 15-MAY-1991; 91GB-00010549.
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PA (MEDI-) MED RES COUNCIL.
XX PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
XX PI Jackson RH, Holliger KP, Marks JD;
XX WPI; 1992-056862/07.
XX PT Producing members of specific binding pairs - by expression in
XX PT recombinant host cells with a secreting replicable genetic display
XX PT package.
XX PS Example 22; Fig 24; 209pp; English.
XX CC The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
XX CC Fv library. The library produces a diverse repertoire of antibody
XX CC fragments specific for 2-phenyl-5-oxazolone (phox). It was prep'd. using
XX CC cDNA generated from mRNA from mice immunised with phox coupled to chicked
XX CC serum albumin. The VH and VL kappa sequences were separately amplified by
XX CC PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
XX CC the phage surface as fusions with gene III. The resulting library of
XX CC clones was diverse; 23 hapten binding clones were sequenced revealing 8
XX CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
XX CC ; AAR21286-92). Most clones were VH-B combinations so a further
XX CC hierarchical library was prep'd. by "crossing" VH-B with the VK
XX CC repertoire. The resulting library was screened for hapten binding and 24
XX CC clones sequenced. 14 new partners (AAR21293-308) for VH-B were
XX CC identified. Nearly all the VK genes were "ox-like"; only f, (from the
XX CC original library) and h, p, q, and r (from the hierarchical library) were
XX CC Vxox1 type genes. Of the 24 hierarchical clones, one was of type "j". The
XX CC Kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest values found.
XX CC This suggests that phage bearing scfv fragments having weak affinity-ies
XX CC can be selected with antigen, probably due to the avidity of the multiple
XX CC antibody heads on the phage. The different combinations could also be
XX CC isolated on a basis of antigen affinity. See also AAR21260-307, 309-311;
XX CC AAR22450, 565-581
XX S0 Sequence 110 AA;

Query Match 95.4%; Score 537; DB 2; Length 110;
Best Local Similarity 95.4%; Pred. No. 1.1e-34;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

Db 1 |||||
 1 DIELTOSPTTMAASGKXITTCSSASSISNNYLMFWQKGFSPKLIYRTSNLASGP 60
 QY 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSSIPRTFGGTGKLEIR 109
 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSSIPRTFGGTGKLEIR 109

RESULT 7
 AAR21288
 ID AAR21288 standard; protein; 110 AA.

XX AAR21288;
 AC
 XX
 DT 21-MAY-1992 (first entry)

XX Murine VL kappa group IV chain "c", specific for phox.

DE Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; plus;
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;
 KM specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers

FT Binding-site 24..35

FT Binding-site 51..57

FT Binding-site 90..98

FT Binding-site /label= CDR3

FT /note= "D-X-G-X-X motif"

XX WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990; 90GB-00015198.

XX 10-JUL-1990; 90GB-00015198.

XX 19-OCT-1990; 90GB-00022845.

XX 12-NOV-1990; 90GB-00024503.

XX 06-MAR-1991; 91GB-00004744.

XX 15-MAY-1991; 91GB-00010549.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX (MEDI-) MED RES COUNCIL.

XX Mccafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;

XX Jackson RH, Holliger KP, Marks JD;

XX WPI; 1992-056862/07.

XX Example 21; Fig 24; 209pp; English.

XX The VK sequence is one of seven (AAR21286-92) found to be expressed from

XX a single chain Fv library from an immunised mouse. The libra-ry produces

XX a diverse repertoire of antibody fragments specific for 2-phenyl-5-

XX oxazolone (phox). It was prep'd. using cDNA generated from mRNA from mice

XX immunised with phox coupled to chicked serum albumin. The VH and VL kappa

XX sequences were separately amplified by PCR (see AAO23474-84) and ligated

XX into fdCMT2 (see AAO23463) for ex-pression on the phage surface as

XX fusions with gene III. The result- ing library of clones was diverse.

XX Twenty three hapten binding clones were sequenced revealing eight

XX different VH genes (A-H) (see AAR21264-71) in a variety of pairings with

XX the seven different VK genes (a-g). Of the twenty three clones sequenced,

XX two were of type "c", and were "ox-like" genes. (See Berek et al. Nature

XX 316 412-418, 1985). They contain the DXGX motif in CDR3, the central Gly

XX of which is needed to create a cavity for phox. Most of the clones were

CC Vd-d combinations. The Kd of VH-B/Vk-b for phox-GABA was 10 uM, one of
 CC the highest values found. This suggests that phage bearing scfv fragments
 CC having weak affinities can be selected with antigen, probably due to the
 CC avidity of the multiple antibody heads on the phage. See also AAR21260-
 CC 307, 309-311; AAR22450, 565-581

XX Sequence 110 AA;

XX Query Match 95.0%; Score 535; DB 2; Length 110;

XX Best Local Similarity 95.4%; Pred. No. 1.66-34;

XX Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASGKXITTCSSASSISNNYLMFWQKGFSPKLIYRTSNLASGP 60
 Db 1 DIELTOSPTTMAASGKXITTCSSASSISNNYLMFWQKGFSPKLIYRTSNLASGP 60
 QY 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSSIPRTFGGTGKLEIR 109
 61 ARFSGSGSTSYSLTIGTMEADVATYYCOQSSSIPRTFGGTGKLEIR 109

RESULT 8
 AAR21298
 ID AAR21298 standard; protein; 110 AA.

XX AAR21298;

XX 21-MAY-1992 (first entry)

XX Murine VL kappa group V chain m specificd for phox.

KM Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; plus;
 KW g3p; binding; adsorption; gene VIII; diverse repertoire;
 KM specific binding pairs; replicable genetic display package.

XX Synthetic.

XX Key Location/Qualifiers

FT Binding-site 24..35

FT Binding-site 51..57

FT Binding-site 90..98

FT Binding-site /label= CDR3

FT /note= "D-X-G-X-X motif"

XX WO9201047-A.

XX 23-JAN-1992.

XX 10-JUL-1990; 90GB-00015198.

XX 10-JUL-1990; 90GB-00015198.

XX 19-OCT-1990; 90GB-00022845.

XX 12-NOV-1990; 90GB-00024503.

XX 06-MAR-1991; 91GB-00004744.

XX 15-MAY-1991; 91GB-00010549.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX (MEDI-) MED RES COUNCIL.

XX Mccafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;

XX Jackson RH, Holliger KP, Marks JD;

XX WPI; 1992-056862/07.

XX Example 22; Fig 24; 209pp; English.

XX The VK sequence is one of 23 (AAR21286-308) expressed from a single chain

Fv library. The library produces a diverse repertoire of antibody fragments specific for 2-benzyl-5-oxazolone (phox). It was prepared using cDNA generated from mRNA from mice immunised with phox coupled to chicked serum albumin. The VH and VL kappa sequences were separately amplified by PCR (AAQ2474-84) and ligated into fdCA22 (AAQ23463) for expression on the phage surface as fusions with gene III. The resulting library of clones was diverse; 23 hapten binding clones were sequenced revealing 8 VH genes (A-H; AAR21264-71) in a variety of pairings with 7 Vk genes (a-g; AAR21286-92). Most clones were VH-B combinations so a further hierarchical library was prepared by "crossing" VH-B with the Vk repertoire. The resulting library was screened for hapten binding and 24 clones sequenced. 14 new partners (AAR21293-308) for VH-B were identified. Nearly all the Vk genes were "ox-like"; only f, (from the original library) and h, p, g, and r (from the hierarchical library) were Vxol1 type genes. Of the 24 hierarchical clones, only one was of type "m". The Kd of VH-B/Vk-d for phox-GABA was 10 nM, one of the highest values found. This suggests that phage bearing scfv fragments having weak affinity-ies can be selected with antigen, probably due to the avidity of the multiple antibody heads on the phage. The different combinations could also be isolated on a basis of antigen affinity. See also AAR21260-307, 309-311; AAR22450, 565-581

Sequence 110 AA;

Query Match 94.5%; Score 532; DB 2; Length 110;
Best Local Similarity 94.5%; Pred. No. 2.8e-34;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTGPTTMAAPGKITTTCGASSISNNYLHWYQKRGFPKLLIYRTSNLAGVP 60
DB 1 DIELTQSPPTTMAAPGKITTTCGASSISNNLHWYQKRGFPKLLIYRTSNLAGVP 60
QY 61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSSIPRTFGGCTKLEIKR 109
DB 61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSSIPRTFGGCTKLEIKR 109

RESULT 9
AA05363
ID AA05363 standard; protein; 297 AA.

XX AAY05363;

DT 30-JUN-1999 (first entry)

XX HBV specific single stranded antibody.

XX Single stranded antibody; hepatitis B virus; HBV core protein;
KW HBV infection; viral proliferation inhibitor; viral DNA synthesis;
KW gene therapy.

XX Mus sp.

XX WO9911792-A1.

XX 11-MAR-1999.

XX 02-SEP-1998; 98WO-JP003921.

XX 02-SEP-1997; 97JP-00237054.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (HAYAH) HAYASHI N.

XX Hayashi N, Yamamoto M, Yamamoto H, Tohdoh N;

XX WPI; 1999-243623/20.

XX N-PSDB; AAX33931.

XX Single-stranded antibody against hepatitis B virus core protein,
PT applicable as (gene) therapeutic agents for treatment of hepatitis B
PT viral infections.

PS Claim 5; Page 55-57; 72pp; English.

XX This sequence is the single-stranded antibody of the invention, that has
CC the capability of binding to a hepatitis B virus (HBV) core protein.
CC Therapeutic agents can be formulated with the antibody for treatment of
CC HBV infections by stopping proliferation of the virus through inhibition
CC of viral DNA synthesis, and the gene encoding the antibody can be applied
XX as an agent to gene therapy

Sequence 297 AA;

Query Match 94.1%; Score 530; DB 2; Length 297;
Best Local Similarity 93.7%; Pred. No. 1.1e-33;
Matches 104; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 1 DSELTGPTTMAAPGKITTTCGASSISNNYLHWYQKRGFPKLLIYRTSNLAGVP 60
DB 169 DIELTQSPPTTMAAPGKITTTCGASSISNNLHWYQKRGFPKLLIYRTSNLAGVP 228

QY 61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSSIPRTFGGCTKLEIKR 109
DB 229 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSSIPRTFGGCTKLEIKR 279

RESULT 10
AAR79162
ID AAR79162 standard; peptide; 109 AA.

XX AAR79162;

XX 25-MAR-2003 (revised)

DT 04-MAR-1996 (first entry)

XX Human Igb receptor-binding, antibody-related peptide light chain.

XX Immunoglobulin E; antibody; receptor; monoclonal; detection;
KW complementarity determining region.

XX Mus sp.

XX Location/qualifiers

XX 24..35

XX /label= CDR1L

XX /note= "all CDR regions are claimed"

XX 51..57

XX /label= CDR2L

XX /note= "all CDR regions are claimed"

XX 90..98

XX /label= CDR3L

XX /note= "all CDR regions are claimed"

XX JP07165799-A.

XX 27-JUN-1995.

XX 22-OCT-1993; 93JP-00264792.

XX 22-OCT-1993; 93JP-00264792.

XX (TSUR/) TSURA T.

XX (ASAK) ASAH BREMERIES LTD.

XX (TORI) TORII YAKUJIN KK.

XX (NIKK-) NIKKA WHISKY KK.

XX WPI; 1995-261292/34.

XX N-PSDB; AAO96289.

XX Novel monoclonal antibody against human high-affinity Igb receptor - and
PT DNA fragment encoding the MAb, for the specific identification of human
PT Fe-epitope R1.

PS Claim 9; Page 16-17; 20pp; Japanese.

Polypeptides which specifically recognise human IgE receptor (Fc-epsilon-R1) have been isolated and sequenced. The new peptides are related to a monoclonal antibody against Fc-epsilon-R1 and are either heavy or light chain molecules. The heavy chain molecules have the general formula FR1-CDRIH-FR2-CDRH-FR3-CDRH-FR4 (corresp. to AAR79153, AAR79155, AAR79157, AAR79159 and AAR79161) and are encoded by AA096280, AA096282, AA096284, AA096286 and AA096288. FR1 is a polypeptide having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly the light chains have the general formula FR5-CDRI-L-FR6-CDRL-FR7-CDRL-FR8 (corresp. to AAR79154, AAR79156, AAR79158, AAR79160 and AAR79162) and are encoded by AA096281, AA096283, AA096285, AA096287 and AA096289. FR5 is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the peptides are derived from mouse hybridoma cells and are useful in the detection of the human Fc-epsilon-R1 or for the elucidation of an antigen recognising region of a monoclonal antibody against human Fc-epsilon-R1. (updated on 25-MAR-2003 to correct PA field.)

Sequence 109 AA;

Query Match 93.8%; Score 528; DB 2; Length 109;
Best Local Similarity 92.7%; Pred. No. 5.7e-34;
Matches 101; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 60
DB 1 DQMTQSPPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 60

QY 61 AAFSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 109
DB 61 AAFSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 109

RESULT 11
AAU72866
AAU72866 standard; protein; 256 AA.

AC AAU72866;

XX 26-FEB-2002 (first entry)

XX P5-3 single chain Fv.

Human; NKGD2; NKGD2 receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI10; helminth; cytotoxic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7; 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

XX Homo sapiens.

XX WO200171005-A2.

XX 27-SEP-2001.

XX 26-MAR-2001; 2001WO-EP003414.

XX 24-MAR-2000; 2000EP-00106467.

XX (KUFE/) KUFER P.

XX Kufner P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;

XX Mayer M, Hofmeister R;

XX WPI; 2002-055119/07.

XX DR N-PSDB; AAS37140.

XX Multifunctional polypeptides comprising binding sites that specifically

recognize extracellular groups of the NKGD2 receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases.

Example 7; Fig 16; 114pp; English.

The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKGD2 receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKGD2 receptor and the polypeptides of the invention

Sequence 256 AA;

Query Match 93.4%; Score 526; DB 5; Length 256;
Best Local Similarity 96.2%; Pred. No. 1.9e-33;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 63
DB 140 LTQSPPTTMAASPGKITTTCSSASSISSNVLMHYOORPGFSPKLIYRTSNLASGV 199

QY 64 SSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 109
DB 200 SSGSGSTSYSLTIGTMEADVATYYCOQGSIPRTFGGKLEIKR 245

RESULT 12

AAU72874
AAU72874 standard; protein; 503 AA.

XX AAU72874;

XX 26-FEB-2002 (first entry)

XX 3B10xP5-23 bispecific single chain Fv.

Human; NKGD2; NKGD2 receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI10; helminth; cytotoxic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7; 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.

XX Homo sapiens.

XX WO200171005-A2.

XX 27-SEP-2001.

XX 26-MAR-2001; 2001WO-EP003414.

XX 24-MAR-2000; 2000EP-00106467.

XX (KUFE/) KUFER P.

XX Kufner P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;

XX Mayer M, Hofmeister R;

```

XX  WPI; 2002-055119/07.
DR  N-PSDB; AAS97146.
XX  Multifunctional polypeptides comprising binding sites that specifically
PT  recognize extracellular groups of the NKG2D receptor complex and domains
PT  which function as receptors or ligands, useful for treating cancers and
PT  infectious diseases.
XX
PS  Example 5; Fig 16; 114pp; English.
XX
CC  The invention relates to a multifunctional polypeptide comprising a
CC  domain with a binding site that specifically recognizes an extracellular
CC  group of the NKG2D receptor complex and a second domain which functions
CC  as a receptor or ligand. The polypeptide and its associated
CC  polynucleotide are used for the preparation of a pharmaceutical
CC  composition for the treatment of cancer, infections and/or autoimmune
CC  conditions. The cancer may be a tumour of the head and neck, stomach,
CC  oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
CC  larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
CC  bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
CC  The infectious diseases can be caused by viruses, bacteria, fungi,
CC  protozoa or helminths. The autoimmune diseases include multiple
CC  sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
CC  uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
CC  diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
CC  autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
CC  receptor and the polypeptides of the invention
XX
SQ  Sequence 503 AA;
XX
Query Match          93.4%; Score 526; DB 5; Length 503;
Best Local Similarity 96.2%; Pred. No. 3.7e-33;
Matches 102; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY  4 LTGSPPTMAASPGKITTTCASASSISSNYLHWYQQRGFSFKLLIYRTSNLAGVPAF 63
DB  387 LTGSPPTMAASPGKITTTCASASSISSNYLHWYQQRGFSFKLLIYRTSNLAGVPAF 446
XX
QY  64 SSGSGSGTYSYLTIGTMEADVAITYCCQGSISIPRTFGGTLEIKR 109
DB  447 SSGSGSGTYSYLTIGTMEADVAITYCCQGSISIPRTFGGTLEIKR 492
XX
RESULT 13
ADR38693
ID  ADR38693 standard; peptide; 109 AA.
XX
AC  ADR38693;
XX
DT  02-DEC-2004 (first entry)
XX
DE  Mouse light chain variable region scfv seqid 95.
XX
KW  antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW  BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW  toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KW  light chain variable region; single chain antibody; scfv.
XX
OS  Mus sp.
XX
PN  US2004175385-A1.
XX
PD  09-SEP-2004.
XX
PF  01-AUG-2003; 2003US-00632706.
XX
PR  31-AUG-1998; 98US-00144886.
XX  01-AUG-2002; 2002US-0400721P.
XX  (REGC ) UNIV CALIFORNIA.
XX  Marks JD, Ameredorfer P;

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XX  WPI; 2004-652009/63.
DR
XX  New isolated antibody that neutralizes botulinum neurotoxin type A,
PT  useful for diagnosing botulism or for treating pathologies associated
PT  with botulinum neurotoxin poisoning.
XX
PS  Example 1, SEQ ID NO 95; 110pp; English.
XX
CC  The invention describes an isolated antibody (I) that specifically binds
CC  to an epitope specifically bound by an antibody expressed by a specific
CC  clone where (I) binds to and neutralises botulinum neurotoxin type A
CC  (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC  specifically bound by an antibody expressed by a clone chosen from clone
CC  S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC  3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC  neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC  comprising BoNT/A neutralising epitope having an epitope that is
CC  specifically bound by an antibody expressed by clones as mentioned in (I)
CC  ; producing (I); and a composition (III) comprising several anti-
CC  botulinum neurotoxin antibodies, where each antibody is specific for a
CC  different epitope of a botulinum neurotoxin and the combination of
CC  antibodies shows greater toxin neutralisation than the single antibodies
CC  in surplus. The following are disclosed: a pharmaceutical composition
CC  comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC  BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC  involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC  specific for a different epitope of the botulinum neurotoxin and the
CC  combination of antibodies shows greater toxin neutralisation than the
CC  single antibodies in surplus. (I) is useful for diagnosing the botulism
CC  or for treating pathologies associated with botulinum neurotoxin
CC  poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC  enables rapid detection or diagnosis of botulism. This is the amino acid
CC  sequence of a mouse light chain variable fragment anti-botulinum toxin
CC  scfv.
XX
SQ  Sequence 109 AA;
XX
Query Match          93.3%; Score 525; DB 8; Length 109;
Best Local Similarity 92.7%; Pred. No. 9.8e-34;
Matches 101; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
QY  1 DSELTQSPPTMAASPGKITTTCASASSISSNYLHWYQQRGFSFKLLIYRTSNLAGV 60
DB  1 DIELTQSPPTMAASPGKITTTCASASSISSNYLHWYQQRGFSFKLLIYRTSNLAGV 60
XX
QY  61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSISIPRTFGGTLEIKR 109
DB  61 ARFSGSGSGTYSYLTIGTMEADVAITYCCQGSISIPRTFGGTLEIKR 109
XX
RESULT 14
AAR21300
ID  AAR21300 standard; protein; 110 AA.
XX
AC  AAR21300;
XX
DT  21-MAY-1992 (first entry)
XX
DE  Murine VL kappa group V chain o specific for phox.
XX
KW  Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; plus;
KW  g3p; binding; adsorption; gene VIII; diverse repertoire;
KW  specific binding pairs; replicable genetic display package.
XX
OS  Synthetic.
XX
PN  Key
XX  Location/Qualifiers
XX  Binding-site 24..35
XX  Binding-site /label= CDR1
XX  Binding-site 51..57
XX  Binding-site /label= CDR2
XX  Binding-site 90..98

```



```
FT /label= CDR3
FT /note= "D-X-G-X-X motif "
XX
XX MO9201047-A.
XX
XX 23-JAN-1992.
XX
XX 10-JUL-1990; 90GB-00015198.
XX
XX 10-JUL-1990; 90GB-00015198.
XX
XX 10-JUL-1990; 90GB-00015198.
XX
XX 19-OCT-1990; 90GB-00022845.
XX
XX 12-NOV-1990; 90GB-00024503.
XX
XX 06-MAR-1991; 91GB-00004744.
XX
XX 15-MAY-1991; 91GB-00010549.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX (MEDI-) MED RES COUNCIL.
XX
XX McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD,
XX Jackson RH, Holliger KP, Marks JD;
XX
XX WPI, 1992-056862/07.
XX
XX Producing members of specific binding pairs - by expression in
XX recombinant host cells with a secreting replicable genetic display
XX package.
XX
XX Example 22; Fig 24; 209pp; English.
XX
XX The VK sequence is one of 23 (AAR21286-308) expressed from a single chain
XX Fv library. The library produces a diverse repertoire of antibody
XX fragments specific for 2-phenyl-5-oxazolone (phox). It was prep'd. using
XX cDNA generated from mRNA from mice immunised with phox coupled to chicken
XX serum albumin. The VH and VL kappa sequences were separately amplified by
XX PCR (AAG2374-84) and ligated into fdCAT2 (AAG22463) for expression on
XX the phage surface as fusions with gene III. The resulting library of
XX clones was diverse; 23 hapten binding clones were sequenced revealing 8
XX VH genes (A-H; AAR21264-71) in a variety of pairings with 7 VK genes (a-g
XX ; AAR21286-92). Most clones were VH-B combinations so a further
XX hierarchical library was prep'd. by "crossing" VH-B with the VK
XX repertoire. The resulting library was screened for hapten binding and 24
XX clones sequenced. 14 new partners (AAR21293-308) for VH-B were
XX identified. Nearly all the VK genes were "ox-like"; only f, (from the
XX original library) and h, p, q, and r (from the hierarchical library) were
XX Vkalpha type genes. Of the 24 hierarchical clones, two were of type "o".
XX The Kd of VH-B/VK-d for phox-GABA was 10 nM, one of the highest values
XX found. This suggests that phage bearing scFv fragments having weak
XX affinity-ies can be selected with antigen, probably due to the avidity of
XX the multiple antibody heads on the phage. The different combinations
XX could also be isolated on a basis of antigen affinity. See also AAR21260-
XX 307, 309-311; AAR22450, 565-581
XX
XX Sequence 110 AA;
SQ
XX
XX Query Match 92.5%; Score 521; DB 2; Length 110;
XX Best Local Similarity 93.6%; Pred. No. 2e-33;
XX Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
DT 04-AUG-1999 (first entry)
XX
XX Mouse scFv fragment 5-3.
XX
XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
XX autoimmune disease; scFv-antibody; single-chain Fv; mouse.
XX
XX Mus sp.
XX
XX MO9925818-A1.
XX
XX 27-MAY-1999.
XX
XX 16-NOV-1998; 98WO-EP007313.
XX
XX 17-NOV-1997; 97EP-00120096.
XX
XX (KUPE/) KUPER P.
XX
XX Kufer P, Raum T, Borchert K, Zettl P, Lutterbuese R;
XX
XX WPI, 1999-338004/28.
XX
XX N-PsDB; AAX77246.
XX
XX Phage display system for identification of binding site domains retaining
XX capacity to bind an epitope.
XX
XX Claim 27; Fig 6.9; 152pp; English.
XX
XX The invention relates to a method of identifying binding site domains
XX (BSD) that retain the capacity of binding to a predetermined epitope when
XX positioned C-terminal of at least one further domain in a recombinant bi-
XX or multivalent polypeptide. The method comprises (a) testing a panel of
XX BSD displayed on the surface of a biological display system as part of a
XX fusion protein for binding to a predetermined epitope, where the fusion
XX protein comprises an additional domain positioned N-terminal of the BSD
XX and an amino acid sequence that mediates anchoring of the fusion protein
XX to the surface of the display system; and (b) identifying a BSD that
XX binds to the predetermined epitope. The method is useful to identify bi-
XX or multivalent polypeptides that comprise antibody binding sites capable
XX of efficiently binding to the corresponding antigen. The polypeptides or
XX antibodies identified by the method are useful therapeutically and
XX diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
XX fragments that bind independently of their position within bifunctional
XX single-chain fusion proteins can be isolated from combinatorial antibody
XX libraries using the new in vitro method. Sequences AAY17957-965 represent
XX mouse scFv fragments
XX
XX Sequence 239 AA;
SQ
XX
XX Query Match 92.5%; Score 521; DB 2; Length 239;
XX Best Local Similarity 96.2%; Pred. No. 4.4e-33;
XX Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Search completed: November 21, 2005, 12:19:58
Job time : 147.932 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 / Search time 26.5513 seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-89

Sequence: 1 DSELTQSPTMAASPEKITT.....QQGSSIRPTGGGTLEIKR 109

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Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Length	DB ID	Description
1	533	94.7	123	2 S05269
2	522	92.7	109	2 S1369
3	522	92.7	124	2 S05267
4	520	92.4	108	2 PS0069
5	516	91.7	106	2 S29583
6	515	91.5	120	2 S66536
7	504	89.5	103	2 S13695
8	497	88.3	102	2 S29588
9	493	87.6	102	2 S29582
10	478	84.9	101	2 S13696
11	478	84.9	102	2 S13697
12	473.5	84.1	103	2 S13698
13	468	83.1	93	2 S17633
14	467	82.9	93	2 S17635
15	464	82.4	93	2 S17631
16	462	82.1	93	2 S17624
17	459	81.5	93	2 S17634
18	458	81.3	93	2 S17636
19	445	79.0	93	2 S17625
20	440	78.2	93	2 S17632
21	436	77.4	130	2 A32513
22	433	76.9	108	2 P10278
23	431	76.6	108	2 P10277
24	427	75.8	108	2 P10276
25	426	75.7	107	2 PC4405
26	425	75.5	140	2 P10013
27	425	75.3	130	2 S04573
28	424	75.3	130	2 B32456
29	423	75.1	107	2 A30562

30	419	74.4	105	2 S26338	Ig kappa chain V r
31	418	74.2	107	2 B30562	Ig kappa chain V r
32	418	74.2	132	2 S05268	Ig kappa chain pre
33	417	74.1	113	2 S03410	Ig kappa chain pre
34	416	73.9	129	1 KVM578	Ig kappa chain pre
35	414	73.5	106	2 B54378	Ig light chain V r
36	414	73.5	108	2 S29581	Ig kappa chain V r
37	412	73.2	106	2 PS0070	Ig kappa chain V r
38	410	72.8	109	2 P10405	Ig light chain V r
39	407	72.3	130	1 J10079	Ig kappa chain pre
40	404	71.8	107	2 PD0011	Ig kappa chain V r
41	404	71.8	109	2 PT0404	Ig light chain V r
42	403	71.6	103	2 S29591	Ig kappa chain V r
43	403	71.6	120	2 A34871	Ig kappa chain V r
44	402	71.4	104	2 UC6076	anti-D-dimer monoc
45	401	71.2	106	2 PS0070	Ig kappa chain V r

ALIGNMENTS

RESULT 1
S05269
Ig kappa chain precursor V-J region (38C13-V4) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C/Accession: S05269; J10064; S03847
R/Levy, S.
submitted to the EMBL Data Library, February 1989
A/Reference number: S05267
A/Accession: S05269
A/Molecule type: mRNA
A/Residues: 1-123 <LBV>
A/Cross-references: UNIPARC:UPI0000115DED; EMBL:X14099; NID:95268; PIDN:CA32261.1; PID
R/Carroll, W.L.; Starnes, C.O.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A/Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explanation
A/Reference number: J10061; MUID:89035985; PMID:3141553
A/Accession: J10064
A/Molecule type: mRNA
A/Residues: 1-121 <CAR>
A/Cross-references: UNIPARC:UPI0000176799; EMBL:X14099
C/Species: Mus musculus (house mouse)
C/KeyWords: heterotetramer; immunoglobulin
F/1-13/Domain: signal sequence (fragment) #status predicted <SIG>
F/14-123/Product: Ig kappa chain (fragment) #status predicted <MAT>
F/14-107/Domain: V region (V-kappa-4) <VRB>
F/28-104/Domain: immunoglobulin homology <IMH>
F/108-123/Domain: J region (J-kappa-4) (fragment) <JRB>
Query Match 94.7%; Score 533; DB 2; Length 123;
Best Local Similarity 97.2%; Pred. No. 4.2e-38;
Matches 103; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 4 LTGSPPTMAASPEKITTGSSASSSTSSNYLHWYQQRPSPKLLIRTSNLSGVPAF 63
Db 17 LTGSPPTMAASPEKITTGSSASSSTSSNYLHWYQQRPSPKLLIRTSNLSGVPAF 76

Oy 64 SGSGSGTYSGLTIGTMEABDVATYCCQGSISIRTPFGGTLEIKR 109
Db 77 SGSGSGTYSGLTIGTMEABDVATYCCQGSISIRTPFGGTLEIKR 122

RESULT 2
S13699
Ig kappa chain V region (hybridoma NCI9-B8G2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S13699
R/Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A/Title: Biallelic immunoglobulin variable region gene expression by Ig-1 B cells due to clc
A/Reference number: S13685; MUID:89338557; PMID:2503389

```
A:Accession: S13699
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-109 <PEN>
A:Cross-references: UNIPARC:UPI000011377B; EMBL:X53352; NID:G55303; PIDN:CAA37438.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match          92.7%; Score 522; DB 2; Length 109;
Best Local Similarity 95.3%; Pred. No. 1.6e-37;
Matches 101; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 63
DB 4 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 63

QY 64 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 109
DB 64 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 109

RESULT 3
S05267
IG kappa chain precursor V-J region (38C13-V3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C:Accession: S05267; J10063; S03845
R:Levy, S.
submitted to the EMBL Data Library, February 1989
A:Reference number: S05267
A:Accession: S05267
A:Molecule type: mRNA
A:Residues: 1-124 <LEV>
A:Cross-references: UNIPARC:UPI0000115DB; EMBL:X14097; NID:G52565; PIDN:CAA32259.1; PID
R:Carroll, W.L.; Stearns, C.O.; Levy, R.; Levy, S.
J. Exp. Med. 168, 1607-1620, 1988
A:Title: Alternative V kappa gene rearrangements in a murine B cell lymphoma. An explant
A:Reference number: J10061; MUID:8905985; PMID:3141553
A:Accession: J10063
A:Molecule type: mRNA
A:Residues: 1-123 <CAR>
A:Cross-references: UNIPARC:UPI0000176798; EMBL:X14097
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-11/Domain: signal sequence (fragment) #status predicted <SIG>
F:14-124/Product: Ig kappa chain (fragment) #status predicted <Mat>
F:14-111/Domain: V region (V-kappa-3) <VRB>
F:29-104/Domain: immunoglobulin homology <IMM>
F:112-124/Domain: J region (J-kappa-4) (fragment) <JRB>

Query Match          92.7%; Score 522; DB 2; Length 124;
Best Local Similarity 95.4%; Pred. No. 1.9e-37;
Matches 103; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 63
DB 17 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 76

QY 64 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 109
DB 77 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 124

RESULT 4
PS0069
IG kappa chain V region (38C13.V6) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: PS0069
R:Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A:Title: Functional immunoglobulin light chain genes are replaced by ongoing rearrangement
```

```
A:Reference number: A92781; MUID:89310348; PMID:2501443
A:Accession: PS0069
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-108 <LEV>
A:Cross-references: UNIPROT:Q9JL78; UNIPARC:UPI00001767C7
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match          92.4%; Score 520; DB 2; Length 108;
Best Local Similarity 96.2%; Pred. No. 2.4e-37;
Matches 101; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 63
DB 4 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 63

QY 64 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 108
DB 64 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 108

RESULT 5
S29583
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S29583
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S29583
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <KAV>
A:Cross-references: UNIPARC:UPI0000113791; EMBL:X59098; NID:G52203; PIDN:CAA41824.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match          91.7%; Score 516; DB 2; Length 106;
Best Local Similarity 97.1%; Pred. No. 5.1e-37;
Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 63
DB 4 LTQSPPTMAASPGKTTTCSASSISSNVLMHYOQRPSPKLIYRTSNLASGVPARF 63

QY 64 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 106
DB 64 SSGSGGTSTLTGTMEADVAITYCCQGSIPRTFGGTLEIKR 106

RESULT 6
S66536
IG light chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S66536
R:Teisclote, G.; Haase, W.; Engel, A.; Michel, H.
Eur. J. Biochem. 231, 823-830, 1995
A:Title: Isolation and structural characterization of trimeric cyanobacterial photosystem
A:Reference number: S66536; MUID:95377318; PMID:7649183
A:Accession: S66536
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <TSI>
A:Cross-references: UNIPARC:UPI00001137B0; EMBL:X88903; NID:G895870; PIDN:CAA61365.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match          91.5%; Score 515; DB 2; Length 120;
```

Best Local Similarity 91.7%; Pred. No. 7, 1e-37;
Matches 100; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DSELTGPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 60
Db 1 DIELTGPALMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 60

Qy 61 ARSGSGSTSYSLITGTMEADVATYYCOQGSIPRTFGGTLIKR 109
Db 61 ARSGSGSTSYSLITGTMEADVATYYCOQGSIPRTFGGTLIKR 109

RESULT 7

S13695

Ig kappa chain - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S13695

R/Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

A/Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl

A/Reference number: S13685; MUID:89338557; PMID:2503389

A/Accession: S13695

A/Molecule type: mRNA

A/Residues: 1-103 <PEN>

C/Cross-references: UNIPARC:UPI0000113777; EMBL:X53348; NID:955296; PIDN:CAA37434.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 89.5%; Score 504; DB 2; Length 103;
Best Local Similarity 97.0%; Pred. No. 5, 2e-36;
Matches 97; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63
Db 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63

Qy 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFGG 103
Db 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFGG 103

RESULT 8

S29588

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S29588

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29588

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-102 <KAV>

C/Cross-references: UNIPARC:UPI0000115F54; EMBL:X59091; NID:952221; PIDN:CAA41817.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 88.3%; Score 497; DB 2; Length 102;
Best Local Similarity 97.0%; Pred. No. 2e-35;
Matches 96; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63
Db 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63

Qy 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFGG 102
Db 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFGG 102

RESULT 9

S29582

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S29582

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29582

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-102 <KAV>

C/Cross-references: UNIPARC:UPI0000115F59; EMBL:X59091; NID:952201; PIDN:CAA41823.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 493; DB 2; Length 102;
Best Local Similarity 96.0%; Pred. No. 4, 4e-35;
Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63
Db 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63

Qy 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFGG 102
Db 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFGG 102

RESULT 10

S13696

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S13696

R/Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

A/Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clc

A/Reference number: S13685; MUID:89338557; PMID:2503389

A/Accession: S13696

A/Molecule type: mRNA

A/Residues: 1-101 <PEN>

C/Cross-references: UNIPARC:UPI0000113778; EMBL:X53349; NID:955297; PIDN:CAA37435.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 478; DB 2; Length 101;
Best Local Similarity 95.9%; Pred. No. 8e-34;
Matches 93; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63
Db 4 LTGSPPTMAASPGKITTTCSSASSISNNYLMHWQORPGFSPKLLIYRTSNLASGVP 63

Qy 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFG 100
Db 64 SGSGSGTSYSLITGTMEADVATYYCOQGSIPRTFG 100

RESULT 11

S13697

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S13697

R/Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.

A/Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clc

A/Reference number: S13685; MUID:89338557; PMID:2503389

A:Accession: S13697
A:Molecule type: mRNA
A:Residues: 1-102 <PEN>
A:Cross-references: UNIPROT:Q9JUL78; UNIPARC:UPI00001767B5; EMBL:X53350
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 84.9%; Score 478; DB 2; Length 102;
Best Local Similarity 93.9%; Pred. No. 8.1e-34;
Matches 93; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ITQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63
DB 4 LTQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63
QY 64 GSGSGSTSYSLTGTMEADVATYYCQGSISIPRTFGG 102
DB 64 GSGSGSTSYSLTGTMEADVATYYCQGSISIPRTFGG 102

RESULT 12

S13698
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S13698
R:Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.; Bur, J. Immunol. 19, 1289-1295, 1989
A:Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A:Reference number: S13685; MUID:89338557; PMID:2503389
A:Accession: S13698
A:Molecule type: mRNA
A:Residues: 1-103 <PEN>
A:Cross-references: UNIPROT:Q9JUL78; UNIPARC:UPI00001767B6; EMBL:X53351
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 473.5; DB 2; Length 103;
Best Local Similarity 94.0%; Pred. No. 2e-33;
Matches 94; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 4 ITQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63
DB 4 LTQSPPTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARF 63
QY 64 GSGSGSTSYSLTGTMEADVATYYCQGSISIPRTFGG 102
DB 64 GSGSGSTSYSLTGTMEADVATYYCQGSISIPRTFGG 102

RESULT 13

S17633
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17633
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17633
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
A:Cross-references: UNIPARC:UPI00001767FA
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 468; DB 2; Length 93;
Best Local Similarity 96.8%; Pred. No. 5.2e-33;
Matches 90; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGGS 68
DB 1 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGGS 60
QY 69 GTSYSLTGTMEADVATYYCQGSISIPRTFGG 101
DB 61 GTSYSLTGTMEADVATYYCQGSISIPRTFGG 93

RESULT 14

S17635
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17635
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17635
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
A:Cross-references: UNIPARC:UPI00001767FC
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 82.9%; Score 467; DB 2; Length 93;
Best Local Similarity 96.8%; Pred. No. 6.3e-33;
Matches 90; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGGS 68
DB 1 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGGS 60
QY 69 GTSYSLTGTMEADVATYYCQGSISIPRTFGG 101
DB 61 GTSYSLTGTMEADVATYYCQGSISIPRTFGG 93

RESULT 15

S17631
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S17631
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17631
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
A:Cross-references: UNIPROT:Q9JUL78; UNIPARC:UPI00001767F8
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:8-83/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 464; DB 2; Length 93;
Best Local Similarity 95.7%; Pred. No. 1.1e-32;
Matches 89; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGGS 68
DB 1 TTMAASPGEKITTTCSASSISSNYLHWYQORPGFSPKLLIYRTSNLASGVPARFSGGS 60
QY 69 GTSYSLTGTMEADVATYYCQGSISIPRTFGG 101
DB 61 GTSYSLTGTMEADVATYYCQGSISIPRTFGG 93

Search completed: November 21, 2005, 12:22:13
Job time : 26.5513 secs

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OW protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 161.304 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-89
Perfect score: 563
Sequence: 1 DSELTQSPPTMAAPGKIKT.....QQGSSIPRTGGGTKLKIR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Length	DB	ID	Description
1	494.5	87.8	101	Q9JL78_MOUSE	Q9JL78 mus musculu
2	454	80.6	114	Q8KLP1_MOUSE	Q8KLP1 mus musculu
3	431	76.6	112	Q8KLP2_MOUSE	Q8KLP2 mus musculu
4	431	76.6	112	Q8KLP3_MOUSE	Q8KLP3 mus musculu
5	428	76.0	134	Q8VD00_MOUSE	Q8VD00 mus musculu
6	417.5	74.2	131	Q81IC3_MOUSE	Q81IC3 mus musculu
7	417	74.1	237	Q569Y8_MOUSE	Q569Y8 mus musculu
8	416	73.9	129	KV4A_MOUSE	P01680 mus musculu
9	411	73.0	106	Q9U410_MOUSE	Q9U410 mus musculu
10	409	72.6	112	Q8KLP0_MOUSE	Q8KLP0 mus musculu
11	405	71.9	235	Q58EV6_MOUSE	Q58EV6 mus musculu
12	401	71.2	107	KV6K_MOUSE	P04940 mus musculu
13	398	70.7	108	KV6K_MOUSE	P04945 mus musculu
14	396	70.3	107	KV6I_MOUSE	P04943 mus musculu
15	395	70.2	107	KV6G_MOUSE	P04941 mus musculu
16	395	70.2	107	KV6H_MOUSE	P04942 mus musculu
17	394	70.0	235	KV6J_MOUSE	P04944 mus musculu
18	394	70.0	107	Q5XFP8_MOUSE	Q5XFP8 mus musculu
19	379.5	67.4	108	KV5K_MOUSE	Q91176 mus musculu
20	376.5	66.9	97	Q9JL76_MOUSE	P01675 mus musculu
21	376	66.8	107	KV6D_MOUSE	P01678 mus musculu
22	376	66.8	107	KV6E_MOUSE	P01645 mus musculu
23	374.5	66.5	108	KV5L_MOUSE	P01646 mus musculu
24	374.5	66.5	108	KV5M_MOUSE	P01648 mus musculu
25	374.5	66.5	108	KV5O_MOUSE	P01643 mus musculu
26	373.5	66.3	108	KV5J_MOUSE	P01647 mus musculu
27	372.5	66.2	108	KV5N_MOUSE	P01679 mus musculu
28	371	65.9	107	KV6E_MOUSE	P01678 mus musculu
29	370	65.7	107	KV6B_MOUSE	Q9JL70 mus musculu
30	368.5	65.5	108	KV3H_MOUSE	Q9JL70 homo sapien
31	368.5	65.5	111	KV3H_MOUSE	P01660 mus musculu

32	368	65.4	107	1	KV6C_MOUSE	P01677 mus musculu
33	367.5	65.3	111	1	KV3R_MOUSE	P01670 mus musculu
34	366	65.0	109	2	Q9JL78_HUMAN	Q9JL78 homo sapien
35	364.5	64.7	236	2	Q6PIH7_HUMAN	Q6PIH7 homo sapien
36	363	64.5	107	2	Q96SA9_HUMAN	Q96SA9 homo sapien
37	362.5	64.4	244	2	Q65ZC8_HUMAN	Q65ZC8 homo sapien
38	362	64.3	129	1	KV3L_HUMAN	P18135 homo sapien
39	361.5	64.2	108	1	KV5P_MOUSE	P01649 mus musculu
40	360.5	64.0	111	2	Q920E9_MOUSE	Q920E9 mus musculu
41	360.5	64.0	236	2	Q7TS98_MOUSE	Q7TS98 mus musculu
42	359.5	63.9	108	1	KV3O_HUMAN	P01607 homo sapien
43	359	63.8	109	1	KV3E_HUMAN	P01623 homo sapien
44	358.5	63.7	108	2	Q9JL77_HUMAN	Q9JL77 homo sapien
45	357.5	63.5	236	2	Q6GMX8_HUMAN	Q6GMX8 homo sapien

ALIGNMENTS

RESULT 1
Q9JL78_MOUSE
ID Q9JL78_MOUSE PRELIMINARY; PRT; 101 AA.
AC Q9JL78;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-mysin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC SPRAIN-A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin".
RT Infect. Immun. 68:5803-5808 (2000).
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=2501443;
RX Levy S., Campbell M.J., Levy R.;
RA "Functional immunoglobulin light chain genes are replaced by ongoing
RT rearrangements of germ-line V kappa genes to downstream J kappa segment
RT in a murine B cell line".
RL J. Exp. Med. 170:1-13 (1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1907718;
RA Claesson T., Hoogenboom H.R., Griffiths A.D., Winter G.;
RT "Making antibody fragments using phage display libraries".
RL Nature 352:624-628 (1991).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=8938557; PubMed=2503389;
RA Pennell C.A., Mercollino T.J., Grdina T.A., Arnold L.W., Houghton G.,
RA Clarke S.H.;
RT "Biased immunoglobulin variable region gene expression by Ly-1 B cells
RT due to clonal selection".
RL Eur. J. Immunol. 19:1289-1295 (1989).
DR EMBL, AF206028; AF69326.1; -, mRNA.
DR PIR, P80069; P80069.
DR PIR, S13697; S13697.
DR PIR, S13698; S13698.
DR PIR, S17631; S17631.
DR HSSP, P01679; 2PBJ.
DR SMR, Q9JL78; 3-101.
DR Ensemble; ENSMUSG00000056850; Mus musculus.

DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 101 101
 SQ SEQUENCE 101 AA; 10778 MW; 0A7F6586A7E6F14D CRC64;

Query Match 87.8%; Score 494.5; DB 2; Length 101;
 Best Local Similarity 96.0%; Pred. No. 1.3e-41;
 Matches 97; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 TMAASPGKITTTCSSASSISSNYLHWYQORPGFSPKLIYRTSNLASGVPARFSGSGS 68
 DB 1 TMAASPGKITTTCSSASSISSNYLHWYQORPGFSPKLIYRTSNLASGVPARFSGSGS 60
 QY 69 GTSYSLTIGTMEADVATYYCOQSSIRP-TRFGGTKLEIR 108
 DB 61 GTSYSLTIGTMEADVATYYCOQSSIRP-TRFGGTKLEIR 101

RESULT 2

QK1F1_MOUSE
 ID QK1F1_MOUSE PRELIMINARY; PRT; 114 AA.
 AC QK1F1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Theriata; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed:2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes."; Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=9238144; PubMed=1512540; DOI=10.1084/jem.176.3.761;
 RA Tiliman D.M., Jou N.T., Hill R.J., Marion T.N.;
 RT "Both IGM and IGG anti-DNA antibodies are the products of clonally
 RT selective B cell stimulation in (NZB x NZM) F1 mice."; J. Exp. Med. 176:1761-1779 (1992).
 RL EMBL; AF516284; AAM64202.1; -; Genomic_DNA.
 DR PIR; A33933; A33933.
 DR PIR; PH1058; PH1058.
 DR HSSP; P01837; 25C8.
 DR SMR; Q8K1F1; 2-114.
 DR Ensembl; ENSMUSG0000059896; Mus musculus.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12163 MW; 8BD9833DBF3BEFD1 CRC64;

Query Match 80.6%; Score 454; DB 2; Length 114;
 Best Local Similarity 80.7%; Pred. No. 1.7e-37;
 Matches 88; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 QY 1 DSELQSPPTMAASPGKITTTCSSASSISSNYLHWYQORPGFSPKLIYRTSNLASGVP 60
 DB 1 DSELQSPPTMAASPGKITTTCSSASSISSNYLHWYQORPGFSPKLIYRTSNLASGVP 60

DB 1 DIVLTQSPAIMSAPGKIVTTCRASSSVSSYLHWYQKSGASPKLIYRTSNLASGVP 60
 QY 61 ARFSGSGGTYSYSLTIGTMEADVATYYCOQSSIRP-TRFGGTKLEIR 109
 DB 61 ARFSGSGGTYSYSLTIGTMEADVATYYCOQSSIRP-TRFGGTKLEIR 109

RESULT 3

QK1F2_MOUSE
 ID QK1F2_MOUSE PRELIMINARY; PRT; 112 AA.
 AC QK1F2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Theriata; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-BALB/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed:2499887;
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes."; Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628 (1989).
 RL EMBL; AF516283; AAM64201.1; -; Genomic_DNA.
 DR PIR; H33932; H33932.
 DR HSSP; P01837; 25C8.
 DR SMR; Q8K1F2; 2-112.
 DR Ensembl; ENSMUSG0000064150; Mus musculus.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 11953 MW; 4716887FADB543BD CRC64;

Query Match 76.6%; Score 431; DB 2; Length 112;
 Best Local Similarity 77.1%; Pred. No. 3.3e-35;
 Matches 84; Conservative 8; Mismatches 15; Indels 2; Gaps 1;

QY 1 DSELQSPPTMAASPGKITTTCSSASSISSNYLHWYQORPGFSPKLIYRTSNLASGVP 60
 DB 1 DIVLTQSPAIMSAPGKIVTTCRASSSVSSYLHWYQKSGASPKLIYRTSNLASGVP 58
 QY 61 ARFSGSGGTYSYSLTIGTMEADVATYYCOQSSIRP-TRFGGTKLEIR 109
 DB 59 ARFSGSGGTYSYSLTIGTMEADVATYYCOQSSIRP-TRFGGTKLEIR 107

RESULT 4

QK1F3_MOUSE
 ID QK1F3_MOUSE PRELIMINARY; PRT; 112 AA.
 AC QK1F3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Anti-VIPase light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Theriata; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALE/c; TISSUE=Hyperimmunized spleen;
 RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed:24998877.
 RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
 RT "Two murine natural polyreactive autoantibodies are encoded by
 RT nonmutated germ-line genes."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE:92381444; PubMed:1512540; DOI=10.1084/jem.176.3.761;
 RA Tilieman D.M., Jou N.T., Hill R.J., Marion T.N.;
 RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
 RT selective B cell stimulation in (NZB x NZW) F1 mice."
 RL J. Exp. Med. 176:761-779(1992).
 DR EMBL; AF516282; AA064200.1; -; Genomic_DNA.
 DR PIR; A33933; A33933.
 DR PIR; PH1085; PH1085.
 DR HSSP; P01837; 25C8.
 DR SMR; Q8K1F3; 2-112.
 DR Ensembl; ENSMUSG0000063156; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 1
 FT SEQUENCE 112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;
 SQ
 Query Match 76.6%; Score 431; DB 2; Length 112;
 Best Local Similarity 78.0%; Pred. No. 3.3e-35;
 Matches 85; Conservative 8; Mismatches 14; Indels 2; Gaps 1;
 QY 1 DSELTOSPTMAASPGKKTITTCASASSISNTLHWYQQRPGSPKLLYRTSNTLASGV 60
 DB 1 DIVLTOSPAIMASPGKKTITTCASASSIS--YMYWYQQRPGSPKMWIRTSNLSAGVP 58
 QY 61 ARPSGSGTSYSLTGTMEADVATYCCQGSISPTFGGKTLEIKR 109
 DB 59 ARPSGSGTSYSLTGTMEADVATYCCQGSISPTFGGKTLEIKR 107
 DB
 RESULT 5
 Q8VDDO MOUSE PRELIMINARY; PRT; 134 AA.
 ID Q8VDDO; Q8VDDO;
 AC Q8VDDO;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Anti-MOG Z12 variable light chain (fragment).
 GN Name=gml502; Synonym=anti-MOG kappa;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALE/c;
 RA Sembli P.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALE/c;
 RA Charnajovsky Y.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed:2427335;
 RA Cation A.J., Brownlee G.G., Staedt L.M., Gerhard W.;
 RT "Structural and functional implications of a restricted antibody

RT response to a defined antigenic region on the influenza virus
 RT hemagglutinin.";
 RL EMBL; AJ416331; CAC94866.1; -, mRNA.
 DR EMBL; AJ416331; CAC94866.1; -, mRNA.
 DR PIR; G27887; G27887.
 DR HSSP; P01834; 1M1M.
 DR SMR; Q8VDDO; 23-134.
 DR Ensembl; ENSMUSG0000062047; Mus musculus.
 DR MG1; 2686348; Gml502.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 FT NON_TER 134
 FT SEQUENCE 134 AA; 14525 MW; CFPD8E2236E2D0CF CRC64;
 SQ
 Query Match 76.0%; Score 428; DB 2; Length 134;
 Best Local Similarity 80.2%; Pred. No. 8.1e-35;
 Matches 85; Conservative 5; Mismatches 14; Indels 2; Gaps 1;
 QY 4 LTQSPPTMAASPGKKTITTCASASSISNTLHWYQQRPGSPKLLYRTSNTLASGV 63
 DB 26 LTQSPPTMAASPGKKTITTCASASSIS--YMYWYQQRPGSPKMWIRTSNLSAGVP 83
 QY 64 SSGSGSGTSYSLTGTMEADVATYCCQGSISPTFGGKTLEIKR 109
 DB 84 SSGSGSGTSYSLTGTMEADVATYCCQGSISPTFGGKTLEIKR 129
 DB
 RESULT 6
 Q81IC3 MOUSE PRELIMINARY; PRT; 131 AA.
 ID Q81IC3; Q81IC3;
 AC Q81IC3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Immunoglobulin gamma-3 kappa chain precursor (fragment).
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MRL/MPJ-1pr/1pr; TISSUE=spleen;
 RX MEDLINE:93156722; PubMed:8429833; DOI=10.1016/0161-5890(93)90089-T;
 RA Takahashi S., Itoh J., Nose M., Ono M., Yamamoto T., Kyogoku M.;
 RT "Cloning and cDNA sequence analysis of nephritogenic monoclonal
 RT antibodies derived from an MRL/lpr lupus mouse."
 RL Mol. Immunol. 30:177-182(1993).
 DR EMBL; D14629; BAA03482.1; -, mRNA.
 DR HSSP; P01679; 2FBJ.
 DR SMR; Q81IC3; 23-131.
 DR Ensembl; ENSMUSG0000058987; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW signal.
 FT SIGNAL 1 22
 FT CHAIN 23 >131
 FT NON_TER 131
 FT SEQUENCE 131 AA; 14083 MW; SE836569466689B CRC64;
 SQ
 Query Match 74.2%; Score 417.5; DB 2; Length 131;
 Best Local Similarity 76.4%; Pred. No. 8.8e-34;
 Matches 81; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
 QY 4 LTQSPPTMAASPGKKTITTCASASSISNTLHWYQQRPGSPKLLYRTSNTLASGV 63
 DB 26 LTQSPPTMAASPGKKTITTCASASSIS--YMYWYQQRPGSPKMWIRTSNLSAGVP 85
 QY 64 SSGSGSGTSYSLTGTMEADVATYCCQGSISPTFGGKTLEIKR 108

Db

86 SGGSGTSLTSSVEAEDATYCCQYDSSPSITFGAGTKLEK 131

Q	RESULT 7	
ID	0569Y8_MOUSE PRELIMINARY;	PRT; 237 AA.
AC	0569Y8_	
DT	10-MAY-2005 (TrEMBLrel. 30, Created)	
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)	
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)	
DE	igk-C protein.	
GN	Name=igk-C;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi;	
OC	Mammalia; Euteleia; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Myrodonta; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	NCLOTOTIDE SSEQUENCE.	
RC	STRAIN-FVB/N. TRISUB=Kidney;	
RX	MEDLINE=22388257; PubMed=12477992; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,	
RA	Diatchenko L., Marziska K., Farmer A.A., Rubin G.W., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,	
RA	Brownstein M.J., Uddin T.B., Tohyama S., Carninci P., Frange C.,	
RA	Rata S.S., Loeuallan N.A., Peters G.J., Abramson R.D., Mullay S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamarate P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butcherfield A., Schein J.E., Jones S.J.M., Skatska U., Smalins D.E.,	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RL	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	NCLOTOTIDE SSEQUENCE.	
RC	STRAIN-FVB/N. TRISUB=Kidney;	
RG	NH MGC Project;	
RL	Submitted (APR-2005) to the EMBL/GenBank/DBD databases.	
DR	EMBL; BC092251; AAH92251.1; -; mRNA.	
DR	SMR; Q569Y8; 23-237.	
DR	InterPro; IPR003599; IG.	
DR	InterPro; IPR007110; IG-1like.	
DR	InterPro; IPR003597; IG cl.	
DR	InterPro; IPR003065; IG_MHC.	
DR	InterPro; IPR003596; IG_v.	
DR	Pfam; PF07654; Cl-secl; 1.	
DR	SMART; SM00409; IG; 2.	
DR	SMART; SM00407; IGcl; 1.	
DR	SMART; SM00406; IGv; 1.	
DR	PROSITE; PSS0835; IG_LIKE; 2.	
DR	PROSITE; PSS00290; IG_MHC; UNKNOWN; 1.	
DR	SEQUENCE 237 AA; 25978 MW; A88596AA417FB932 CRC64;	

	RESULT 8		
KV4A_MOUSE			
ID	_KV4A_MOUSE	STANDARD;	PRT; 129 AA.
AC	P01680;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	10-MAY-2005 (Rel. 47, Last annotation update)		
DS	IG kappa chain V-IIV region S107B precursor.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridea; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RK	MEHLINIE=82115300; Pubmed=6799208; DOI=10.1016/0092-8674(81)90033-7;		
RA	Kwan S.-P., Max E.E., Seidman J.G., Leder P., Schaffr M.D.;		
RT	"Two kappa immunoglobulin genes are expressed in the myeloma S107." ;		
RL	Cell 26:57-66(1981).		
CC	-I- MISCELLANEOUS: This protein, in which there is a deletion of two		
CC	amino acids at the V-J recombination site (after position 118), is		
CC	synthesised but not secreted in cells that express and secrete the		
CC	normal kappa chain S107.		
CC	-----		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		

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          RESULT 9
          Q9U410 MOUSE
          ID Q9U410_ MOUSE PRELIMINARY; PRT; 106 AA
          AC Q9U410;

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DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DB Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30
DB Immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12567627;
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Yu X.C., Xiong Y., Yin C.C.,
RA Huang H.L., Guan X.H.;
RT Cloning and sequence analysis of the light chain variable region
RT gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma
RT japonicum.
RL Zhongguo Ji Sheng Chong Xue Yu Ji Sheng Chong Bing Za Zhi
RL 18:257-259(2000).
DR EMBL; AF207620; AAF19434.1; -; Genomic_DNA.
DR HSSP; P01679; 2PBJ.
DR SMR; Q9U410; 4-106.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 11478 MW; P20F544426BAE63B CRC64;

Query Match 72.6%; Score 411; DB 2; Length 106;
Best Local Similarity 76.2%; Pred. No. 3.1e-33;
Matches 80; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 4 LTGSPPTMAASPGRKTTTTCSSASSISNTLHWYQQRPGSPKLLIRTSNLASGV 63
DB 4 LTGSPAIMSASPGRKVTMTCSASSSVS--YYWYLOKRGSSPRLLIYDTSNLASGV 61

QY 64 SGSSGSGSYSLTIGTMEADVATYTCQGSISIRTFGGGTLEIRK 108
DB 62 SGSSGSGSYSLTISRMEADVATYTCQGSISIRTFGGGTLEIRK 106

RESULT 10
OSKIF0 MOUSE PRELIMINARY; PRT; 112 AA.
ID OSKIF0_MOUSE PRELIMINARY; PRT; 112 AA.
AC OSKIF0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DB Anti-vipase light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAH/c; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=249887;
RA Baccala R., Quang T.V., Gilbert M., Terrynek T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR EMBL; AF516285; AAM64203.1; -; Genomic_DNA.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; 1OKQ.

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DR SMR; Q8KIF0; 3-112.
DR Ensemble; ENSMUSG00000062047; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11901 MW; F6444663201AA239 CRC64;

Query Match 72.6%; Score 409; DB 2; Length 112;
Best Local Similarity 74.3%; Pred. No. 5.2e-33;
Matches 81; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 1 DSELTGSPPTMAASPGRKTTTTCSSASSISNTLHWYQQRPGSPKLLIRTSNLASGV 60
DB 1 DSELTGSPAIMSASPGRKVTMTCSASSSVS--YHWYQQRSGTSPKMIYDTSKLASGV 58

QY 61 ARFSGSGSYSLTIGTMEADVATYTCQGSISIRTFGGGTLEIRK 109
DB 59 ARFSGSGSYSLTISRMEADVATYTCQGSISIRTFGGGTLEIRK 107

RESULT 11
OS8EV6 MOUSE PRELIMINARY; PRT; 235 AA.
ID OS8EV6_MOUSE PRELIMINARY; PRT; 235 AA.
AC OS8EV6;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Pelting E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Abramson R.D., Mullaby S.J.,
RA Rana S.S., Loggiano N.A., Peters G.J., Malek J.A., Gunnaracne P.H.,
RA Bosak S.A., McEwan P.V., McKernan K.J., Hale S., Garcia A.M., Gay L.J.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalando D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,
RA Roderfeldt Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091738; AAH91738.1; -; mRNA.
DR SMR; Q58EV6; 23-235.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c.
DR InterPro; IPR003066; Ig_MHC.

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DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; Cl-secl.1.
 DR SMART; SM00409; Igc1.2.
 DR SMART; SM00407; Igc1.1.
 DR SMART; SM00406; Igc1.1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 DR SEQUENCE 235 AA; 35719 MW; BE454ABDD2578252 CRC64;

Query Match 71.9%; Score 405; DB 2; Length 235;
 Best Local Similarity 74.5%; Pred. No. 3.1e-32;
 Matches 79; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOORPGFSPKLIYRTSNLASGVPAF 63
 AC P04940;
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DB 26 LTQSPALMSAPGQVMTTCASASSVS--YMHYQOKSGTSPKRWIYDTSKLASGVPAF 83
 QY 64 SSGSGGTSTSLTITGMEADVATYYCQOGSSIPRTFGGKTLEIKR 109
 DB 84 SSGSGGTSTSLTITGMEADVATYYCQOWTSNPLTFGAGTKLDLKR 129

RESULT 12
 KV6F_MOUSE STANDARD; PRT; 107 AA.

AC P04940;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-VI region NQ2-17.4.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification."
 RL Nature 304:320-324(1983).
 CC -1- FUNCTION: Anti-2-phenyl oxazolone (PHOX) Antibody.
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 CC EMBL; K00735; AAA38680.1; -; mRNA.
 DR HSSP; P04940; 1-107.
 DR SMR; P04940; 1-107.
 DR Ensemble; ENSMUSG0000062047; Mus musculus.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 96 Complementarity-determining-3.
 FT REGION 97 106 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11561 MW; 6F694284EBCFA686 CRC64;

Query Match 71.2%; Score 401; DB 1; Length 107;
 Best Local Similarity 74.5%; Pred. No. 3.1e-32;
 Matches 79; Conservative 9; Mismatches 16; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOORPGFSPKLIYRTSNLASGVPAF 63
 AC P04940;
 DT 13-AUG-1987 (Rel. 05, Created)
 DB 26 LTQSPALMSAPGQVMTTCASASSVS--YMHYQOKSGTSPKRWIYDTSKLASGVPAF 61
 QY 64 SSGSGGTSTSLTITGMEADVATYYCQOGSSIPRTFGGKTLEIKR 109
 DB 62 SSGSGGTSTSLTITGMEADVATYYCQOWSSNPLTFGAGTKLEIKR 107

RESULT 13
 KV6F_MOUSE STANDARD; PRT; 108 AA.

AC P04945;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig kappa chain V-VI region NQ2-6.1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83271467; PubMed=6877353;
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
 RT "mRNA sequences define an unusually restricted IgG response to 2-phenylloxazolone and its early diversification."
 RL Nature 304:320-324(1983).
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL; K00746; AAA38691.1; -; mRNA.
 DR HSSP; O91W12; 1AY1.
 DR SMR; P04945; 1-108.
 DR Ensemble; ENSMUSG0000062686; Mus musculus.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
 FT REGION 1 23 Framework-1.
 FT REGION 24 33 Complementarity-determining-1.
 FT REGION 34 48 Framework-2.
 FT REGION 49 55 Complementarity-determining-2.
 FT REGION 56 87 Framework-3.
 FT REGION 88 98 Complementarity-determining-3.
 FT REGION 99 108 Framework-4.
 FT DISULFID 23 87 By similarity.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11713 MW; DABF235CDB680AC6 CRC64;

Query Match 70.7%; Score 398; DB 1; Length 108;
 Best Local Similarity 73.8%; Pred. No. 6.3e-32;
 Matches 79; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

QY 4 LTQSPPTMAASPGKITTTCASASSISSNVLMHYOORPGFSPKLIYRTSNLASGVPAF 63
 AC P04945;
 DT 13-AUG-1987 (Rel. 05, Created)
 DB 4 LTQSPALMSAPGQVMTTCASASSVS--YMHYQOKSGTSPKRWIYDTSKLASGVPAF 61
 QY 64 SSGSGGTSTSLTITGMEADVATYYCQOGSSIP--RTFGGKTLEIKR 108
 DB 62 SSGSGGTSTSLTITGMEADVATYYCQOWSSNPLTFGAGTKLEIKR 108

RESULT 14
 KV6I_MOUSE STANDARD; PRT; 107 AA.

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AC P04943;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NO6-8.3.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
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removed.
CC -----
CC EMBL; K00740; AAA38685.1; -; mRNA.
CC HSSP; P01679; 2PBJ.
CC SMR; P04943; 1-107.
CC Ensembl; ENSMUSG0000062047; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC SMART; SM00406; IGV; 1.
CC DR POSTITE; PSS0835; Ig_LIKE; 1.
CC Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
CC REGION 1 23 Framework-1.
CC REGION 24 33 Complementarity-determining-1.
CC REGION 34 48 Framework-2.
CC REGION 49 55 Complementarity-determining-2.
CC REGION 56 87 Framework-3.
CC REGION 88 96 Complementarity-determining-3.
CC REGION 97 106 Framework-4.
CC REGION 107 107 By similarity.
CC DISULFID 23 87
CC NON_TER 107 107
CC SEQUENCE 107 AA; 11573 MW; 6F694824ECF0C8E6 CRC64;

Query Match 70.3%; Score 396; DB 1; Length 107;
Best Local Similarity 73.6%; Pred. No. 9.8e-32;
Matches 78; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTOSPTMAASPGKITTTCSSASSISNTLHWYQORPGFSPKLLIYRTSLASGVPARF 63
DB 4 LTOSPAIMASPGQKVTMTCSASSVS--YHWYQOKSGTSPKWIYDTSKLASGVPARF 61

QY 64 SSGSGSSTSLTGTMEADVATYCCQGSIPRTFGGTLEIKR 109
DB 62 SSGSATSSTLTSMQADATYCCQWSSNPLTFAGTLEIKR 107

RESULT 15
KV6G_MOUSE STANDARD; PRT; 107 AA.
ID P04941;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-VI region NO2-48.2.2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milestein C.;
RT "mRNA sequences define an unusually restricted Igg response to 2-
phenyloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.
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use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC EMBL; K00737; AAA38682.1; -; mRNA.
CC HSSP; Q91W12; 1AY1.
CC SMR; P04941; 1-103.
CC Ensembl; ENSMUSG0000062047; Mus musculus.
CC InterPro; IPR007110; Ig-like.
CC SMART; SM00406; IGV; 1.
CC DR POSTITE; PSS0835; Ig_LIKE; 1.
CC Hybridoma; Immunoglobulin domain; Immunoglobulin V region.
CC REGION 1 23 Framework-1.
CC REGION 24 33 Complementarity-determining-1.
CC REGION 34 48 Framework-2.
CC REGION 49 55 Complementarity-determining-2.
CC REGION 56 87 Framework-3.
CC REGION 88 96 Complementarity-determining-3.
CC REGION 97 106 Framework-4.
CC REGION 107 107 By similarity.
CC DISULFID 23 87
CC NON_TER 107 107
CC SEQUENCE 107 AA; 11557 MW; 7248DA9BF354934 CRC64;

Query Match 70.2%; Score 395; DB 1; Length 107;
Best Local Similarity 73.6%; Pred. No. 1.2e-31;
Matches 76; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTOSPTMAASPGKITTTCSSASSISNTLHWYQORPGFSPKLLIYRTSLASGVPARF 63
DB 4 LTOSPAIMASPGQKVTMTCSASSVS--YHWYQOKSGTSPKWIYDTSKLASGVPARF 61

QY 64 SSGSGSSTSLTGTMEADVATYCCQGSIPRTFGGTLEIKR 109
DB 62 SSGSATSSTLTSMQADATYCCQWSSNPLTFAGTLEIKR 107

Search completed: November 21, 2005, 12:04:06
Job time : 161.304 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 ; Search time 41.1245 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-89
Perfect score: 563
Sequence: 1 DSELTQSPPTMAASPERKIT.....QQGSSIPRTFGGTLLEIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA: *
2: /cgn2_6/prodata/1/1aa/5.COMB.pep: *
3: /cgn2_6/prodata/1/1aa/6.COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RR.COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	97.3	109	1	US-08-553-497A-14 Sequence 14, Appl
2	541	96.1	110	2	US-09-726-219A-247 Sequence 247, App
3	541	96.1	110	2	US-09-196-522-247 Sequence 247, App
4	540	95.9	110	2	US-09-726-219A-249 Sequence 249, App
5	540	95.9	110	2	US-09-196-522-249 Sequence 249, App
6	537	95.4	110	2	US-09-726-219A-245 Sequence 245, App
7	537	95.4	110	2	US-09-196-522-245 Sequence 245, App
8	535	95.0	110	2	US-09-726-219A-258 Sequence 258, App
9	535	95.0	110	2	US-09-196-522-258 Sequence 258, App
10	532	94.5	110	2	US-09-726-219A-238 Sequence 238, App
11	532	94.5	110	2	US-09-726-219A-248 Sequence 248, App
12	532	94.5	110	2	US-09-196-522-238 Sequence 238, App
13	532	94.5	110	2	US-09-196-522-248 Sequence 248, App
14	530	94.1	297	2	US-09-486-814A-2 Sequence 2, Appl1
15	527	93.6	110	2	US-09-726-219A-250 Sequence 250, App
16	527	93.6	110	2	US-09-196-522-250 Sequence 250, App
17	524	93.1	110	2	US-09-726-219A-246 Sequence 246, App
18	524	93.1	110	2	US-09-196-522-246 Sequence 246, App
19	518	92.0	110	2	US-09-726-219A-239 Sequence 239, App
20	518	92.0	110	2	US-09-196-522-239 Sequence 239, App
21	496	88.1	103	2	US-09-486-814A-6 Sequence 6, Appl1
22	455	80.8	108	2	US-08-881-037-74 Sequence 74, Appl
23	455	80.8	110	2	US-09-726-219A-255 Sequence 255, App
24	455	80.8	110	2	US-09-726-219A-256 Sequence 256, App
25	455	80.8	110	2	US-09-196-522-255 Sequence 255, App
26	455	80.8	110	2	US-09-196-522-256 Sequence 256, App
27	452	80.3	110	2	US-09-726-219A-257 Sequence 257, App

28	452	80.3	110	2	US-09-196-542-257	Sequence 257, App
29	450	79.9	110	2	US-09-726-219A-237	Sequence 237, App
30	450	79.9	110	2	US-09-196-542-237	Sequence 237, App
31	447	79.4	108	2	US-09-726-219A-240	Sequence 240, App
32	447	79.4	108	2	US-09-196-542-240	Sequence 240, App
33	444	78.9	110	2	US-09-726-219A-254	Sequence 254, App
34	444	78.9	110	2	US-09-196-542-254	Sequence 254, App
35	440	78.2	129	1	US-08-116-776B-2	Sequence 2, Appl1
36	440	78.2	129	1	US-08-438-502-2	Sequence 2, Appl1
37	440	78.2	129	1	US-08-483-528B-92	Sequence 92, Appl
38	439	78.0	108	2	US-09-726-219A-242	Sequence 242, App
39	439	78.0	108	2	US-09-196-522-242	Sequence 242, App
40	439	78.0	258	2	US-09-526-738A-2	Sequence 2, Appl1
41	439	78.0	258	2	US-09-526-738A-4	Sequence 4, Appl1
42	437	77.6	106	2	US-09-798-688-8	Sequence 8, Appl1
43	437	77.6	235	2	US-09-171-945-17	Sequence 17, Appl
44	437	77.6	235	2	US-09-910-059-17	Sequence 17, Appl
45	437	77.6	238	2	US-09-798-689-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-553-497A-14
Sequence 14, Application US/08553497A
Patent No. 5844093
GENERAL INFORMATION:
APPLICANT: KETTERBOROUGH, C. A.
APPLICANT: BENDIG, MARY M.
APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSON, DETLEF
APPLICANT: ADAM, JAUME
APPLICANT: MITJANS, FRANCESC
APPLICANT: ROSEIL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PILATS, JAUME
TITLE OF INVENTION: ANTI-BGFR SINGLE-CHAIN FVS AND ANTI-BGFR
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-14

Query Match 97.3%; Score 548; DB 1; Length 109;
Best Local Similarity 97.2%; Pred. No. 4,9e-46;
Matches 106; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASGKETTTCASASSISSNYLHWYQKRGFPKLLIYRTSNLAGVP 60
DB 1 DIELTOSPTTMAASGKETTTCASASSISSNYLHWYQKRGFPKLLIYRTSNLAGVP 60
QY 61 ARFSGSGSGTSLTIGTMEADVAITYCCQGSIPRTFGGTLEIKR 109
DB 61 ARFSGSGSGTSLTIGTMEADVAITYCCQGSIPRTFGGTLEIKR 109

RESULT 2

US-09-726-219A-247
Sequence 247, Application US/09726219A
Patent No. 6806079

GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kaeper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A

PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-06
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 247
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VL of scfv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-247

Query Match 96.1%; Score 541; DB 2; Length 110;

Best Local Similarity 96.3%; Pred. No. 2.3e-45;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASGKETTTCASASSISSNYLHWYQKRGFPKLLIYRTSNLAGVP 60
DB 1 DIELTOSPTTMAASGKETTTCASASSISSNYLHWYQKRGFPKLLIYRTSNLAGVP 60
QY 61 ARFSGSGSGTSLTIGTMEADVAITYCCQGSIPRTFGGTLEIKR 109
DB 61 ARFSGSGSGTSLTIGTMEADVAITYCCQGSIPRTFGGTLEIKR 109

RESULT 3

US-09-196-522-247
Sequence 247, Application US/09196522
Patent No. 6916605

GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kaeper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00004
CURRENT APPLICATION NUMBER: US/09/196,522

PRIOR FILING DATE: 1998-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-06
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 247
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VL of scfv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-247

Query Match 96.1%; Score 541; DB 2; Length 110;
Best Local Similarity 96.3%; Pred. No. 2.3e-45;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DSELTOSPTTMAASGKETTTCASASSISSNYLHWYQKRGFPKLLIYRTSNLAGVP 60
DB 1 DIELTOSPTTMAASGKETTTCASASSISSNYLHWYQKRGFPKLLIYRTSNLAGVP 60
QY 61 ARFSGSGSGTSLTIGTMEADVAITYCCQGSIPRTFGGTLEIKR 109

Db 61 ARFSGSGGTSYSLTIGTMEADVATYYCOQSSIPFTFGGTYLRIKR 109

RESULT 4
US-09-726-219A-249
Sequence 249, Application US/09726219A
Patent No. 6806079

GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patentin version 3.1
SEQ ID NO 249
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-249

Query Match 95.9%; Score 540; DB 2: Length 110;
Best Local Similarity 96.3%; Pred. No. 2.9e-45;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSELTOSPTTMAASPEKITTTCASSSISSNYLHWYQORPGFSPKLLIYRTSNLASGVP 60
Db 1 DIELTOSPTTMAASPEKITTTCASSSISSNYLHWYQORPGFSPKLLIYRTSNLASGVP 60

Qy 61 ARFSGSGGTSYSLTIGTMEADVATYYCOQSSIPFTFGGTYLRIKR 109
Db 61 ARFSGSGGTSYSLTIGTMEADVATYYCOQSSIPFTFGGTYLRIKR 109

RESULT 5
US-09-196-522-249
Sequence 249, Application US/09196522
Patent No. 691605

GENERAL INFORMATION:

APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00004
CURRENT APPLICATION NUMBER: US/09/196,522
CURRENT FILING DATE: 1998-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: Patentin version 3.1
SEQ ID NO 249
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-249

Query Match 95.9%; Score 540; DB 2: Length 110;
Best Local Similarity 96.3%; Pred. No. 2.9e-45;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DSELTOSPTTMAASPEKITTTCASSSISSNYLHWYQORPGFSPKLLIYRTSNLASGVP 60
Db 1 DIELTOSPTTMAASPEKITTTCASSSISSNYLHWYQORPGFSPKLLIYRTSNLASGVP 60

Qy 61 ARFSGSGGTSYSLTIGTMEADVATYYCOQSSIPFTFGGTYLRIKR 109
Db 61 ARFSGSGGTSYSLTIGTMEADVATYYCOQSSIPFTFGGTYLRIKR 109

RESULT 6
US-09-726-219A-245
Sequence 245, Application US/09726219A
Patent No. 6806079
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus

```

/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00013
/ CURRENT APPLICATION NUMBER: US/09/726,219A
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 245
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-245

Query Match      95.4% Score 537, DB 2, Length 110;
Best Local Similarity 95.4%; Pred. No. 5,7e-45;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 DSELTQSPTTMAASGKRTTTCSSASSISSNYLHWYQORGFSPKLIYTSNLASGP 60
Db 1 DIELTQSPTTMAASGKRTTTCSSASSISSNYLHWYQORGFSPKLIYTSNLASGP 60

Cy 61 ARFSGSGSGTSYSLTIGTMEADVATYYCCQSSISPTFGGKTLKIR 109
Db 61 ARFSGSGSGTSYSLTIGTMEADVATYYCCQSSISPTFGGKTLKIR 109

RESULT 7
US-09-196-522-245
/ Sequence 245, Application US/09196522
/ Patent No. 6916605
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
```

```

/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00004
/ CURRENT APPLICATION NUMBER: US/09/196,522
/ PRIOR FILING DATE: 1998-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 245
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-245

Query Match      95.4% Score 537, DB 2, Length 110;
Best Local Similarity 95.4%; Pred. No. 5,7e-45;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 DSELTQSPTTMAASGKRTTTCSSASSISSNYLHWYQORGFSPKLIYTSNLASGP 60
Db 1 DIELTQSPTTMAASGKRTTTCSSASSISSNYLHWYQORGFSPKLIYTSNLASGP 60

Cy 61 ARFSGSGSGTSYSLTIGTMEADVATYYCCQSSISPTFGGKTLKIR 109
Db 61 ARFSGSGSGTSYSLTIGTMEADVATYYCCQSSISPTFGGKTLKIR 109

RESULT 8
US-09-726-219A-258
/ Sequence 258, Application US/09726219A
/ Patent No. 6806079
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00013
/ CURRENT APPLICATION NUMBER: US/09/726,219A
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
```

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/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 258
/ LENGTH: 110
/ TYPE: PR1
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-258

Query Match          95.0%; Score 535; DB 2; Length 110;
Best Local Similarity 95.4%; Pred. No. 9e-45;
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPTTMAAPGPKITTTCSASSISSNTLHWYQRPFGSPKLLIYRTSNLAVGP 60
   |||||
DB 1 DIELTQSPTTMAAPGPKITTTCSASSISSNTLHWYQRPFGSPKLLIYRTSNLAVGP 60
   |||||

QY 61 ARPSGSGGTSYSLTGTGMEADVAITYCOQSSISPTFGGKLEIKR 109
   |||||
DB 61 ARPSGSGGTSYSLTGTGMEADVAITYCOQSSISPTFGGKLEIKR 109
   |||||

RESULT 9
US-09-196-522-258
/ Sequence 258, Application US/09196522
/ Patent No. 6916605
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Jackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00004
/ CURRENT APPLICATION NUMBER: US/09/196,522
/ PRIOR FILING DATE: 1998-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
```

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/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 258
/ LENGTH: 110
/ TYPE: PR1
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-258

Query Match          95.0%; Score 535; DB 2; Length 110;
Best Local Similarity 95.4%; Pred. No. 9e-45;
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPTTMAAPGPKITTTCSASSISSNTLHWYQRPFGSPKLLIYRTSNLAVGP 60
   |||||
DB 1 DIELTQSPTTMAAPGPKITTTCSASSISSNTLHWYQRPFGSPKLLIYRTSNLAVGP 60
   |||||

QY 61 ARPSGSGGTSYSLTGTGMEADVAITYCOQSSISPTFGGKLEIKR 109
   |||||
DB 61 ARPSGSGGTSYSLTGTGMEADVAITYCOQSSISPTFGGKLEIKR 109
   |||||

RESULT 10
US-09-726-219A-238
/ Sequence 238, Application US/09726219A
/ Patent No. 6806079
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Jackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 213839-00013
/ CURRENT APPLICATION NUMBER: US/09/726,219A
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
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QY 61 ARFSGSGSTSYSLTIGTMEADVATYYCCQGSSTPRTFGGTLKLEIKR 109
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 Db 61 ARFSGSGSTSYSLTIGTMEADVATYYCCQGSSTPRTFGGTLKLEIKR 109
 |||||

RESULT 13
 US-09-196-522-248
 ; Sequence 248, Application US/09196522
 ; Patent No. 6916605
 ; GENERAL INFORMATION:
 ; APPLICANT: Cambridge Antibody Technology Limited
 ; APPLICANT: Cambridge Antibody Technology Limited
 ; APPLICANT: Medical Research Council
 ; APPLICANT: McCafferty, John
 ; APPLICANT: Pope, Anthony
 ; APPLICANT: Johnson, Kevin
 ; APPLICANT: Hoogenboom, Hendricus
 ; APPLICANT: Griffiths, Andrew
 ; APPLICANT: Jackson, Ronald
 ; APPLICANT: Holliger, Kasper
 ; APPLICANT: Marks, James
 ; APPLICANT: Clarkson, Timothy
 ; APPLICANT: Chiswell, David
 ; APPLICANT: Winter, Gregory
 ; APPLICANT: Bonnett, Timothy
 ; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
 ; FILE REFERENCE: 213839-00004
 ; CURRENT APPLICATION NUMBER: US/09/196,522
 ; CURRENT FILING DATE: 1998-11-28
 ; PRIOR APPLICATION NUMBER: GB 9015198.6
 ; PRIOR FILING DATE: 1990-07-10
 ; PRIOR APPLICATION NUMBER: GB 9022845.3
 ; PRIOR FILING DATE: 1990-10-19
 ; PRIOR APPLICATION NUMBER: GB 9022845.3
 ; PRIOR FILING DATE: 1990-10-19
 ; PRIOR APPLICATION NUMBER: GB 9022845.3
 ; PRIOR FILING DATE: 1990-10-19
 ; PRIOR APPLICATION NUMBER: GB 9024503.6
 ; PRIOR FILING DATE: 1990-11-12
 ; PRIOR APPLICATION NUMBER: GB 9104744.9
 ; PRIOR FILING DATE: 1991-03-06
 ; PRIOR APPLICATION NUMBER: GB 9110549.4
 ; PRIOR FILING DATE: 1991-05-15
 ; PRIOR APPLICATION NUMBER: PCT/GB91/01134
 ; PRIOR FILING DATE: 1991-07-10
 ; PRIOR APPLICATION NUMBER: US 07/971,857
 ; PRIOR FILING DATE: 1993-01-08
 ; PRIOR APPLICATION NUMBER: US 08/484,893
 ; PRIOR FILING DATE: 1995-06-07
 ; NUMBER OF SEQ ID NOS: 272
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 248
 ; LENGTH: 110
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURES:
 ; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone

US-09-196-522-248
 Query Match 94.5%; Score 532; DB 2; Length 110;
 Best Local Similarity 94.5%; Pred. No. 1.8e-44;
 Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTGSPPTMAASPGKITTTCSSASSISNTLHWYQORPGSPPLTLIRTSNLAAGVP 60
 |||||
 Db 1 DIELTGPTTMAASPGKITTTCSSASSISNTLHWYQORPGSPPLTLIRTSNLAAGVP 60
 |||||

QY 61 ARFSGSGSTSYSLTIGTMEADVATYYCCQGSSTPRTFGGTLKLEIKR 109
 |||||
 Db 61 ARFSGSGSTSYSLTIGTMEADVATYYCCQGSSTPRTFGGTLKLEIKR 109
 |||||

RESULT 14
 US-09-486-814A-2
 ; Sequence 2, Application US/09486814A

```

; Patent No. 6562599
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Masato
; APPLICANT: HAYASHI, No. 656259910
; APPLICANT: YAMAMOTO, Hiroko
; APPLICANT: TODOH, Naoki
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
; TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
; TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
; FILE REFERENCE: 0020-4682P
; CURRENT APPLICATION NUMBER: US/09/486,814A
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Mus sp., strain: Balb/c, tissue: spleen
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(145)
; OTHER INFORMATION: Identification Method: P
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (177)..(279)
; OTHER INFORMATION: Identification Method: P
US-09-486-814A-2

Query Match          94.1%; Score 530; DB 2; Length 297;
Best Local Similarity 93.7%; Pred. No. 8,7e-44;
Matches 104; Conservative 2; Mismatches 3; Indels 2; Gaps 1.;

QY      1 DSELTOSPTTMAASPGEXKITTCSSASSISSNYLHWYQQRFSPKLLITYRSLASGVP 60
DB      169 DIETLOSTTTMAAPGXKITTCSSASSISSNYLHWYQQKFSPKLLITYRSLASGP 228
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QY      61 ARFGSGSGGSYSYLITGTMEADVAITYCCOGSSIPR--TTCGGTKLEIKR 109
DB      229 ARFGSGSGGSYSYLITGTMEADVAITYCCOGSSIPRLTFKGAGTKLEIKR 279
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RESULT 15
US-09-726-219A-250
; Sequence 250, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Jackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 ; Search time 134.952 Seconds
(without alignments)
337.478 Million cell updates/sec

Title: US-10-632-706-89

Perfect score: 1 DSELTQSPPTMAASPGKKT.....QQGSSIPRTGGTLEIKR 109

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubpaa/us07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubpaa/us08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubpaa/us09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubpaa/us10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubpaa/us10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubpaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	563	100.0	109	3	US-09-144-886-92
2	563	100.0	109	4	US-10-632-706-89
3	541	96.1	110	4	US-10-803-622-247
4	541	96.1	110	4	US-10-803-622-247
5	540	95.9	110	4	US-10-803-622-249
6	540	95.9	110	4	US-10-803-622-249
7	537	95.4	110	4	US-10-803-622-245
8	537	95.4	110	4	US-10-803-622-245
9	535	95.0	110	4	US-10-803-622-258
10	535	95.0	110	4	US-10-803-622-258
11	532	94.5	109	3	US-09-144-886-98
12	532	94.5	110	4	US-10-803-622-238
13	532	94.5	110	4	US-10-803-622-248
14	532	94.5	110	4	US-10-803-622-238
15	532	94.5	110	4	US-10-803-622-248
16	527	93.6	110	4	US-10-803-622-250
17	527	93.6	110	4	US-10-803-622-250
18	526	93.4	256	4	US-10-233-656-61
19	526	93.4	503	4	US-10-233-656-77
20	525	93.3	109	4	US-10-632-706-95
21	524	93.1	110	4	US-10-803-622-246
22	524	93.1	110	4	US-10-803-622-246
23	518	92.0	110	4	US-10-803-622-239
24	518	92.0	110	4	US-10-803-622-239
25	494	87.7	109	5	US-10-831-459-19
26	455	80.8	110	4	US-10-803-622-255
27	455	80.8	110	4	US-10-803-622-256

28	455	80.8	110	4	US-10-803-622-255	Sequence 255, App
29	455	80.8	110	4	US-10-803-622-256	Sequence 256, App
30	452	80.3	110	4	US-10-803-622-257	Sequence 257, App
31	452	80.3	110	4	US-10-803-622-257	Sequence 257, App
32	450	79.9	109	3	US-09-144-886-91	Sequence 91, App1
33	450	79.9	109	3	US-09-144-886-91	Sequence 91, App1
34	450	79.9	110	4	US-10-632-706-88	Sequence 88, App1
35	450	79.9	110	4	US-10-803-622-237	Sequence 237, App
36	447	79.4	110	4	US-10-803-622-237	Sequence 237, App
37	447	79.4	108	4	US-10-803-622-240	Sequence 240, App
38	444	78.9	107	4	US-10-632-706-87	Sequence 87, App1
39	444	78.9	110	4	US-10-803-622-254	Sequence 254, App
40	444	78.9	110	4	US-10-803-622-254	Sequence 254, App
41	444	78.9	242	4	US-10-259-087A-20	Sequence 20, App1
42	444	78.9	242	4	US-10-689-006-20	Sequence 20, App1
43	443	78.7	109	4	US-10-461-876-12	Sequence 12, App1
44	443	78.7	109	5	US-10-461-885-12	Sequence 12, App1
45	442	78.5	107	3	US-09-144-886-90	Sequence 90, App1

ALIGNMENTS

RESULT 1
US-09-144-886-92
Sequence 92, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize Botulinum Neurotoxin
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144, 886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 92
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-92
OTHER INFORMATION: IB3 region VL epitope 3

Query Match 100.0%; Score 563; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.7e-42;
Matches 109; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DSELTQSPPTMAASPGKKTITTCASASSIS\$NYLHWYQORPSPKLLITRTSLAGVP 60
DB 1 DSELTQSPPTMAASPGKKTITTCASASSIS\$NYLHWYQORPSPKLLITRTSLAGVP 60
QY 61 ARFGSGSGTSTLTITGMAEDVATYCCOQSSIPRTGGTLEIKR 109
DB 61 ARFGSGSGTSTLTITGMAEDVATYCCOQSSIPRTGGTLEIKR 109

RESULT 2
US-10-632-706-89
Sequence 89, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM

FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632, 706
CURRENT FILING DATE: 2003-08-01
PRIORITY APPLICATION NUMBER: US 60/400, 721
PRIORITY FILING DATE: 2002-08-01

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/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 89
/ LENGTH: 109
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody
US-10-632-706-89

Query Match          100.0%; Score 563; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5-42;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DSELTQSPPTMAAPGEEKITTTCSASSSSISNYLHWYQORPFPSPKLLIYRTSNLASGVP 60
DB      1 DSELTQSPPTMAAPGEEKITTTCSASSSSISNYLHWYQORPFPSPKLLIYRTSNLASGVP 60

QY      61 ARFSGSGGTSTSLTIGTMEADVAITYCCQSSSIPTFGGKLEIKR 109
DB      61 ARFSGSGGTSTSLTIGTMEADVAITYCCQSSSIPTFGGKLEIKR 109

RESULT 3
US-10-803-622-247
/ Sequence 247, Application US/10803622
/ Publication No. US2004015721A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 247
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
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/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-247

Query Match          96.1%; Score 541; DB 4; Length 110;
Best Local Similarity 96.3%; Pred. No. 5e-40;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DSELTQSPPTMAAPGEEKITTTCSASSSSISNYLHWYQORPFPSPKLLIYRTSNLASGVP 60
DB      1 DSELTQSPPTMAAPGEEKITTTCSASSSSISNYLHWYQORPFPSPKLLIYRTSNLASGVP 60

QY      61 ARFSGSGGTSTSLTIGTMEADVAITYCCQSSSIPTFGGKLEIKR 109
DB      61 ARFSGSGGTSTSLTIGTMEADVAITYCCQSSSIPTFGGKLEIKR 109

RESULT 4
US-10-803-653-247
/ Sequence 247, Application US/10803653
/ Publication No. US2004015721A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 247
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-247

Query Match          96.1%; Score 541; DB 4; Length 110;
Best Local Similarity 96.3%; Pred. No. 5e-40;
Matches 105; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```



```

/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clarkson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
/ PRIOR FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 245
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-245

Query Match          95.4%; Score 537; DB 4; Length 110;
Best Local Similarity 95.4%; Pred. No. 1.1e-39;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 DSELTGSPPTMAAPGKRIITTCSSASSISSNYLHWYQORGFSPKLIYRTSNLASGVP 60
Db 1 DIELTQSPPTMAAPGKRIITTCSSASSISSNYLHWYQORGFSPKLIYRTSNLASGVP 60

Cy 61 ARFGSSGSGTSYSLTIGTMEADVAITYCCQSSISPTFGGTLKLR 109
Db 61 ARFGSSGSGTSYSLTIGTMEADVAITYCCQSSISPTFGGTLKLR 109

RESULT 8
US-10-803-653-245
/ Sequence 245; Application US/10803653
/ Publication No. US20040157215A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clarkson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
```

```

/ APPLICANT: Marks, James
/ APPLICANT: Jackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ PRIOR FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 245
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-245

Query Match          95.4%; Score 537; DB 4; Length 110;
Best Local Similarity 95.4%; Pred. No. 1.1e-39;
Matches 104; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 DSELTGSPPTMAAPGKRIITTCSSASSISSNYLHWYQORGFSPKLIYRTSNLASGVP 60
Db 1 DIELTQSPPTMAAPGKRIITTCSSASSISSNYLHWYQORGFSPKLIYRTSNLASGVP 60

Cy 61 ARFGSSGSGTSYSLTIGTMEADVAITYCCQSSISPTFGGTLKLR 109
Db 61 ARFGSSGSGTSYSLTIGTMEADVAITYCCQSSISPTFGGTLKLR 109

RESULT 9
US-10-803-622-258
/ Sequence 258; Application US/10803622
/ Publication No. US20040157214A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clarkson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
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CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 258
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolon
US-10-803-622-258

Query Match          95.0%; Score 535; DB 4; Length 110;
Best Local Similarity 95.4%; Pred. No. 1.7e-39;
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPPTMAAPGKRTTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60
DB 1 DIETLQSPPTMAAPGKRTTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60

QY 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSISPTFGGKLEIKR 109
DB 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSISPTFGGKLEIKR 109

RESULT 10
US-10-803-653-258
Sequence 258, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Grifflche, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 1839-00013
CURRENT APPLICATION NUMBER: US/10/803,653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 258
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolon
US-10-803-622-258
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PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 258
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolon
US-10-803-653-258

Query Match          95.0%; Score 535; DB 4; Length 110;
Best Local Similarity 95.4%; Pred. No. 1.7e-39;
Matches 104; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSELTQSPPTMAAPGKRTTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60
DB 1 DIETLQSPPTMAAPGKRTTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60

QY 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSISPTFGGKLEIKR 109
DB 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSISPTFGGKLEIKR 109

RESULT 11
US-09-144-886-98
Sequence 98, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 98
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
OTHER INFORMATION: 2B8 region VL epitope 4
US-09-144-886-98

Query Match          94.5%; Score 532; DB 3; Length 109;
Best Local Similarity 94.5%; Pred. No. 3.1e-39;
Matches 103; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSELTQSPPTMAAPGKRTTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60
DB 1 DIETLQSPPTMAAPGKRTTTCSSASSISNYLHWYQORPGSPKLLIYRTSNLASGVP 60

QY 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSISPTFGGKLEIKR 109
DB 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSISPTFGGKLEIKR 109

RESULT 12
US-10-803-622-238
Sequence 238, Application US/10803622
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/ Publication No. US20040157214A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
/ PRIOR FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1991-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 238
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-238

Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3,1e-39;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSELTQSPPTMAAPGEEKITTTCSASSISSTNYLHWYQKRGFSPKLIYRTSNLASGP 60
Db 1 DIELTQSPPTMAAPGEEKITTTCSASSISSTNYLHWYQKRGFSPKLIYRTSNLASGP 60

Qy 61 ARFSGSGSGTYSYLITGTMEADVAITYYCOQSSIPRTFGGGTKLEIKR 109
Db 61 ARFSGSGSGTYSYLITGTMEADVAITYYCOQSSIPRTFGGGTKLEIKR 109

RESULT 13
US-10-803-622-248
/ Sequence 248, Application US/10803622
/ Publication No. US20040157214A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
```

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/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,622
/ PRIOR FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1991-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 248
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-248

Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3,1e-39;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSELTQSPPTMAAPGEEKITTTCSASSISSTNYLHWYQKRGFSPKLIYRTSNLASGP 60
Db 1 DIELTQSPPTMAAPGEEKITTTCSASSISSTNYLHWYQKRGFSPKLIYRTSNLASGP 60

Qy 61 ARFSGSGSGTYSYLITGTMEADVAITYYCOQSSIPRTFGGGTKLEIKR 109
Db 61 ARFSGSGSGTYSYLITGTMEADVAITYYCOQSSIPRTFGGGTKLEIKR 109

RESULT 14
US-10-803-653-238
/ Sequence 238, Application US/10803653
/ Publication No. US20040157215A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Griffiths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
```

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/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Method for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ CURRENT FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 238
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-238

Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.1e-39; Indels 0; Gaps 0;
Matches 103; Conservative 2; Mismatches 4;

QY 1 DSELTOSPTTMAASPGKITTTCSSASSISNVLHWYQORPGFSPKLLIYRTSNLASGVP 60
DB 1 DIELTOSPTTMAASPGKITTTCSSASSISNVLHWYQORPGFSPKLLIYRTSNLASGVP 60

QY 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSSIPRTFGGTKLEIKR 109
DB 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSGSTIPLTFAGTKLEIKR 109

RESULT 15
US-10-803-653-248
/ Sequence 248, Application US/10803653
/ Publication No. US20040157215A1
/ GENERAL INFORMATION:
/ APPLICANT: Cambridge Antibody Technology
/ APPLICANT: Cambridge Antibody Technology Limited
/ APPLICANT: Medical Research Council
/ APPLICANT: McCafferty, John
/ APPLICANT: Pope, Anthony
/ APPLICANT: Johnson, Kevin
/ APPLICANT: Hoogenboom, Hendricus
/ APPLICANT: Grifflths, Andrew
/ APPLICANT: Jackson, Ronald
/ APPLICANT: Holliger, Kasper
/ APPLICANT: Marks, James
/ APPLICANT: Clackson, Timothy
/ APPLICANT: Chiswell, David
/ APPLICANT: Winter, Gregory
/ APPLICANT: Bonert, Timothy
/ TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
/ FILE REFERENCE: 13839-00013
/ CURRENT APPLICATION NUMBER: US/10/803,653
/ CURRENT FILING DATE: 2004-03-18
/ PRIOR APPLICATION NUMBER: GB 9015198.6
/ PRIOR FILING DATE: 1990-07-10
/ PRIOR APPLICATION NUMBER: GB 9022845.3
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/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9022845.3
/ PRIOR FILING DATE: 1990-10-19
/ PRIOR APPLICATION NUMBER: GB 9024503.6
/ PRIOR FILING DATE: 1990-11-12
/ PRIOR APPLICATION NUMBER: GB 9104744.9
/ PRIOR FILING DATE: 1991-03-06
/ PRIOR APPLICATION NUMBER: GB 9110549.4
/ PRIOR FILING DATE: 1991-05-15
/ PRIOR APPLICATION NUMBER: PCT/GB91/01134
/ PRIOR FILING DATE: 1991-07-10
/ PRIOR APPLICATION NUMBER: US 07/971,857
/ PRIOR FILING DATE: 1993-01-08
/ PRIOR APPLICATION NUMBER: US 08/484,893
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 272
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 248
/ LENGTH: 110
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-248

Query Match          94.5%; Score 532; DB 4; Length 110;
Best Local Similarity 94.5%; Pred. No. 3.1e-39; Indels 0; Gaps 0;
Matches 103; Conservative 2; Mismatches 4;

QY 1 DSELTOSPTTMAASPGKITTTCSSASSISNVLHWYQORPGFSPKLLIYRTSNLASGVP 60
DB 1 DIELTOSPTTMAASPGKITTTCSSASSISNVLHWYQORPGFSPKLLIYRTSNLASGVP 60

QY 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSSSIPRTFGGTKLEIKR 109
DB 61 ARPSGSGSGTSYSLTIGTMEADVATYYCOQSGGIRYTFGGTKLEIKR 109

Search completed: November 21, 2005, 12:33:35
Job time : 135.952 secs
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 12:04:27 ; Search time 1.99634 Seconds
(without alignments)
61.686 Million cell updates/sec

Title: US-10-632-706-89

Perfect score: 563
Sequence: 1 DSELYQSPPTMAASPEKTKIT.....QQGSSIPRTFGGTYKLEIKR 109

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
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4: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	398	70.7	106	7	US-11-174-186-1 Sequence 1, Appl1
2	398	70.7	213	7	US-11-174-186-42 Sequence 42, Appl1
3	393	69.8	106	7	US-11-174-186-9 Sequence 9, Appl1
4	391	69.4	106	7	US-11-174-186-7 Sequence 7, Appl1
5	391	69.4	213	7	US-11-172-320-4 Sequence 4, Appl1
6	390	69.3	106	7	US-11-174-186-8 Sequence 8, Appl1
7	390	69.3	248	1	US-10-512-184-36 Sequence 36, Appl1
8	390	69.3	615	1	US-10-512-184-50 Sequence 50, Appl1
9	387	68.7	106	7	US-11-174-186-15 Sequence 15, Appl1
10	382	67.9	106	7	US-11-174-186-16 Sequence 16, Appl1
11	381	67.7	213	7	US-11-172-320-8 Sequence 8, Appl1
12	379.5	67.1	110	1	US-10-648-816-5 Sequence 5, Appl1
13	377.5	67.0	110	1	US-10-648-816-1 Sequence 1, Appl1
14	377	67.0	106	7	US-11-174-186-10 Sequence 10, Appl1
15	377	67.0	106	7	US-11-174-186-14 Sequence 14, Appl1
16	374	66.4	106	7	US-11-174-186-11 Sequence 11, Appl1
17	374	66.4	106	7	US-11-174-186-12 Sequence 12, Appl1
18	374	66.4	106	7	US-11-174-186-13 Sequence 13, Appl1
19	370.5	65.8	128	1	US-10-721-763-31 Sequence 31, Appl1
20	369.5	65.6	110	1	US-10-648-816-2 Sequence 2, Appl1
21	369.5	65.6	110	1	US-10-648-816-3 Sequence 3, Appl1
22	369.5	65.6	110	1	US-10-648-816-4 Sequence 4, Appl1
23	369.5	65.6	110	1	US-10-648-816-6 Sequence 6, Appl1
24	369.5	65.6	110	1	US-10-648-816-7 Sequence 7, Appl1
25	369.5	65.6	110	1	US-10-648-816-8 Sequence 8, Appl1

26	367.5	65.3	543	1	US-10-495-664-3 Sequence 3, Appl1
27	355.5	63.1	129	1	US-10-721-763-19 Sequence 19, Appl1
28	355	63.1	106	7	US-11-174-186-5 Sequence 5, Appl1
29	354.5	63.0	111	7	US-11-077-978-1 Sequence 1, Appl1
30	352.5	62.6	131	1	US-10-721-763-27 Sequence 27, Appl1
31	349.5	62.1	129	1	US-10-721-763-23 Sequence 23, Appl1
32	346.5	61.5	126	1	US-10-839-799-47 Sequence 47, Appl1
33	346.5	61.5	126	1	US-10-839-799-65 Sequence 65, Appl1
34	345.5	61.4	126	1	US-10-839-799-85 Sequence 85, Appl1
35	345.5	61.4	259	1	US-10-512-184-31 Sequence 31, Appl1
36	345.5	61.4	329	1	US-10-512-184-68 Sequence 68, Appl1
37	343.5	61.0	111	7	US-11-077-978-4 Sequence 4, Appl1
38	343.5	61.0	127	1	US-10-721-763-35 Sequence 35, Appl1
39	343.5	61.0	236	7	US-11-144-248-48 Sequence 48, Appl1
40	343.5	61.0	259	1	US-10-512-184-34 Sequence 34, Appl1
41	343.5	61.0	263	1	US-10-512-184-29 Sequence 29, Appl1
42	343.5	61.0	371	1	US-10-512-184-71 Sequence 71, Appl1
43	342.5	61.0	626	1	US-10-512-184-49 Sequence 49, Appl1
44	342.5	60.8	126	1	US-10-839-799-43 Sequence 43, Appl1
45	342.5	60.8	126	1	US-10-839-799-53 Sequence 53, Appl1

ALIGNMENTS

RESULT 1
US-11-174-186-1
; Sequence 1, Application US/11/174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Glilies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; PRIOR FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VK mouse
US-11-174-186-1

Query Match 70.7%; Score 398; DB 7; Length 106;
Best Local Similarity 75.2%; Pred. No. 2, 4e-19;
Matches 79; Conservative 7; Mismatches 17; Indels 2; Gaps 1;

QY 4 LNSPTMAASGCKTTTCASASSISNYLHMYYOORPQSPPLTYRTSNLASGVPARP 63
DB 4 LQSPAIMASGCKTWTCSASSVS--YMLMYQKPSRPFWFTDSNLASGFPARP 61

QY 64 SSGSGTSYSLTGTWEADVATYYCOQGSJIPRTFGGTYKLEIK 108
DB 62 SSGSGTSYSLTISWEADATYYCHQRSQPYRTFGGTYKLEIK 106

RESULT 2
US-11-174-186-42
; Sequence 42, Application US/11/174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Glilies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186

```

; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: light chain
US-11-174-186-42
```

```

Query Match      70.7%; Score 398; DB 7; Length 213;
Best Local Similarity 73.6%; Pred. No. 4, 1e-19;
Matches 78; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
```

```

Qy 4 LTGSPPTMAASPGRKITTTCASASSISSNYLHWYQORPGFSPKLLIYRTSNLAGVPAFP 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSVS--YMLWYQKQKQSSPKPWFPTSNLAGSFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGGTISLTITGMEADVAITYCCQGSISPTFGGCTKLEIKR 109
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGGTISLTITGMEADVAITYCHQRSQGYPTFGGCTKLEIKR 107
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 3

```

US-11-174-186-9
; Sequence 9, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: VK8 light chain
US-11-174-186-9
```

```

Query Match      69.8%; Score 393; DB 7; Length 106;
Best Local Similarity 73.3%; Pred. No. 4, 9e-19;
Matches 77; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
```

```

Qy 4 LTGSPPTMAASPGRKITTTCASASSISSNYLHWYQORPGFSPKLLIYRTSNLAGVPAFP 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSVS--YMLWYQKQKQSSPKPWFPTSNLAGSFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGGTISLTITGMEADVAITYCCQGSISPTFGGCTKLEIKR 108
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGGTISLTITGMEADVAITYCHQRSQGYPTFGGCTKLEIKR 106
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 4

```

US-11-174-186-7
; Sequence 7, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
```

```

; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: VK6 light chain
US-11-174-186-7
```

```

Query Match      69.4%; Score 391; DB 7; Length 106;
Best Local Similarity 70.5%; Pred. No. 6, 4e-19;
Matches 74; Conservative 13; Mismatches 16; Indels 2; Gaps 1;
```

```

Qy 4 LTGSPPTMAASPGRKITTTCASASSISSNYLHWYQORPGFSPKLLIYRTSNLAGVPAFP 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSVS--YMLWYQKQKQAPKLLIYRTSNLAGSFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGGTISLTITGMEADVAITYCCQGSISPTFGGCTKLEIKR 108
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGGTIDYTLTISLSPEDFAVYVYCHQRSQGYPTFGGCTKLEIKR 106
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 5

```

US-11-172-320-4
; Sequence 4, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Anke
; APPLICANT: Adolf, Guenther
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Humanised Murine Antibody BiMA 4 Light Chain
US-11-172-320-4
```

```

Query Match      69.4%; Score 391; DB 7; Length 213;
Best Local Similarity 70.8%; Pred. No. 1, 1e-16;
Matches 75; Conservative 14; Mismatches 15; Indels 2; Gaps 1;
```

```

Qy 4 LTGSPPTMAASPGRKITTTCASASSISSNYLHWYQORPGFSPKLLIYRTSNLAGVPAFP 63
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 4 LTGSPATLSLSPGRVTLTCSASSSVS--NYLWYQKQKQAPRLLIYRTSNLAGSFPARF 61
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 64 SSGSGGTISLTITGMEADVAITYCCQGSISPTFGGCTKLEIKR 109
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 SSGSGGTIDYTLTISLSPEDFAVYVYCHQWSNPLTFGGCTKLEIKR 107
    |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 6

```

US-11-174-186-8
; Sequence 8, Application US/11174186
```

Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gullies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xiang
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.3
SEQ ID NO 8
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: VK7 light chain
US-11-174-186-8

Query Match 69.3%; Score 390; DB 7; Length 106;
Best Local Similarity 73.3%; Pred. No. 7, 4e-19;
Matches 77; Conservative 8; Mismatches 18; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCSSASSISNYLHWYQORPGFSPKLLIYRTSNLASGVPAF 63
DB 4 LTQSPMAASPGKITTTCSSASSIS--YMLWYQKPGSPKPIFDTSNLASGVPARF 61

QY 64 SSGSGSGTSLTGTMEADVATYYCOGSSIPRTGGGKLEIK 108
DB 62 SSGSGSGTSLTISMSPEADATYYCHORSGYPTGGGKLEIK 106

RESULT 7
US-10-512-184-36
Sequence 36, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1.
SEQ ID NO 36
LENGTH: 248
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with
OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match 69.3%; Score 390; DB 1; Length 248;
Best Local Similarity 70.6%; Pred. No. 1, 4e-18;
Matches 77; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 DSELTQSPPTMAASPGKITTTCSSASSISNYLHWYQORPGFSPKLLIYRTSNLASGVPAF 60
DB 141 DIVLQSPPTMAASPGKITTTCSSASSIS--NYIYQKSGTSPKPIFDTSNLASGVP 198

QY 61 ARFSGSGTSLTGTMEADVATYYCOGSSIPRTGGGKLEIK 109
DB 199 VRFSGSGTSLTISMSPEADATYYCHORSGYPTGGGKLEIK 247

RESULT 8
US-10-512-184-50

Sequence 50, Application US/10512184
Publication No. US20050244901A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 50
LENGTH: 615
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fusion protein
OTHER INFORMATION: comprising the leader peptide - chitinase - linker
OTHER INFORMATION: - scFv SS2 - cmc/his6.
US-10-512-184-50

Query Match 69.3%; Score 390; DB 1; Length 615;
Best Local Similarity 70.6%; Pred. No. 2, 6e-18;
Matches 77; Conservative 11; Mismatches 19; Indels 2; Gaps 1;

QY 1 DSELTQSPPTMAASPGKITTTCSSASSISNYLHWYQORPGFSPKLLIYRTSNLASGVPAF 60
DB 482 DIVLQSPPTMAASPGKITTTCSSASSIS--YMLWYQKPGSPKPIFDTSNLASGVPARF 539

QY 61 ARFSGSGTSLTGTMEADVATYYCOGSSIPRTGGGKLEIK 109
DB 540 VRFSGSGTSLTISMSPEADATYYCHORSGYPTGGGKLEIK 588

RESULT 9
US-11-174-186-15
Sequence 15, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gullies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xiang
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.3
SEQ ID NO 15
LENGTH: 106
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VK5
US-11-174-186-15

Query Match 68.7%; Score 387; DB 7; Length 106;
Best Local Similarity 71.4%; Pred. No. 1, 1e-18;
Matches 75; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTQSPPTMAASPGKITTTCSSASSISNYLHWYQORPGFSPKLLIYRTSNLASGVPAF 63
DB 4 LTQSPMAASPGKITTTCSSASSIS--YMLWYQKPGSPKPIFDTSNLASGVPARF 61

QY 64 SSGSGSGTSLTGTMEADVATYYCOGSSIPRTGGGKLEIK 108
DB 62 SSGSGSGTSLTISMSPEADATYYCHORSGYPTGGGKLEIK 106

RESULT 10

US-11-174-186-16
; Sequence 16, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gilles, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: KS VK mouse
US-11-174-186-16

Query Match 67.9%; Score 382; DB 7; Length 106;
Best Local Similarity 70.5%; Pred. No. 2,2e-18;
Matches 74; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

QY 4 LTGSPFTMAASPGKITTTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGVPAF 63
DB 4 LTGSPATISASPGKRVITTCASASSVS--YMLMWYQKQSSPKPIPTSNLASGVPAF 61
QY 64 SSGSGGTYSYLTIGTMEADVATYYCCQGSISIPRTFGGTKEIK 108
DB 62 SSGSGGTYSYLTIGTMEADVATYYCHQRRGYPYTFGGTKEIK 106

RESULT 11
US-11-172-320-8
; Sequence 8, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1.
; SEQ ID NO 8
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Humanised Antibody BiMA 8 Light Chain
US-11-172-320-8

Query Match 67.7%; Score 381; DB 7; Length 213;
Best Local Similarity 68.9%; Pred. No. 4,2e-18;
Matches 73; Conservative 15; Mismatches 16; Indels 2; Gaps 1;

QY 4 LTGSPFTMAASPGKITTTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGVPAF 63
DB 4 LTGSPATISASPGKRVITTCASASSIS--NYIWMYQKQKQAPRIIYITSNLASGVPAF 61

QY 64 SSGSGGTYSYLTIGTMEADVATYYCCQGSISIPRTFGGTKEIKR 109
DB 62 SSGSGGTYSYLTIGTMEADVATYYCQWSSNPLTFGGTKEIKR 107

RESULT 12
US-10-648-816-5
; Sequence 5, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 5
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-5

Query Match 67.4%; Score 379.5; DB 1; Length 110;
Best Local Similarity 65.1%; Pred. No. 3,2e-18;
Matches 71; Conservative 22; Mismatches 15; Indels 1; Gaps 1;

QY 1 DSELTQSPFTMAASPGKITTTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGV 60
DB 1 DIQLTQSPSSIASAVGKRVITTCASADPI-SNYLNMWYQKQKAPKVLIFRTSSLSHSGVP 59
QY 61 ARFGSGGTYSYLTIGTMEADVATYYCCQGSISIPRTFGGTKEIKR 109
DB 60 SRFGSGGTIDFTLITSLQPEDPATYYCQYSTVPTWTFGGTKEIKR 108

RESULT 13
US-10-648-816-1
; Sequence 1, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-1

Query Match 67.1%; Score 377.5; DB 1; Length 110;
Best Local Similarity 64.2%; Pred. No. 4,2e-18;
Matches 70; Conservative 23; Mismatches 15; Indels 1; Gaps 1;

QY 1 DSELTQSPFTMAASPGKITTTCASASSISNLYLHWYQRRGFSPKLIYRTSNLASGV 60
DB 1 DIQMTQSPSSIASAVGKRVITTCASADPI-SNYLNMWYQKQKAPKVLIFRTSSLSHSGVP 59

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CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) and a composition (II) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarily determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX Sequence 11 AA;

Query Match Best Local Similarity 100.0%; Score 60; DB 8; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
 Db 1 LATYYFGLDV 11

RESULT 2

ID ADR38725 standard; peptide; 11 AA.

XX ADR38725;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain variable region CDR3 seqid 127.

XX anti-bacterial; antibody; botulinum neurotoxin type A; BONT/A;

XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;

XX heavy chain variable region; complementarily determining region; CDR3.

XX Mus sp.

XX US2004175385-A1.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amerdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

XX useful for diagnosing botulism or for treating pathologies associated

XX with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 127; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC 825, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,

CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) and a composition (II) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarily determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX Sequence 11 AA;

Query Match Best Local Similarity 100.0%; Score 60; DB 8; Length 11;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
 Db 1 LATYYFGLDV 11

RESULT 3

ID AEB45960 standard; protein; 122 AA.

XX AEB45960;

XX 06-OCT-2005 (first entry)

XX Human monoclonal anti-MadCAM antibody related protein #4.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM;

XX inflammation; inflammatory bowel disease; Crohn's disease;

XX ulcerative colitis; diverticular disease; gastritis; liver disease;

XX primary biliary cirrhosis; primary sclerosing cholangitis;

XX insulin dependent diabetes; graft versus host disease; anti-inflammatory;

XX immunosuppressive; antibody.

XX Homo sapiens.

XX WO2005067620-A2.

XX 28-JUL-2005.

XX 07-JAN-2005; 2005MO-US000370.

XX 09-JAN-2004; 2004US-0535490P.

XX (PFIZ) PFIZER INC.

XX (ABGR-) ABGENIX INC.

XX Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendocho M;

XX WPI; 2005-554958/56.

XX New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.

PS Example 5, Fig 1; 167pp; English.

The invention relates to a human monoclonal antibody or its antigen-binding portion that specifically binds to mucosal addressin cell adhesion molecule (MAdCAM). The invention also relates to a hybridoma cell line that produces the human monoclonal antibody, a pharmaceutical composition comprising an amount of the monoclonal antibody or its antigen-binding portion and a pharmaceutical carrier, a method of treating inflammatory disease in a subject, an isolated cell line that produces the monoclonal antibody or its antigen-binding portion or the heavy chain or light chain of the antibody or of its portion, an isolated nucleic acid molecule comprising a nucleotide sequence encoding the heavy chain or its antigen-binding portion or the light chain or its antigen-binding portion of an antibody described above, a vector comprising the nucleic acid molecule, where the vector optionally comprises an expression control sequence operably linked to the nucleic acid molecule, a host cell comprising the vector or the nucleic acid molecule above, a method of producing a human monoclonal antibody or its antigen-binding portion that specifically binds MAdCAM, a method of isolating an antibody or its antigen-binding portion that specifically binds to MAdCAM, a method of treating a subject in need of a human antibody or its antigen-binding portion that specifically binds to MAdCAM and inhibits binding to alpha4beta7, a method of inhibiting alpha4beta7 binding to cells expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte-endothelial cell adhesion, migration and infiltration into tissues, a method of inhibiting alpha4beta7/MAdCAM-dependent cellular adhesion, inhibiting the MAdCAM-mediated recruitment of lymphocytes to gastrointestinal lymphoid tissue, a method of diagnosing a disorder characterized by circulating soluble human MAdCAM and detecting inflammation in a subject. The antibody, composition and methods are useful for diagnosing and treating inflammatory disease, e.g. inflammatory bowel disease, Crohn's disease, ulcerative colitis, diverticular disease, gastritis, liver disease, primary biliary cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and graft versus host disease. This sequence represents a human monoclonal anti-MAdCAM antibody related protein of the invention.

SQ Sequence 122 AA;

Query Match	80.0%	Score 48	DB 9	Length 122
Similarity	63.6%	Pred. No. 2.5		
Best Local				
Matches	7	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0

```
QY      1 LATYYYFGLDV 11
          : ||||: ||
Db     100 VVTYYYGMDV 110
```

RESULT 4
ADD28082
ID ADD28082 standard; protein; 114 AA

AC ADD28082;

DT 15-JAN-2004 (first entry)

DE Lymphoma related immunoglobulin variable region

KM B-cell; malignant; immunoglobulin, immunoglobulin variable region.
 KM Ig variable region; glycosylation site; lymphoma; B cell receptor.
 KM cytosolic; gene therapy; glycosylation inhibitor;
 KM non-Hodgkin's lymphoma.

OS Synthetic.

OS Homo sapiens

PN WO2003074059-A2

PD 12-SEP-2003

PF 24-FEB-2003; 2003WO-GB000783

PR 07-MAR-2002; 2002GB-00005395.

XX
PA (CANC-) CANCER RES TECHNOLOGY LTD.

PI Zhu D, Stevenson F,

DR WPI, 2003-902720/82

```

pr      Classifying a B-cell as malignant or normal by isolating a sequence
pr      representing an Ig variable region from the B cell, detecting the
pr      presence of a glycosylation site and classifying the cell as malignant or
pr      normal.

```

PS Disclosure; Flg 3; 61pp; English

CC The present invention describes a method for classifying a B-cell as
CC malignant or normal comprising: (a) isolating a sequence representing an
CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the
CC presence of a glycosylation site; and (c) classifying the cell as
CC malignant or normal on the basis of the presence or absence of a
CC glycosylation site. Also described: (1) treating a patient suffering from
CC or at risk of having lymphoma; (2) screening for substances capable of
CC inhibiting glycosylation of the Ig variable region of the B cell receptor
CC ; and (3) screening for substances (5) capable of inhibiting the
CC interaction between lectins of the type found in the germinal centre and
CC N-glycans found on the surface of Ig of lymphoma cells. (5) has
CC cytostatic activity, and can be used in gene therapy, and as a
CC glycosylation inhibitor. The method is useful in classifying a B-cell as
CC malignant or normal. The glycosylation inhibitor is useful in preparing a
CC medicament for treating non-Hodgkin's lymphoma. The present sequence
CC represents an Ig variable region sequence which is used in the
CC exemplification of the present invention.

SQ Sequence 114 AA:

Query Match	78.3%	Score 47	DB 7	Length 114
Best Local Similarity	77.8%	Pred. No.	3.4	
Matches 7; Conservative	2	Mismatches	0	Gaps 0

QY	3	TYYYFGLDV	11
		: :	
Db	106	TYYYGMDV	114

RESULT 5
ADD28323
ID ADD28323 standard; protein; 129 AA

AC ADD28323

DT 15-JAN-2004 (first entry)

AA	DE	Human heterodimeric antibody heavy chain variable region	SEQ ID NO:101
1			1
2			2
3			3
4			4
5			5
6			6
7			7
8			8
9			9
10			10
11			11
12			12
13			13
14			14
15			15
16			16
17			17
18			18
19			19
20			20
21			21
22			22
23			23
24			24
25			25
26			26
27			27
28			28
29			29
30			30
31			31
32			32
33			33
34			34
35			35
36			36
37			37
38			38
39			39
40			40
41			41
42			42
43			43
44			44
45			45
46			46
47			47
48			48
49			49
50			50
51			51
52			52
53			53
54			54
55			55
56			56
57			57
58			58
59			59
60			60
61			61
62			62
63			63
64			64
65			65
66			66
67			67
68			68
69			69
70			70
71			71
72			72
73			73
74			74
75			75
76			76
77			77
78			78
79			79
80			80
81			81
82			82
83			83
84			84
85			85
86			86
87			87
88			88
89			89
90			90
91			91
92			92
93			93
94			94
95			95
96			96
97			97
98			98
99			99
100			100

human heterodimeric antibody; human; antibody; binding affinity;
protective antigen; *Bacillus anthracis*; anthrax infection; cell receptor;
edema factor; lethal factor; virulence; antibacterial; immunotherapy;
anti-toxin; anti-infective; anthrax; botulinum; smallpox;
Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

OS Synthetic.

OS Homo sapiens

PN WO2003076568-A2.

PD 18-SEP-2003

PF 11-FBB-2003; 2003WO-US004206.

PR 11-FEB-2002; 2002US-0356086P

PR 27-SEP-2002; 2002US-0414053P

XX

PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Wild MA;
 XX
 DR WPI, 2003-722327/68.
 XX
 PT New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.
 XX
 PS Claim 11, SEQ ID NO 101, 67pp; English.
 XX
 CC The present invention describes a human heterodimeric antibody (I)
 CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
 CC protective antigen of Bacillus anthracis or a molecule involved in
 CC anthrax infection that blocks binding of the antigen or molecule to cell
 CC receptors, edema factor and lethal factor. (I) has virulence and
 CC antibacterial activities, and can be used in immunotherapy. The
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
 CC present sequence represents a human heterodimeric antibody heavy chain
 CC variable region amino acid sequence, which is used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 129 AA;

Query Match 78.3%; Score 47; DB 7; Length 129;
 Best Local Similarity 77.8%; Pred. No. 3.9;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
 ||||:|
 Db 105 TTYTGMVDV 113

RESULT 6
 ADD28237
 ID ADD28237 standard; protein; 134 AA.

AC ADD28237;
 XX
 DT 15-JAN-2004 (first entry)
 XX

DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:15.

XX human heterodimeric antibody; human; antibody; binding affinity;
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
 KW edema factor; lethal factor; virulence; antibacterial; immunotherapy;
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

OS Synthetic.
 OS Homo sapiens.

XX MO2003076568-A2.

XX 18-SEP-2003.

XX 11-FEB-2003; 2003WO-US004206.

XX 11-FEB-2002; 2002US-0356086P.

XX 29-APR-2002; 2002US-0376408P.

XX 27-SEP-2002; 2002US-0414053P.

XX 25-NOV-2002; 2002US-042807P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Wild MA;

XX WPI; 2003-722327/68.

XX

PT New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.
 XX
 PS Claim 6, SEQ ID NO 15, 67pp; English.

XX The present invention describes a human heterodimeric antibody (I)
 CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
 CC protective antigen of Bacillus anthracis or a molecule involved in
 CC anthrax infection that blocks binding of the antigen or molecule to cell
 CC receptors, edema factor and lethal factor. (I) has virulence and
 CC antibacterial activities, and can be used in immunotherapy. The
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
 CC present sequence represents a human heterodimeric antibody heavy chain
 CC variable region amino acid sequence, which is used in the exemplification
 CC of the present invention.
 XX

SQ Sequence 134 AA;

Query Match 78.3%; Score 47; DB 7; Length 134;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
 ||||:|
 Db 110 TTYTGMVDV 118

RESULT 7
 ADV86824
 ID ADV86824 standard; protein; 134 AA.

AC ADV86824;

XX 10-MAR-2005 (first entry)

DE Bacillus anthracis toxin Fab 9 K 2e G pro heavy chain variable region.

XX Bioreactor; Bacillus anthracis infection; vaccine; diagnosis;

KW antibacterial; antibody; heavy chain variable region.

OS Homo sapiens.

XX NO2004110362-A2.

XX 23-DEC-2004.

XX 26-MAY-2004; 2004WO-US016557.

XX 02-JUN-2003; 2003US-00452593.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Frederickson S, Wild MA, Maruyama T, Nolan MJ;

XX WPI; 2005-057715/06.

XX Treating an animal with anthrax infection by administering an antibody to
 PT the protective antigen of Bacillus anthracis, and blocking binding to
 PT cell receptors, edema factor or lethal factor.

XX Claim 7, SEQ ID NO 15, 87pp; English.

XX A claimed method for treating an animal infected with Bacillus anthracis
 CC comprises administering an antibody or antibody fragment that binds to a
 CC molecule involved in anthrax infection and which has the ability to block
 CC the binding of the molecule to at least one of a cell receptor, PA63,
 CC PA63 heptamer, PA83, edema factor and lethal factor. A claimed method for
 CC determining exposure to B. anthracis comprises assaying a sample for the
 CC presence of a molecule selected from cell receptors, PA63, PA63 heptamer,

CC PA83, edema factor or lethal factor with an antibody that has binding
 CC affinity for the molecule, where the presence of elevated levels of the
 CC antibody correlates with the presence of a disease associated with B.
 CC anthrax. Alternatively, the method involves assaying for the presence
 CC of an antibody to a cell receptor, PA63, PA63 heptamer, PA83, edema
 CC factor or lethal factor with a secondary antibody having binding affinity
 CC for the antibody, where the presence of elevated levels of the secondary
 CC antibody correlates with the presence of B. anthracis in a subject. In
 CC all cases, the antibody (full-length or functional fragment) may comprise
 CC a heavy chain variable region selected from a group of sequences ADV86810
 CC -ADV86827, a light chain kappa region selected from a group of sequences
 CC ADV86828-ADV86835 and a light chain lambda region selected from a group
 CC of sequences ADV86836-ADV86847. Diagnostic kits are provided. A claimed
 CC vaccine comprises a multimer of anthrax toxin PA63. The methods and
 CC compositions of the present invention are also useful for producing anti-
 CC toxins or anti-infectives to infective agents such as anthrax, botulinum,
 CC smallpox, Venezuelan equine encephalomyelitis and West Nile virus. The
 CC present sequence is that of the heavy chain variable region of a human
 CC Fab (designated 9 K 2e G pro) with positive reactivity to anthrax
 CC proteins PA63 and PA83. Phage libraries were developed from mRNA isolated
 CC from blood and bone marrow samples of donors who had been vaccinated
 CC against anthrax. The libraries were panned against PA83 and PA63, and
 CC sequence analysis was performed on positive responders. Neutralization of
 CC anthrax toxin activity by purified Fabs was demonstrated.

SO Sequence 134 AA;

Query Match 78.3%; Score 47; DB 9; Length 134;
 Best Local Similarity 77.8%; Pred. No. 4;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYTGGLDV 11
 ||||:|:
 Db 110 TTYTGGMDV 118

RESULT 8
 ADR28082
 ID ADR28082 standard; protein; 244 AA.

AC ADR28082;
 DT 07-OCT-2004 (first entry)
 XX NPB polypeptide scFv27, seq id 29.

DE NPB polypeptide scFv27, seq id 29.
 XX Cytostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;
 KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

OS Mus sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FH 87.103
 FT /note="complementary determining region claimed under
 FT claim 5"
 XX

PN WO2004056874-A2.

PD 08-JUL-2004.

PF 22-DEC-2003; 2003WO-EP014756.

PR 20-DEC-2003; 2002US-0435893P.

PR 15-JAN-2003; 2003EP-0000615.

XX (XERI-) XERION PHARM AG.
 PA (TUFT) UNIV TUFTS.

PI Unger CM, Beese G, Zehetmeier C, Iain B, Torella C, Niewoehner J;
 XX Jay DG, Bustace BK, Krauer R, Jensen KH;

DR WPI, 2004-507700/48.

DR N-PSDB; ADR2811C.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,
 PT that modulates neuropilin-1 function or inhibits NP-1 dependent
 PT angiogenesis of endothelial cells and/or invasion of tumor cells useful
 PT for treating cancer.

PS Claim 3, SEQ ID NO 29, 120pp, English.

XX The invention relates to a neuropilin binder (NPB) (1) which is a
 CC polypeptide, antibody, scFv, antibody fragment or bioconjugate, that
 CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent
 CC angiogenesis of endothelial cells and/or invasion of tumour cells,
 CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further
 CC disclosed is an ex vivo method of determining the dependency of the
 CC invasiveness of a naturally occurring invasive cancer cell on the
 CC functionality of NP-1. The NPB of the invention is an inhibitor of
 CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of
 CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention
 CC is useful for detecting NP-1 expression, modulation of NP-1 function,
 CC particularly modulation or inhibition of NP-dependent invasion or
 CC adhesion of cells, preferably tumour cells. It is useful in the
 CC manufacture of medicament for the treatment or prevention of NP-dependent
 CC angiogenesis and non-physiological blood vessel growth, particularly
 CC correlated with a tumour. It is also useful for treatment or prevention
 CC of cancer and/or metastasis of tumour cells. The current sequence
 CC represents a single chain antibody neuropilin binder (NPB) polypeptide.

SO Sequence 244 AA;

Query Match 78.3%; Score 47; DB 8; Length 244;
 Best Local Similarity 77.8%; Pred. No. 4.7;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTYTGGLDV 11
 ||||:|:
 Db 95 TTYTGGMDV 103

RESULT 9
 AEB45891
 ID AEB45891 standard; protein; 468 AA.

AC AEB45891;

DT 06-OCT-2005 (first entry)
 XX Human monoclonal anti-MAdCAM antibody #37.

DE Human monoclonal anti-MAdCAM antibody #37.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;
 KW inflammation; inflammatory bowel disease; Crohn's disease;
 KW ulcerative colitis; diverticular disease; gastritis; liver disease;
 KW primary biliary cirrhosis; primary sclerosing cholangitis;
 KW insulin dependent diabetes; graft versus host disease; anti-inflammatory;
 KW gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;
 KW immunosuppressive; antibody.

OS Homo sapiens.

PN WO2005067620-A2.

PD 28-JUL-2005.

PF 07-JAN-2005; 2005WO-US000370.

PR 09-JAN-2004; 2004US-0535490P.

XX (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.

PI (PFIZ) PFIZER LTD.

XX Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendschko M;

XX

DR WPI; 2005-554958/56.
 DR N-PSDB; AEB45890.
 XX
 XX New antibody to Mucosal Adhesin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.
 XX
 XX Claim 8; SEQ ID NO 56; 167bp; English.
 PS
 XX The invention relates to a human monoclonal antibody or its antigen-
 CC binding portion that specifically binds to mucosal adhesin cell
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma
 CC cell line that produces the human monoclonal antibody, a pharmaceutical
 CC composition comprising an amount of the monoclonal antibody or its
 CC antigen-binding portion and a pharmaceutical carrier, a method of
 CC treating inflammatory disease in a subject, an isolated cell line that
 CC produces the monoclonal antibody or its antigen-binding portion or the
 CC heavy chain or light chain of the antibody or of its portion, an isolated
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
 CC chain or its antigen-binding portion or the light chain or its antigen-
 CC binding portion of an antibody described above, a vector comprising the
 CC nucleic acid molecule, where the vector optionally comprises an
 CC expression control sequence operably linked to the nucleic acid molecule,
 CC a host cell comprising the vector or the nucleic acid molecule above,
 CC a method of producing a human monoclonal antibody or its antigen-binding
 CC portion that specifically binds MAdCAM, a method of isolating an antibody
 CC or its antigen-binding portion that specifically binds to MAdCAM, a
 CC method of treating a subject in need of a human antibody or its antigen-
 CC binding portion that specifically binds to MAdCAM and inhibits binding to
 CC alpha-beta7, a method of inhibiting alpha-beta7 binding to cells
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte
 CC endothelial cell adhesion, migration and infiltration into tissues, a
 CC method of inhibiting alpha-beta7/MAdCAM-dependent cellular adhesion,
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
 CC characterized by circulating soluble human MAdCAM and detecting
 CC inflammation in a subject. The antibody, composition and methods are
 CC useful for diagnosing and treating inflammatory disease, e.g.
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC diverticular disease, gastritis, liver disease, primary biliary
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
 CC graft versus host disease. This sequence represents a human monoclonal
 CC anti-MAdCAM antibody of the invention.
 CC
 XX
 SQ Sequence 468 AA;
 Query Match 78.3%; Score 47; DB 9; Length 468;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTYTFFGADV 11
 DB 123 TTYTFFGADV 131
 RESULT 10
 AEB45853
 ID AEB45853 standard; protein; 469 AA.
 XX
 AC AEB45853;
 XX
 DT 06-OCT-2005 (first entry)
 XX
 XX Human monoclonal anti-MAdCAM antibody #9.
 XX
 KM Monoclonal antibody; mucosal adhesin cell adhesion molecule; MAdCAM;
 KM inflammation; inflammatory bowel disease; Crohn's disease;
 KM ulcerative colitis; diverticular disease; gastritis; liver disease;
 KM primary biliary cirrhosis; primary sclerosing cholangitis;
 KM insulin dependent diabetes; graft versus host disease; anti-inflammatory;
 KM gastrointestinal-gen.; antineur; hepatotropic; antidiabetic;
 KM immunosuppressive; antibody.

XX
 OS Homo sapiens.
 XX
 PN WO2005067620-A2.
 XX
 PD 28-JUL-2005.
 XX
 PF 07-JAN-2005; 2005WO-US000370.
 XX
 PR 09-JAN-2004; 2004US-0535490P.
 XX
 PA (PFIZ) PFIZER INC.
 PA (ABGE-) ABGENIX INC.
 PA (PFIZ) PFIZER LTD.
 XX
 PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendelcho M;
 XX
 DR WPI; 2005-554958/56.
 DR N-PSDB; AEB45852.
 XX
 XX New antibody to Mucosal Adhesin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.
 XX
 XX Claim 8; SEQ ID NO 18; 167bp; English.
 PS
 XX The invention relates to a human monoclonal antibody or its antigen-
 CC binding portion that specifically binds to mucosal adhesin cell
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma
 CC cell line that produces the human monoclonal antibody, a pharmaceutical
 CC composition comprising an amount of the monoclonal antibody or its
 CC antigen-binding portion and a pharmaceutical carrier, a method of
 CC treating inflammatory disease in a subject, an isolated cell line that
 CC produces the monoclonal antibody or its antigen-binding portion or the
 CC heavy chain or light chain of the antibody or of its portion, an isolated
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
 CC chain or its antigen-binding portion or the light chain or its antigen-
 CC binding portion of an antibody described above, a vector comprising the
 CC nucleic acid molecule, where the vector optionally comprises an
 CC expression control sequence operably linked to the nucleic acid molecule,
 CC a host cell comprising the vector or the nucleic acid molecule above,
 CC a method of producing a human monoclonal antibody or its antigen-binding
 CC portion that specifically binds MAdCAM, a method of isolating an antibody
 CC or its antigen-binding portion that specifically binds to MAdCAM, a
 CC method of treating a subject in need of a human antibody or its antigen-
 CC binding portion that specifically binds to MAdCAM and inhibits binding to
 CC alpha-beta7, a method of inhibiting alpha-beta7 binding to cells
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte
 CC endothelial cell adhesion, migration and infiltration into tissues, a
 CC method of inhibiting alpha-beta7/MAdCAM-dependent cellular adhesion,
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
 CC characterized by circulating soluble human MAdCAM and detecting
 CC inflammation in a subject. The antibody, composition and methods are
 CC useful for diagnosing and treating inflammatory disease, e.g.
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC diverticular disease, gastritis, liver disease, primary biliary
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
 CC graft versus host disease. This sequence represents a human monoclonal
 CC anti-MAdCAM antibody of the invention.
 CC
 XX
 SQ Sequence 469 AA;
 Query Match 78.3%; Score 47; DB 9; Length 469;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTYTFFGADV 11
 DB 123 TTYTFFGADV 131

RESULT 11
 ADR38712 standard; peptide; 13 AA.
 XX ADR38712;
 DT 02-DEC-2004 (first entry)
 XX
 DE Mouse heavy chain variable region CDR3 seqid 114.
 XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KW heavy chain variable region; complementarity determining region; CDR3.
 OS Mus sp.
 XX
 XX US2004175385-A1.
 XX
 XX 09-SEP-2004.
 XX
 XX 01-AUG-2003; 2003US-00632706.
 XX
 XX 31-AUG-1998; 98US-00144886.
 XX 01-AUG-2002; 2002US-0400721P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Marks JD, Amerdorter P;
 XX
 XX WPI; 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX
 XX Example 3; SEQ ID NO 114; 110pp; English.
 XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC 525, C35, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI (V), WRI (T), 3-1,
 CC 3-8, 3-10 and INC1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 76.7%; Score 46; DB 8; Length 13;
 Best Local Similarity 70.0%; Pred. No. 0.5;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 4 ANYYYGMDV 13
 RESULT 12
 ADM04816
 ID ADM04816 standard; peptide; 21 AA.
 XX ADM04816;
 AC
 DT 07-APR-2005 (first entry)
 XX
 DE PAP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.
 XX
 KW Cytostatic; Vascotropic; heavy chain variable domain;
 KW proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 XX
 OS Unidentified.
 XX
 XX US2005009136-A1.
 XX
 XX 13-JAN-2005.
 XX
 XX 19-FEB-2004; 2004US-00783311.
 XX
 XX 19-FEB-2003; 2003US-0448515P.
 XX
 XX (DYAX-) DYAX CORP.
 XX
 XX Nixon A, Hogan S;
 XX
 XX WPI; 2005-080519/09.
 XX
 PT New pregnancy-associated plasma protein-A (PAP-A) binding proteins
 PT comprising immunoglobulin variable domain sequences, useful for
 PT diagnosing, preventing or treating diseases such as cancer.
 XX
 XX Example; SEQ ID NO 141; 168pp; English.
 XX
 CC The present invention relates to novel proteins (I) that bind to
 CC pregnancy-associated plasma protein A (PAP-A ADM04676). (I) comprises a
 CC first and second immunoglobulin variable domain sequence which binds to
 CC PAP-A. Also claimed are proteins (II) which comprise light chain (LC)
 CC and heavy chain immunoglobulin variable domain sequences which binds to
 CC PAP-A. The proteins are useful for diagnosing, preventing or treating
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
 CC of vascular smooth muscle cells following e.g., balloon angioplasty
 CC (which may cause restenosis). The proteins are especially useful for
 CC useful for treating diseases involving IGF regulated growth. The present
 CC sequence is one such immunoglobulin variable domain sequence.
 XX
 XX Sequence 21 AA;
 SQ
 Query Match 76.7%; Score 46; DB 9; Length 21;
 Best Local Similarity 63.6%; Pred. No. 0.83;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LATYYFGLDV 11
 DB 11 LGNYYYGMVDV 21
 RESULT 13
 ADZ41994
 ID ADZ41994 standard; peptide; 126 AA.
 XX ADZ41994;
 AC
 DT 30-JUN-2005 (first entry)
 XX
 DE Ig H chain variable region, B-CLL set II peptide #4.
 XX
 KW Antibody; antibody engineering; antibody therapy;
 KW light chain variable region; heavy chain variable region;

KM chronic lymphocytic leukemia; cytostatic; Hodgkins disease; lymphoma;
 KM Burkitts lymphoma; multiple myeloma; systemic lupus erythematosus;
 KM antinflammatory; dermatological; immunosuppressive; myasthenia gravis;
 KM muscular-gen.; neuroprotective; Graves disease; antithyroid;
 KM insulin dependent diabetes; diabetes mellitus; antidiabetic;
 KM autoimmune hemolytic anemia; antianemic.
 OS Homo sapiens.
 XX
 XX MO2005034733-A2.
 PN
 XX
 PD 21-APR-2005.
 XX
 PF 08-OCT-2004; 2004MO-US033176.
 XX
 PF 08-OCT-2003; 2003US-0509473P.
 XX
 PR (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
 PA
 XX
 PI Messmer BT, Chiorazzi N, Albesiano E;
 XX
 DR WPI; 2005-306220/31.
 XX
 PT New isolated and purified preparation of light chain and heavy chain
 PT antibody genes, useful for diagnosing, preventing or treating B cell
 PT chronic lymphocytic leukemia, or in screening for agents that may treat
 PT such disease.
 XX
 XX
 PS Disclosure; Fig 2, 58pp; English.
 CC The new invention relates to combinations of light chain antibody genes
 CC and heavy chain antibody genes, useful for treating B cell chronic
 CC lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating
 CC CD5+ B lymphocytes. These cells express low levels of surface membrane Ig
 CC that serves as the receptor for antigen (BCR). Analysis of V region gene
 CC cassette usage has shown that distribution of variable region gene
 CC increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies
 CC that the structure of the antibody molecule, and antigen specificity,
 CC play a role in the leukemic transformation of particular B cells. The
 CC present invention discloses that a significant proportion of B-CLL
 CC patients with aggressive disease share the same classes of VH, D, JH, VL
 CC and JH antibody genes, forming sets of patients with highly homologous B
 CC cell receptors. Alternatively, the patients have a disorder selected from
 CC Hodgkins' disease, non-Hodgkins' lymphoma, Burkitt's lymphoma, myeloma or
 CC systemic lupus erythematosus, myasthenia gravis, Grave's disease, type I
 CC diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune
 CC hemolytic anemia. The new members of the antibody genes are: VH4-39/D6-
 CC 13/JH5/VLkappa012/2/JLkappa1/kappa2 (Set II); VH4-34/D5-
 CC 5/JH6/VLkappa017/JLkappa1/kappa2 (Set III); VH1-69/D3-
 CC 21/JH6/VLlambda37/JLlambda3 (Set IV); VH1-69/D3-
 CC 16/JH3/VLkappa27/JLkappa1/kappa4 (Set IV); VH1-69/D3-
 CC 10/JH6/VLlambda1c/JLlambda1 (Set V); VH1-02/D6-
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIA); VH1-03/D6-
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIB); VH1-18/D6-
 CC 51/D6-19/JH4/VLkappa012/2/JLkappa1 (Set VIC); VH1-46/D6-19/JH4 (Set VID); VH5-
 CC 3/JH4/VLkappa019/JLkappa4 (Set VII); and VH1-69/D2-
 CC 2/JH6/VLkappa16/2/JLkappa3 (Set VIII). Treating a patient having B-CLL
 CC with the above genes comprises administering an agent that binds to the
 CC antigen-binding region of an antibody encoded by the antibody genes. The
 CC agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The
 CC present sequence is an Ig H chain variable region, B-CLL set II peptide.
 XX
 XX
 SQ Sequence 126 AA;
 Query Match 76.7%; Score 46; DB 9; Length 126;
 Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LATYYFGLDV 11
 DB 105 LKRYYYGLDV 115

RESULT 14
 ADM04810
 ID ADM04810 standard; protein; 140 AA.
 XX
 XX ADM04810;
 AC
 XX
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE PAPP-A immunoglobulin variable domain AB D03 heavy chain SEQ ID 135.
 XX
 XX Cytostatic; Vasotropic; heavy chain variable domain;
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 XX
 XX
 OS Unidentified.
 XX
 XX US2005009136-A1.
 PN
 XX
 PD 13-JAN-2005.
 XX
 PF 19-FEB-2004; 2004US-00783311.
 XX
 PR 19-FEB-2003; 2003US-0448515P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 XX
 PI Nixon A, Hogan S;
 XX
 DR WPI; 2005-080519/09.
 XX
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
 PT comprising immunoglobulin variable domain sequences, useful for
 PT diagnosing, preventing or treating diseases such as cancer.
 XX
 PS Example; SEQ ID NO 135; 168pp; English.
 XX
 XX The present invention relates to novel proteins (I) that bind to
 XX pregnancy-associated plasma protein A (PAPP-A ADM04676). (I) comprises a
 XX first and second immunoglobulin variable domain sequence which binds to
 XX PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
 XX and heavy chain immunoglobulin variable domain sequences which binds to
 XX PAPP-A. The proteins are useful for diagnosing, preventing or treating
 XX proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
 XX (which may cause restenosis). The proteins are especially useful for
 XX useful for treating diseases involving IGF regulated growth. The present
 XX sequence is one such immunoglobulin variable domain sequence.
 XX
 XX
 SQ Sequence 140 AA;
 Query Match 76.7%; Score 46; DB 9; Length 140;
 Best Local Similarity 63.6%; Pred. No. 6.3;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LATYYFGLDV 11
 DB 109 LGNYYYGMDV 119
 RESULT 15
 ADM04952
 ID ADM04952 standard; peptide; 16 AA.
 XX
 XX ADM04952;
 AC
 XX
 XX 07-APR-2005 (first entry)
 DT
 XX
 DE PAPP-A immunoglobulin variable domain AB F03 heavy chain CDR3 SEQ ID 277.
 XX
 XX Cytostatic; Vasotropic; heavy chain variable domain;
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 XX

OS Unidentified.

XX US2005009136-A1.

XX 13-JAN-2005.

XX 19-FEB-2004; 2004US-00783311.

XX 19-FEB-2003; 2003US-0448515P.

XX (DYAX-) DYAX CORP.

XX Nixon A, Hogan S;

XX WPI; 2005-080519/09.

XX New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
PT comprising immunoglobulin variable domain sequences, useful for
PT diagnosing, preventing or treating diseases such as cancer.

XX Example; SEQ ID NO 277; 168bp; English.

XX The present invention relates to novel proteins (I) that bind to
CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a
CC first and second immunoglobulin variable domain sequence which binds to
CC PAPP-A. Also claimed are proteins (II) which comprise light chain (Lc)
CC and heavy chain immunoglobulin variable domain sequences which binds to
CC PAPP-A. The proteins are useful for diagnosing, preventing or treating
CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
CC of vascular smooth muscle cells following e.g., balloon angioplasty
CC (which may cause restenosis). The proteins are especially useful for
CC useful for treating diseases involving IGF regulated growth. The present
CC sequence is one such immunoglobulin variable domain sequence.

XX Sequence 16 AA;

Query Match 75.0%; Score 45; DB 9; Length 16;
Best Local Similarity 63.6%; Pred. No. 0.92;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYRGLDV 11
: |||||:
Db 6 VAGYYTGMDV 16

Search completed: November 21, 2005, 12:20:00
Job time : 16.7271 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:36 / Search time 2.67949 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-126
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	43	71.7	19 2 PH1307	Ig heavy chain DJ
2	43	71.7	23 2 PH1361	Ig heavy chain DJ
3	43	71.7	29 2 PH1328	Ig heavy chain DJ
4	43	71.7	160 2 D70189	conserved hypochet
5	43	71.7	160 2 S05271	Ig heavy chain pre
6	43	71.7	408 2 E70380	Na+/H+-exchanging
7	42	70.0	19 2 PH1304	Ig heavy chain DJ
8	42	70.0	19 2 S43960	Ig mu chain V regi
9	42	70.0	23 2 PH1364	Ig heavy chain DJ
10	42	70.0	24 2 PT0258	Ig heavy chain CDR
11	42	70.0	27 2 PH1371	Ig heavy chain DJ
12	42	70.0	27 2 PH1355	Ig heavy chain V r
13	42	70.0	74 2 S26793	Ig heavy chain V r
14	42	70.0	118 2 PH1666	Ig heavy chain V r
15	42	70.0	119 2 PH0961	Ig heavy chain V r
16	42	70.0	120 2 PH1650	Ig heavy chain V r
17	42	70.0	125 2 S24686	Ig heavy chain V6
18	42	70.0	128 2 S46797	Ig heavy chain V r
19	42	70.0	132 2 PH0954	Ig heavy chain V r
20	42	70.0	133 2 C33548	Ig heavy chain V-1
21	42	70.0	136 2 A49047	Ig heavy chain V r
22	42	70.0	147 2 I37780	Ig variable region
23	42	70.0	627 2 S14683	Ig mu chain precu
24	40	66.7	22 2 PH1325	Ig heavy chain DJ
25	39.5	65.8	581 2 E83729	adenine deaminase
26	39	65.0	126 2 S44107	Ig heavy chain V-D
27	39	65.0	375 2 A83788	spore germination
28	38	63.3	22 2 PH1359	Ig heavy chain DJ
29	38	63.3	45 2 PL0094	Ig heavy chain V r

30	38	63.3	287 2 T27056	hypothetical prote
31	38	63.3	473 2 H86240	hypothetical prote
32	38	63.3	979 2 A39792	transcription acti
33	37	61.7	14 2 PH1601	Ig H chain V-D-J r
34	37	61.7	126 1 MHHUOU	Ig heavy chain V-I
35	37	61.7	276 2 S16892	probable transposa
36	37	61.7	447 2 T09809	NADH2 dehydrogenas
37	37	61.7	448 2 T12006	glycerol-3-phospha
38	37	61.7	527 2 C70130	conditioned medium
39	37	61.7	571 2 A42138	conditioned medium
40	37	61.7	571 2 S24482	sel-1 protein - Ca
41	37	61.7	685 2 T22223	Ig heavy chain V r
42	36.5	60.8	120 2 E49590	hypothetical prote
43	36.5	60.8	316 2 C75205	Ig heavy chain DJ
44	36	60.0	18 2 PH1368	30S ribosomal prot
45	36	60.0	145 2 H97707	

ALIGNMENTS

RESULT 1

PH1307
Ig heavy chain DJ region (clone C96-119) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_reviseion 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1307
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1307
A/Molecule type: DNA
A/Residues: 1-19 <WAS>
A/Cross-references: UNIPARC:UPI0000176935
C/Suprafamily: immunoglobulin V region; immunoglobulin
C/Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 19;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYFGLDV 11
DB 6 SYYYGMDV 14

RESULT 2

PH1361
Ig heavy chain DJ region (clone C178-122B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_reviseion 30-Sep-1993 #text_change 07-May-1999
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1361
A/Molecule type: DNA
A/Residues: 1-23 <WAS>
A/Cross-references: UNIPARC:UPI0000176948
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 23;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
DB 8 LFPYYYGMDV 18

```
RESULT 3
PH1328
Ig heavy chain DJ region (clone C113-148) - human (fragment)
A/Residues: 1-160 <KIS2>
A/Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1328
R/Maserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovere, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:11460419
A/Accession: PH1328
A/Molecule type: DNA
A/Residues: 1-29 <MAS>
A/Cross-references: UNIPARC:UPI0000176939
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match      71.7%; Score 43; DB 2; Length 29;
Best Local Similarity 66.7%; Pred. No. 0.36;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTYTFFGLDV 11
      :|||:|:|
Db      16 SYTYGMDV 24

RESULT 4
D70189
conserved hypothetical integral membrane protein BB0717 - Lyme disease spirochete
C/Species: Borrelia burgdorferi (Lyme disease spirochete)
C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C/Accession: D70189
R/Fraser, C.M.; Casjens, S.; Hang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavac, A.R.; Quackenbush, J.; Salberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A/Authors: Smith, H.O.; Venter, J.C.
A/Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A/Reference number: A70100; MUID:98065943; PMID:9403665
A/Accession: D70189
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-160 <KLB>
A/Cross-references: UNIPROT:O51659; UNIPARC:UPI0000575B2; GB:AE001171; GB:AE000783; NID
A/Experimental source: strain B31

Query Match      71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 60.0%; Pred. No. 2;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 ATYYFFGLDV 11
      |||:|:|
Db      23 ATYYFSIDI 32

RESULT 5
S05271
Ig heavy chain precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C/Accession: S05271; S04602
R/Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A/Reference number: S05270
A/Accession: S05271
A/Molecule type: mRNA
A/Residues: 1-160 <KIS1>
A/Cross-references: UNIPROT:Q96B89; UNIPARC:UPI0000176B50; EMBL:X14584
R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A/Reference number: S04601; MUID:89296497; PMID:2500644
A/Accession: S04602
```

```
A/Molecule type: mRNA
A/Residues: 1-144 <KIS2>
A/Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C/Superfamily: immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <Sig>
F/20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match      71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTYTFFGLDV 11
      :|||:|:|
Db      125 SYTYGMDV 133

RESULT 6
E70380
Na+/H+-exchanging protein - Aquifex aeolicus
N/Alternate names: Na+/H+ antiporter
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: E70380
R/Decker, G.; Warren, P.V.; Gassterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; Ove
r Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: E70380
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1408 <AQF>
A/Cross-references: UNIPROT:O67072; UNIPARC:UPI0000564AB; GB:AE000714; NID:92983446; PII
C/Experimental source: strain VFS
C/Genetics:
A/Gene: napA2
C/Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match      71.7%; Score 43; DB 2; Length 408;
Best Local Similarity 54.5%; Pred. No. 5.2;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 LATYYFGLDV 11
      :|||:|:|
Db      116 IVSYFFGLDL 126

RESULT 7
PH1304
Ig heavy chain DJ region (clone C439-111) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1304
R/Maserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovere, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:11460419
A/Accession: PH1304
A/Molecule type: DNA
A/Residues: 1-19 <MAS>
A/Cross-references: UNIPARC:UPI0000176934
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query Match      70.0%; Score 42; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 YYYTFFGLDV 11
      |||:|:|
Db      7 YYYTGMDV 14
```

RESULT 8

S43960
Ig mu chain V region (clone 18) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C/Accession: S43960
R/Magnier, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A/Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A/Reference number: S43956; MUID:94248036; PMID:8190623
A/Accession: S43960
A/Molecule type: DNA
A/Residues: 1-19 <WAS>
A/Cross-references: UNIPARC:UPI000017690D
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin

Query Match
Best Local Similarity 70.0%; Score 42; DB 2; Length 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
Db 10 YYYGMDV 17

RESULT 9

PH1364
Ig heavy chain DJ region (clone C178-136A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1364
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1364
A/Molecule type: DNA
A/Residues: 1-23 <WAS>
A/Cross-references: UNIPARC:UPI0000176949
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 70.0%; Score 42; DB 2; Length 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
Db 11 YYYGMDV 18

RESULT 10

PT0258
Ig heavy chain CDR3 region (clone 2-118B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-May-1997
C/Accession: PT0258
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0258
A/Molecule type: DNA
A/Residues: 1-24 <YAM>
A/Cross-references: UNIPARC:UPI0000176940
A/Experimental source: B lymphocyte
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 24;

Best Local Similarity 75.0%; Pred. No. 0.44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
Db 12 YYYGMDV 19

RESULT 11

PH1371
Ig heavy chain DJ region (clone C111-145) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1371
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1371
A/Molecule type: DNA
A/Residues: 1-27 <WAS>
A/Cross-references: UNIPARC:UPI000017694B
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 70.0%; Score 42; DB 2; Length 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
Db 15 YYYGMDV 22

RESULT 12

PH1355
Ig heavy chain DJ region (clone C100-136) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1355
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1355
A/Molecule type: DNA
A/Residues: 1-27 <WAS>
A/Cross-references: UNIPARC:UPI0000176945
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 70.0%; Score 42; DB 2; Length 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
Db 15 YYYGMDV 22

RESULT 13

S26793
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26793
R/Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam1
A/Reference number: S26786; MUID:92111632; PMID:1730251
A/Accession: S26793
A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 1-74 <MOR>
A/Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:932787; PIDD:CAA43353.1; PIR
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
|||:|:
Db 56 YYYGMDV 63

RESULT 14

PH166
Ig heavy chain V region (clone 6C9) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH166
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylo
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH166
A/Molecule type: mRNA
A/Residues: 1-118 <HIL>
A/Cross-references: UNIPARC:UPI0000176BE7
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
|||:|:
Db 100 YYYGMDV 107

RESULT 15

PH0961
Ig heavy chain V region (G6+ T-L33) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C/Accession: PH0961
R/Martin, T.; Duffy, S.F.; Carson, D.A.; Kilps, T.J.
J. Exp. Med. 175, 983-991, 1992
A/Title: Evidence for somatic selection of natural autoantibodies.
A/Reference number: PH0952; MUID:92202880; PMID:1552291
A/Accession: PH0961
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-119 <MAR>
A/Cross-references: UNIPARC:UPI0000176CE5
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-30/Region: framework 1
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/36-50/Region: framework 2
F/51-67/Region: complementarity-determining 2
F/68-98/Region: framework 3
F/99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;
Best Local Similarity 75.0%; Pred. No. 2.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
|||:|:

Db 101 YYYGMDV 108

Search completed: November 21, 2005, 12:22:14
Job time: 3.67949 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55, Search time 16.2784 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-126
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	44	73.3	Q4N9V2_THRPA	Q4N9V2 theileria p
2	44	73.3	Q4UFX8_THRAN	Q4UFX8 theileria a
3	43	71.7	O51659_BOBBU	O51659 borrelia bu
4	43	71.7	O660F6_BOBGA	O660F6 borrelia ga
5	43	71.7	O67072_AOUAR	O67072 aquifex aco
6	42	70.0	Q7VY71_BOBPE	Q7VY71 bordetella
7	42	70.0	Q7W926_BOBPA	Q7W926 bordetella
8	42	70.0	Q7WKH1_BOBBA	Q7WKH1 bordetella
9	42	70.0	Q4OAL0_LEIMA	Q4OAL0 leishmania
10	42	70.0	O89NT9_BRABA	O89NT9 bradyrhizob
11	42	70.0	Q7AN07_NANEO	Q7AN07 nanorchaeu
12	42	70.0	O6GMY2_HUMAN	O6GMY2 homo sapien
13	42	70.0	O96X97_SULTO	O96X97 sulfolobus
14	42	70.0	O4FWX4_LEIMA	O4FWX4 leishmania
15	41	68.3	O6A0Z1_DESPS	O6A0Z1 desulfofale
16	41	66.7	O6F6N6_ACTAD	O6F6N6 acinetobact
17	40	66.7	O4ZUB1_PERSY	O4ZUB1 pseudomonas
18	40	66.7	O6D0Z3_ERECT	O6D0Z3 erwinia car
19	40	66.7	O8EU78_OCRSH	O8EU78 ocreospori
20	40	66.7	O8C3X8_MOUSE	O8C3X8 mus musculu
21	40	66.7	O5AAV6_CANAL	O5AAV6 candida alb
22	40	66.7	O6WEO5_ARALY	O6WEO5 arabidopsis
23	40	66.7	Q4OBV4_LEIMA	Q4OBV4 leishmania
24	39.5	65.8	Y637_BRCHD	O9K49 bacillus ha
25	39	65.0	O52G31_MAGGR	O52G31 magnaporthe
26	39	65.0	O5YXQ2_NOCFA	O5YXQ2 nocardia fa
27	39	65.0	O97BK3_THERVO	O97BK3 thermoplaem
28	39	65.0	O9KDV6_BACDH	O9KDV6 bacillus ha
29	39	65.0	O82700_MEDTR	O82700 medicago tr
30	39	65.0	O95TAS_MEDTR	O95TAS medicago tr
31	39	65.0	O6ZBX7_ORISA	O6ZBX7 oryza sativ

32	39	65.0	451	2	O6ZBX6_ORISA	O6ZBX6 oryza sativ
33	39	65.0	478	2	O6P181_HUMAN	O6P181 homo sapien
34	39	65.0	662	2	O88T15_LACPL	O88T15 lactobacill
35	39	65.0	701	1	LSP2_DROME	O21388 drosophila
36	39	65.0	779	2	O65S21_MANSW	O65S21 manheimia
37	39	65.0	780	2	O7VQH6_CANBR	O7VQH6 candidatus
38	38	63.3	116	2	O7Z3Y6_HUMAN	O7Z3Y6 homo sapien
39	38	63.3	148	2	O5TMY6_HUMAN	O5TMY6 anophelis g
40	38	63.3	159	2	O96QSO_HUMAN	O96QSO homo sapien
41	38	63.3	239	2	O5X0G3_LEGPI	O5X0G3 legionella
42	38	63.3	243	2	O5Z2F4_LEGPI	O5Z2F4 legionella
43	38	63.3	307	2	O6NSD3_RHOPA	O6NSD3 rhodospendo
44	38	63.3	350	2	O8TVTS_METKA	O8TVTS methanopyru
45	38	63.3	366	2	O9XTT1_CABEL	O9XTT1 caenorhabdi

ALIGNMENTS

RESULT 1
Q4N9V2_THRPA PRELIMINARY; PRT; 1348 AA.
ID Q4N9V2_THRPA PRELIMINARY; PRT; 1348 AA.
AC Q4N9V2_THRPA PRELIMINARY; PRT; 1348 AA.
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TP01_0021;
OS Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga.
RA Gardner M.J., Bishop R., Shah T., de Villiers B.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoib A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Uteback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA Taracha B.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.,
RA "Genome sequence of Theileria parva, a bovine pathogen that transforms
lymphocytes.";
RT Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga.
RA Gardner M., Bishop R., Shah T., de Villiers B., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoib A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Uteback T., Feldblyum T., Pertea M., Allen J., Taracha B.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.,
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AAGK0100001; EMBL3265.1; -; Genomic DNA.
DR EMBL; AAGK0100001; EMBL3265.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 1348 AA; 155635 MW; 474C3A40C23B8C5F CRC64;
Query Match 73.3%; Score 44; DB 2; Length 1348;
Beef Local Similarity 87.5%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Q4UFY8_THEAN PRELIMINARY; PRT; 2262 AA.
 ID Q4UFY8
 AC Q4UFY8
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=TAL9710;
 OS Theileria annulata.
 OC Eukaryote; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 NCBI_TaxID=5874;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Beriman M.,
 RA Hall N., Barrell B.G.;
 RT "The chromosome 1 sequence of Theileria annulata."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 RM EMBL, CR940347; CA174001.1; -; Genomic DNA.
 DR Hypothetical protein.
 KW SEQUENCE 2262 AA; 262068 MW; FD9E8915243EF512 CRC64;

Query Match 73.3%; Score 44; DB 2; Length 2262;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYVFGLD 10
 Db 1244 STYVFGLD 1251

RESULT 3

051659 BORBU PRELIMINARY; PRT; 160 AA.
 ID 051659 BORBU
 AC 051659;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Conserved hypothetical integral membrane protein.
 GN OrderedLocustNames=B80717;
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
 OC Borrelia burgdorferi group.
 NCBI_TaxID=139;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/375511;
 RA Frazer C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Ladhira R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
 RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
 RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
 RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
 RA Gocayne J.D., Weidman J.F., Utterback T.R., Matthey L., McDonald L.A.,
 RA Artiach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
 RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 burgdorferi."
 RL Nature 390:580-586(1997).
 DR EMBL, AF001171; AAC67057.1; -; Genomic DNA.
 DR PIR, D70189; D70189.
 DR TIGR, BB0717; -.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 160 AA; 19300 MW; 9DB28A497C0F5737 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 160;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYVFGLDV 11

Db 23 ATYVFSIDI 32

RESULT 4

Q660F6_BORGA PRELIMINARY; PRT; 160 AA.
 ID Q660F6_BORGA
 AC Q660F6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Conserved hypothetical integral membrane protein.
 GN OrderedLocustNames=BG0739;
 OS Borrelia garinii.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
 OC Borrelia burgdorferi group.
 NCBI_TaxID=29519;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PRI;
 RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
 RA Schulte-Spechtel U., Wilske B., Suenkel U., Plazzer M.;
 RT "Comparative analysis of the Borrelia garinii genome."
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, CP000013; AA07565.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 160 AA; 19293 MW; B65B15C5197BF89 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 160;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYVFGLDV 11
 Db 23 ATYVFSIDI 32

RESULT 5

067072_AQUAR PRELIMINARY; PRT; 408 AA.
 ID 067072_AQUAR
 AC 067072;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Na(+)/H(+) antiporter.
 GN Name=napA2; OrderedLocustNames=AQ_929;
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 NCBI_TaxID=63363;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/328311;
 RA Dackert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
 RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 aeolicus."
 RL Nature 392:353-358(1998).
 DR EMBL, AE000714; AAC07034.1; -; Genomic DNA.
 DR PIR, E70380; E70380.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0015299; F:resolute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 KM Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 408 AA; 43582 MW; 7E05B4B387A6C506 CRC64;

Query Match 71.7%; Score 43; DB 2; Length 408;
 Best Local Similarity 54.5%; Pred. No. 28;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYVYFGLDV 11
:|||||:
Db 116 IVSYVFFGLDL 126

RESULT 6

Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
ID Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
AC Q7VY71
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smow; OrderedLocuNames=BPI487;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
NCBI_TaxID=520;
[1]

NUCLEOTIDE SEQUENCE.

RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640415; CAB3176.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP transpDctP.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 40021 MW; 03F1C2B6FC51D502 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ATYVYFGLD 10
:|||||:
Db 98 ASYVFFGKD 106

Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
ID Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
AC Q7W926;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smow; OrderedLocuNames=BPI1948;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
[1]

NUCLEOTIDE SEQUENCE.

RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640443; CAB32632.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP transpDctP.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39997 MW; 8AB672BA3BF09AD CRC64;

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640428; CAB37248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP transpDctP.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39967 MW; 970BC4608CF1D88 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ATYVYFGLD 10
:|||||:
Db 98 ASYVFFGKD 106

RESULT 8
Q7W926 BORBR PRELIMINARY; PRT; 364 AA.
ID Q7W926 BORBR PRELIMINARY; PRT; 364 AA.
AC Q7W926;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smow; OrderedLocuNames=BBI2136;
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
[1]

NUCLEOTIDE SEQUENCE.
RC STRAIN=RB50 / ATCC BAA-589;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640443; CAB32632.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP transpDctP.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39997 MW; 8AB672BA3BF09AD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLD 10
Db 98 ASYYFGKD 106

RESULT 9

04QAL0_LEIMA

ID 04QAL0_LEIMA PRELIMINARY; PRT; 378 AA.

AC 04QAL0;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DE Hypothetical protein.

GN ORFNames=LmjP25_0840;

OS Leishmania major.

OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI_TaxID=5664;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Friedlin.

RA Peacock C.S., Murphy L., Ivens A.C., Bertman M., Blackwell J.,

RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,

RA Saunders D., Seeger K., Warren T., Rajadream M., and Barrell B.G.;

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; C7005264; CAJ04989.1; -; Genomic_DNA.

KM Hypothetical protein.

SEQUENCE 378 AA; 41605 MW; 9E3EE7C7C1F04839 CRC64;

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 378;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTFFGL 9
Db 112 TTYTFFGL 118

RESULT 10

089NT9_BRAJA

ID 089NT9_BRAJA PRELIMINARY; PRT; 382 AA.

AC 089NT9;

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Oridiploasmic mannitol-binding protein.

GN OrderedLocustNames=blt3745;

OS Bradyrhizobium japonicum.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Bradyrhizobiaceae; Bradyrhizobium.

OX NCBI_TaxID=375;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=USDA 110;

RX MEDLINE=22484998; PubMed=12597275;

RA Kaneko T., Nakanura Y., Sato S., Minamisawa K., Uchiumi T.,

RA Sasamoto S., Watanabe A., Idegawa K., Iriyuchi M., Kawashima K.,

RA Kohara M., Matsumoto M., Shimpo S., Tsunoka H., Wada T., Yamada M.,

RA Tabata S.;

RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium

RL DNA Res. 9:189-197(2002).

DR EMBL; BA000040; BAC9010.1; -; Genomic_DNA.

DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR006311; Tat.

DR InterPro; IPR004682; TRAP transpDcCP.

DR Pfam; PF03480; SBP_bac_7; 1.

DR TIGRFAMs; TIGR01405; TAT_signal_seq; 1.

KM Complete proteome.

SEQUENCE 382 AA; 42090 MW; 23C264980A9F9B8D CRC64;

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 382;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLD 10
Db 117 ASYYFGKD 125

RESULT 11

074N07_NANEO

ID 074N07_NANEO PRELIMINARY; PRT; 594 AA.

AC 074N07;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE NEQ353.

GN OrderedLocustNames=NEQ353;

OS Nanoarchaeum equitans.

OC Archaea; Nanoarchaeota; Nanoarchaeum.

OX NCBI_TaxID=160232;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K14-M;

RX PubMed=14566062; DOI=10.1073/pnas.1735403100;

RA Materson E., Hohn M.J., Abel I., Graham D.E., Adams M.D., Barnstead M.,

RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,

RA Mathur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,

RA Scell D., Stetter K.O., Short J.M., Wooldraver M.;

RT "The genome of Nanoarchaeum equitans: Insights into early archaeal

evolution and derived parasitism."

RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).

DR EMBL; AEO17199; AAR3202.1; -; Genomic_DNA.

KM Complete proteome.

SEQUENCE 594 AA; 69673 MW; FD2E60ACF00CD9F4 CRC64;

Query Match Best Local Similarity 70.0%; Score 42; DB 2; Length 594;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
Db 569 LSRHYFGVDI 579

RESULT 12

06GM72_HUMAN

ID 06GM72_HUMAN PRELIMINARY; PRT; 606 AA.

AC 06GM72;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE IGHM protein.

GN Name=IGHM;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Earchontoglires; Primates; Catarrhini; Homidae;

OC Homo

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,

RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guaratane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyminski M.I., Skalska U., Smallus D.B.,
 RA Schermer A., Schein J.B., Jones S.U.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH NCI Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073758; AAH73758.1; -, mRNA.
 DR SMR; O6GMV2; 20-256.
 DR InterPro; IPR003599; IG-like.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG-v.
 DR Pfam; PF07654; CI-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE 606 AA; 66185 MW; B6B3B5114FAC5 CRC64;
 Query Match 70.0%; Score 42; DB 2; Length 606;
 Best Local Similarity 75.0%; Pred. No. 63;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 YYYRGLDV 11
 Db 135 YYYRGMV 142
 RESULT 13
 ID Q96X97_SUITO PRELIMINARY; PRT; 1062 AA.
 AC Q96X97;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 GN 1062aa long hypothetical thermoprotein.
 OS OrderedLocustNames=ST2615;
 OC Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JCM 10545 / ?;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosooyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7.";
 RL DNA Res. 8:123-140(2001).
 DR EMBL; BA000023; BAB67731.1; -, Genomic-DNA.
 DR InterPro; IPR007981; Peptidase_A5.
 DR Pfam; PF05317; Thermopain; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 1062 AA; 118024 MW; 166F4ED60A040B4 CRC64;
 Query Match 70.0%; Score 42; DB 2; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 TTYRFL 9
 Db 623 TTYRFL 629
 RESULT 14
 ID Q4FWX4_LEIMA PRELIMINARY; PRT; 3212 AA.
 AC Q4FWX4;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=LMO_1075;
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Friedlin;
 RX PubMed=16020728; DOI=10.1126/science.1112680;
 RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
 RA Berriman M., Slek B., Rajandream M.A., Adlem E., Aert R., Anupama A.,
 RA Apostolou Z., Attipoe P., Baeson N., Bauser C., Beck A., Beverley S.M.,
 RA Blanchettin G., Borzym K., Bothe G., Brusch C.V., Collins M.,
 RA Cadag B., Clarion L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
 RA Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
 RA Farelina G., Foster N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
 RA Gobie A., Goffeau A., Harris D., Hertz-Powder C., Hilbert H., Horn D.,
 RA Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,
 RA Lord A., Louie T., Marra M., Maury D., Matthews K., Michael S.,
 RA Mottner J.C., Muller-Auer S., Munden H., Nelson S., Nordertsch H.,
 RA Oliver K., O'Neill S., Pentony M., Pohl T.M., Price C., Purnelle B.,
 RA Quail M.A., Rabinowitch E., Reinhardt R., Rieger M., Rinta J.,
 RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
 RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
 RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
 RA Voickaert G., Wambolt R., Warren T., Wedler H., Woodward J., Zhou S.,
 RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
 RA Myler P.J.;
 RT "The genome of the Kinetoplastid Parasite, Leishmania major.";
 RL Science 309:436-442(2005).
 DR EMBL; CP000081; AAZ14365.1; -, Genomic-DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 3212 AA; 342958 MW; E26BA125060F9A6B CRC64;
 Query Match 70.0%; Score 42; DB 2; Length 3212;
 Best Local Similarity 70.0%; Pred. No. 3.3e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LATYYRGLD 10
 Db 164 LATYYRGLD 173
 RESULT 15
 ID Q6A0Z1_DESPS PRELIMINARY; PRT; 716 AA.
 AC Q6A0Z1;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Related to mercuroic reductase.
 GN OrderedLocustNames=DP0504;
 OS Desulfococcus psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
 OC Desulfobulbaceae; Desulfococcus.
 OX NCBI_TaxID=84980;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LSV54 / DSM 12343;

RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann U., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL: CR522870; CAG35233.1; -; genomic_DNA.
DR GO: GO:0005737; C:cytoplasm; IEA.
DR GO: GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR GO: GO:0050660; F:PAD binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001327; FAD_DYR_redox.
DR InterPro: IPR000815; Hg_reductase.
DR InterPro: IPR005162; pntine_S.
DR InterPro: IPR01100; Pyr_redox.
DR InterPro: IPR04099; Pyr_redox_dim.
DR Pfam: PF00070; Pyr_redox; 2.
DR Pfam: PF02852; Pyr_redox_dim; 1.
DR PRINTS: PR00368; FADPNR.
DR PRINTS: PR00945; HGRDTRSE.
DR PRINTS: PR00411; PNDROTASEI.
DR PRODOM: PD000139; FAD_Pyr_redox; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
DR PROSITE: PS00076; PYRIDINE_REDOX_1; 1.
KW Complete proteome.
SQ SEQUENCE 716 AA; 78725 MW; 68EFC0600DE44094 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 716;
Best local similarity 60.0%; Pred. NO. 1.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFRGLD 10
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DB 14 VSAYYFRGLD 23

Search completed: November 21, 2005, 12:04:09
Job time : 19.2784 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 ; Search time 4.15018 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-126
Perfect score: 60
Sequence: 1 IATYYPGLDV 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	71.7	33	1	US-08-053-131-78 Sequence 78, Appl
2	43	71.7	33	1	US-08-645-641-78 Sequence 78, Appl
3	43	71.7	33	1	US-07-853-408B-78 Sequence 78, Appl
4	43	71.7	33	1	US-08-096-762-78 Sequence 78, Appl
5	43	71.7	33	1	US-08-308-865-78 Sequence 78, Appl
6	43	71.7	33	2	US-09-042-353-275 Sequence 275, App
7	43	71.7	33	2	US-08-758-417A-123 Sequence 123, App
8	43	71.7	33	4	PCT-US92-10983-78 Sequence 78, Appl
9	43	71.7	125	2	US-09-840-459-84 Sequence 84, Appl
10	43	71.7	125	2	US-09-497-625A-84 Sequence 84, Appl
11	42	70.0	29	1	US-08-053-131-73 Sequence 73, Appl
12	42	70.0	29	1	US-08-645-641-73 Sequence 73, Appl
13	42	70.0	29	1	US-07-853-408B-73 Sequence 73, Appl
14	42	70.0	29	1	US-08-096-762-73 Sequence 73, Appl
15	42	70.0	29	1	US-08-308-865-73 Sequence 73, Appl
16	42	70.0	29	2	US-09-042-353-270 Sequence 270, App
17	42	70.0	29	2	US-08-758-417A-118 Sequence 118, App
18	42	70.0	29	4	PCT-US92-10983-73 Sequence 73, Appl
19	42	70.0	31	1	US-08-053-131-83 Sequence 83, Appl
20	42	70.0	31	1	US-08-645-641-83 Sequence 83, Appl
21	42	70.0	31	1	US-07-853-408B-83 Sequence 83, Appl
22	42	70.0	31	1	US-08-096-762-83 Sequence 83, Appl
23	42	70.0	31	1	US-08-308-865-83 Sequence 83, Appl
24	42	70.0	31	2	US-09-042-353-280 Sequence 280, App
25	42	70.0	31	2	US-08-758-417A-128 Sequence 128, App
26	42	70.0	31	4	PCT-US92-10983-83 Sequence 83, Appl
27	42	70.0	36	1	US-08-053-131-84 Sequence 84, Appl

28	42	70.0	36	1	US-08-645-641-84 Sequence 84, Appl
29	42	70.0	36	1	US-07-853-408B-84 Sequence 84, Appl
30	42	70.0	36	1	US-08-096-762-84 Sequence 84, Appl
31	42	70.0	36	1	US-08-308-865-84 Sequence 84, Appl
32	42	70.0	36	2	US-09-042-353-281 Sequence 129, App
33	42	70.0	36	2	US-08-758-417A-129 Sequence 84, Appl
34	42	70.0	36	4	PCT-US92-10983-84 Sequence 88, Appl
35	42	70.0	119	2	US-09-840-459-88 Sequence 88, Appl
36	42	70.0	119	2	US-09-497-625A-88 Sequence 77, Appl
37	42	70.0	128	2	US-09-840-459-77 Sequence 79, Appl
38	42	70.0	128	2	US-09-840-459-79 Sequence 77, Appl
39	42	70.0	128	2	US-09-497-625A-77 Sequence 79, Appl
40	42	70.0	128	2	US-09-497-625A-79 Sequence 80, Appl
41	42	70.0	167	2	US-09-472-087-80 Sequence 64, Appl
42	42	70.0	236	2	US-09-456-090A-64 Sequence 104, App
43	42	70.0	236	2	US-09-456-090A-104 Sequence 64, Appl
44	42	70.0	236	2	US-09-453-234-64 Sequence 104, App
45	42	70.0	236	2	US-09-453-234-104 Sequence 104, App

ALIGNMENTS

RESULT 1
US-08-053-131-78
Sequence 78, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
NUMBER OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend Knourle and Crew
STREET: One Market Plaza, Stewart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053.131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/653,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-053-131-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYYYFGLDV 11
:|:|:|:
Db 10 SYYYGMDV 18

RESULT 2

US-08-645-641-78
Sequence 78, Application US/08645641
Patent No. 5719032
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-MAY-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-641-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYYYFGLDV 11
:|:|:|:
Db 10 SYYYGMDV 18

RESULT 3

US-07-853-408B-78
Sequence 78, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-853-408B-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYYYFGLDV 11
:|:|:|:
Db 10 SYYYGMDV 18

RESULT 4

US-08-096-762-78
Sequence 78, Application US/08096762
Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knoutle and Crew
STREET: One Market Plaza, Stewart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGDGV 11
:||||:|
DB 10 SYYTGGMDV 18

RESULT 5
US-08-308-865-78

Sequence 78, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSER: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGDGV 11
:||||:|
DB 10 SYYTGGMDV 18

RESULT 6
US-09-042-353-275

Sequence 275, Application US/09042353
Patent No. 625458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 625458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION: NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-042-353-275

Query Match 71.7%; Score 43; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGLDV 11
:|:|:|:
Db 10 SYTYGMDV 18

RESULT 7
US-08-758-417A-123
Sequence 123, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996

APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION: NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS: LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-08-758-417A-123

Query Match 71.7%; Score 43; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGLDV 11
:|:|:|:
Db 10 SYTYGMDV 18

RESULT 8
PCT-US92-10983-78
Sequence 78, Application PC/TUS9210983
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic Non-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10983
FILING DATE: 19921217
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-10983-78

Query Match 71.7%; Score 43; DB 4; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGDGV 11
Db 10 STYYGMDV 18

RESULT 9
US-09-840-459-84
Sequence 84, Application US/09840459
Patent No. 6696550
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 84
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-84

Query Match 71.7%; Score 43; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGDGV 11
Db 106 STYYGMDV 114

RESULT 10
US-09-497-625A-84
Sequence 84, Application US/09497625A
Patent No. 6727349
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-004
CURRENT APPLICATION NUMBER: US/09/497,625A
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 84
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-09-497-625A-84

Query Match 71.7%; Score 43; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGDGV 11
Db 106 STYYGMDV 114

RESULT 11
US-08-053-131-73
Sequence 73, Application US/0805131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Londerg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-053-131-73

Query Match
Best Local Similarity 70.0%; Score 42; DB 1; Length 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGDLV 11
Db 7 YYYGMDV 14

RESULT 12
US-08-645-641-73
Sequence 73, Application US/08645641
Patent No. 5719032

GENERAL INFORMATION:

APPLICANT: Lonberg, Nils

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for

NUMBER OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/645,641

FILING DATE: 20-MAY-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/904,068

FILING DATE: 23-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14643-000913

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-645-641-73

Query Match
Best Local Similarity 70.0%; Score 42; DB 1; Length 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGDLV 11
Db 7 YYYGMDV 14

RESULT 13
US-07-853-408B-73
Sequence 73, Application US/07853408B
Patent No. 5789650

GENERAL INFORMATION:

APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/853,408B

FILING DATE: 19920318

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 14643-9

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 73:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-853-408B-73

Query Match
Best Local Similarity 70.0%; Score 42; DB 1; Length 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGDLV 11
Db 7 YYYGMDV 14

RESULT 14
US-08-096-762-73
Sequence 73, Application US/08096762
Patent No. 5814318

GENERAL INFORMATION:

APPLICANT: Lonberg, Nils

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for

NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Hourie and Crew

STREET: One Market Plaza, Stewart Tower, Suite 200

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/096,762

FILING DATE: 22-JUL-1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/053,131

FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO.: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11
|||:|:
Db 7 YYYGMDV 14

RESULT 15
US-08-308-865-73
Sequence 73, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nile
Applicant: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSER: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGGLDV 11
|||:|:
Db 7 YYYGMDV 14

Search completed: November 21, 2005, 12:07:38
Job time : 5.15018 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:50:51 ; Search time 13.619 Seconds
(without alignments)
337.478 Million cell updates/sec

Title: US-10-632-706-126
Perfect score: 60
Sequence: 1 LATYYFGGLDV 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications RA-Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	60	100.0	11 4 US-10-632-706-126	Sequence 126, App
2	60	100.0	11 4 US-10-632-706-127	Sequence 127, App
3	48	80.0	122 6 US-11-031-485-116	Sequence 116, App
4	47	78.3	129 4 US-10-364-743-101	Sequence 101, App
5	47	78.3	129 5 US-10-452-593-101	Sequence 101, App
6	47	78.3	134 4 US-10-364-743-15	Sequence 15, App1
7	47	78.3	134 5 US-10-452-593-15	Sequence 15, App1
8	47	78.3	468 6 US-11-031-485-18	Sequence 56, App1
9	47	78.3	469 6 US-11-031-485-18	Sequence 18, App1
10	46	76.7	13 4 US-10-632-706-114	Sequence 114, App
11	46	76.7	21 5 US-10-783-311-141	Sequence 141, App
12	46	76.7	140 5 US-10-783-311-135	Sequence 135, App
13	45	75.0	16 5 US-10-783-311-277	Sequence 277, App
14	45	75.0	21 5 US-09-880-748-3068	Sequence 3068, App
15	45	75.0	21 4 US-10-293-418-3068	Sequence 3068, App
16	45	75.0	117 6 US-11-009-731-47	Sequence 47, App1
17	45	75.0	135 5 US-10-783-311-271	Sequence 271, App
18	45	75.0	256 3 US-09-880-748-1600	Sequence 1600, App
19	45	75.0	256 4 US-10-293-418-1600	Sequence 1600, App
20	44	73.3	16 3 US-09-880-748-2129	Sequence 2129, App
21	44	73.3	16 4 US-10-293-418-2129	Sequence 2129, App
22	44	73.3	17 3 US-09-880-748-2876	Sequence 2876, App
23	44	73.3	17 4 US-10-293-418-2876	Sequence 2876, App
24	44	73.3	18 5 US-10-984-960A-8	Sequence 8, App1
25	44	73.3	117 4 US-10-041-860-206	Sequence 206, App1
26	44	73.3	123 4 US-10-309-762-18	Sequence 18, App1
27	44	73.3	123 4 US-10-309-762-19	Sequence 19, App1

ALIGNMENTS

28	44	73.3	124 4 US-10-292-088-106	Sequence 106, App
29	44	73.3	127 4 US-10-041-860-31	Sequence 31, App1
30	44	73.3	127 4 US-10-041-860-243	Sequence 243, App
31	44	73.3	127 4 US-10-041-860-325	Sequence 325, App
32	44	73.3	127 4 US-10-665-383-42	Sequence 42, App1
33	44	73.3	127 4 US-10-466-242-53	Sequence 53, App1
34	44	73.3	127 5 US-10-984-960A-2	Sequence 2, App1
35	44	73.3	129 4 US-10-292-088-10	Sequence 10, App1
36	44	73.3	124 4 US-10-364-743-16	Sequence 16, App1
37	44	73.3	134 4 US-10-364-743-109	Sequence 109, App
38	44	73.3	134 4 US-10-364-743-110	Sequence 110, App
39	44	73.3	134 5 US-10-452-593-16	Sequence 16, App1
40	44	73.3	134 5 US-10-452-593-109	Sequence 109, App1
41	44	73.3	134 5 US-10-452-593-110	Sequence 110, App
42	44	73.3	145 5 US-10-644-277-146	Sequence 146, App
43	44	73.3	157 5 US-10-473-287-34	Sequence 34, App1
44	44	73.3	157 5 US-10-473-287-63	Sequence 63, App1
45	44	73.3	249 5 US-10-935-290-61	Sequence 61, App1

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RESULT 1
US-10-632-706-126
; Sequence 126, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-126
Query Match      100.0%; Score 60; DB 4; Length 11;
Best local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy      1 LATYYFGGLDV 11
Db      1 LATYYFGGLDV 11
RESULT 2
US-10-632-706-127
; Sequence 127, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 127
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-127

Query Match 100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
DB 1 LATYYFGLDV 11

RESULT 3
US-11-031-485-116
Sequence 116, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULEN, NICHOLAS
APPLICANT: KELLMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAK-FREDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MACCAM
FILE REFERENCE: ABX-DF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 116
LENGTH: 122
TYPE: PRT
ORGANISM: Homo sapiens
US-11-031-485-116

Query Match 80.0%; Score 48; DB 6; Length 122;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
DB 100 VTTYGGMDV 110

RESULT 4
US-10-364-743-101
Sequence 101, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: NO. US20040009178A1an, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 101
LENGTH: 129

TYPE: PRT
ORGANISM: human
US-10-364-743-101

Query Match 78.3%; Score 47; DB 4; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
DB 105 TTYYGMDV 113

RESULT 5
US-10-452-593-101
Sequence 101, Application US/10452593
Publication No. US20040258699A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: Nolan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 98 CIP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: US 10/364,743
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/356,086
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 101
LENGTH: 129
TYPE: PRT
ORGANISM: human
US-10-452-593-101

Query Match 78.3%; Score 47; DB 5; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
DB 105 TTYYGMDV 113

RESULT 6
US-10-364-743-15
Sequence 15, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: NO. US20040009178A1an, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)
CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15
LENGTH: 134
TYPE: PRT

ORGANISM: human
US-10-364-743-15

Query Match 78.3%; Score 47; DB 4; Length 134;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
DB 110 TTYTFFGLDV 118

RESULT 7

US-10-452-593-15
Sequence 15, Application US/10452593
Publication No. US20040258699A1
GENERAL INFORMATION:
APPLICANT: Bowdlen, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A..
APPLICANT: Maruyama, Toshiaki
APPLICANT: Nolan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 98 CIP (1087-73 CIP)
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: US/10/364,743
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/356,086
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15
LENGTH: 134
TYPE: PRT
ORGANISM: human
US-10-452-593-15

Query Match 78.3%; Score 47; DB 5; Length 134;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
DB 110 TTYTFFGLDV 118

RESULT 8

US-11-031-485-56
Sequence 56, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, STRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAR-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MADCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 56
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens

US-11-031-485-56

Query Match 78.3%; Score 47; DB 6; Length 468;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
DB 123 TTYTFFGLDV 131

RESULT 9

US-11-031-485-18
Sequence 18, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, STRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAR-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MADCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 18
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
DB 123 TTYTFFGLDV 131

RESULT 10

US-10-632-706-114
Sequence 114, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 0.64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLDV 11
| | | | |
Db 4 ANYYGMDV 13

RESULT 11
US-10-783-311-141
; Sequence 141, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-141

Query Match 76.7%; Score 46; DB 5; Length 21;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
| | | | |
Db 11 LGNYYYGMDV 21

RESULT 12
US-10-783-311-135
; Sequence 135, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-135

Query Match 76.7%; Score 46; DB 5; Length 140;
Best Local Similarity 63.6%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
| | | | |
Db 109 LGNYYYGMDV 119

RESULT 13
US-10-783-311-277
; Sequence 277, Application US/10783311

; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-277

Query Match 75.0%; Score 45; DB 5; Length 16;
Best Local Similarity 63.6%; Pred. No. 1.2;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
| | | | |
Db 6 VAGYYYGMDV 16

RESULT 14
US-09-880-748-3068
; Sequence 3068, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3068

Query Match 75.0%; Score 45; DB 3; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLDV 11
| | | | |
Db 12 APYYYGMDV 21

RESULT 15
US-10-293-418-3068
; Sequence 3068, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

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FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3068
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-3068
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Query Match 75.0% Score 45 DB 4 Length 21
Best Local Similarity 70.0% Pred. No. 1.5
Matches 7 Conservative 2 Mismatches 1 Indels 0 Gaps 0
```

```
QY 2 ATYYFGLDV 11
DB 12 APYYGMDV 21
```

Search completed: November 21, 2005, 12:33:36
Job time : 14.619 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 12:04:27 ; Search time 0.201465 Seconds
(without alignments)
61.686 Million cell updates/sec

Title: US-10-632-706-126
Perfect score: 60
Sequence: 1 LARYYFGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	43	71.7	306	7	US-11-017-550-47
2	42	70.0	124	7	US-11-144-248-8
3	42	70.0	125	7	US-11-144-248-16
4	42	70.0	174	7	US-11-144-248-4
5	42	70.0	470	7	US-11-144-248-45
6	42	70.0	470	7	US-11-144-248-46
7	42	70.0	470	7	US-11-144-248-49
8	42	70.0	473	7	US-11-144-248-50
9	40	66.7	113	7	US-11-144-248-20
10	36	60.0	306	7	US-11-017-550-42
11	35	58.3	87	1	US-10-839-799-112
12	35	58.3	145	1	US-10-721-763-29
13	35	58.3	154	1	US-11-017-550-37
14	33	55.0	306	7	US-11-017-550-46
15	33	55.0	2280	7	US-11-022-562-211
16	32	53.0	61	1	US-10-997-201A-9
17	31	51.7	167	1	US-10-967-457-79
18	31	51.7	428	1	US-10-632-150-6
19	31	51.7	828	1	US-10-501-039-2
20	30	50.0	285	7	US-11-082-389-324
21	30	50.0	306	7	US-11-017-550-46
22	30	50.0	475	7	US-10-510-386-98
23	29	48.3	103	7	US-11-074-176-156
24	29	48.3	306	7	US-11-017-550-38
25	29	48.3	306	7	US-11-017-550-60

26	29	48.3	312	7	US-11-082-389-346	Sequence 346, App
27	29	48.3	366	7	US-11-022-542-228	Sequence 228, App
28	29	48.3	500	1	US-10-957-569-18	Sequence 18, App
29	28	46.7	21	1	US-10-939-890-526	Sequence 526, App
30	28	46.7	120	1	US-10-932-334-78	Sequence 78, App
31	28	46.7	306	7	US-11-017-590-58	Sequence 58, App
32	28	46.7	317	1	US-10-674-767-2	Sequence 2, App
33	28	46.7	425	1	US-10-336-763A-2	Sequence 2, App
34	28	46.7	525	1	US-10-131-826A-56	Sequence 56, App
35	28	46.7	654	7	US-11-046-668-4	Sequence 4, App
36	28	46.7	683	7	US-11-046-668-2	Sequence 2, App
37	28	46.7	1857	7	US-11-057-058-60	Sequence 60, App
38	28	46.7	1857	7	US-11-057-058-61	Sequence 61, App
39	27	45.0	10	7	US-11-057-708-25	Sequence 25, App
40	27	45.0	122	1	US-10-932-334-73	Sequence 73, App
41	27	45.0	277	1	US-10-510-386-96	Sequence 96, App
42	27	45.0	302	7	US-11-182-592-6	Sequence 6, App
43	27	45.0	353	7	US-11-182-592-4	Sequence 4, App
44	27	45.0	393	1	US-10-523-588-13	Sequence 13, App
45	27	45.0	394	1	US-10-131-826A-520	Sequence 520, App

ALIGNMENTS

RESULT 1
US-11-017-550-47
; Sequence 47, Application US/11017550
; Publication No. US20050250183A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Schultz, Peter G
; APPLICANT: Wang, Lei
; APPLICANT: Anderson, John C
; APPLICANT: Chin, Jason
; APPLICANT: Liu, David R
; APPLICANT: Magliery, Thomas
; APPLICANT: Meggers, Eric L
; APPLICANT: Mehl, Ryan A
; APPLICANT: Paetznick, Mirol
; APPLICANT: Santoro, Stephen W
; APPLICANT: Zhang, Zhiwen
; TITLE OR INVENTION: In Vivo Incorporation of Unnatural Amino Acids
; FILE REFERENCE: 54-000120US
; CURRENT APPLICATION NUMBER: US/11/017,550
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/126,927
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/285,030
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 60/355,514
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
US-11-017-550-47
Query Match 71.7%; Score 43; DB 7; Length 306;
Best Local Similarity 77.8%; Pred. No. 0.15;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 TYYFGLDV 11
DB 158 TYYFGLDV 166
RESULT 2
US-11-144-248-8
; Sequence 8, Application US/11144248
; Publication No. US20050244408A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-8
```

```
Query Match 70.0%; Score 42; DB 7; Length 124;
Best Local Similarity 75.0%; Pred. No. 0.092;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YYYFGLDV 11
DB 106 YYYGMDV 113
```

```
RESULT 3
US-11-144-248-16
/ Sequence 16, Application US/11/144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-16
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```
Query Match 70.0%; Score 42; DB 7; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.092;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 4 YYYFGLDV 11
DB 107 YYYGMDV 114
```

```
RESULT 4
US-11-144-248-4
/ Sequence 4, Application US/11/144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 174
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-4
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```
Query Match 70.0%; Score 42; DB 7; Length 174;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YYYFGLDV 11
DB 99 YYYGMDV 106
```

```
RESULT 5
US-11-144-248-45
/ Sequence 45, Application US/11/144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 45
/ LENGTH: 470
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-45
```

```
Query Match 70.0%; Score 42; DB 7; Length 470;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YYYFGLDV 11
DB 126 YYYGMDV 133
```

```
RESULT 6
US-11-144-248-46
/ Sequence 46, Application US/11/144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
```

```
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-46
```

```
Query Match
Best Local Similarity 70.0%; Score 42; DB 7; Length 470;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YYYFGLDV 11
|||:|:|
Db 126 YYYGMDV 133
```

```
RESULT 7
US-11-144-248-49
Sequence 49, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-49
```

```
Query Match
Best Local Similarity 70.0%; Score 42; DB 7; Length 470;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YYYFGLDV 11
|||:|:|
Db 126 YYYGMDV 133
```

```
RESULT 8
US-11-144-248-50
Sequence 50, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
```

```
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 473
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-50
```

```
Query Match
Best Local Similarity 70.0%; Score 42; DB 7; Length 473;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 YYYFGLDV 11
|||:|:|
Db 129 YYYGMDV 136
```

```
RESULT 9
US-11-144-248-20
Sequence 20, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-20
```

```
Query Match
Best Local Similarity 66.7%; Score 40; DB 7; Length 113;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 ATYYFGLDV 11
:::|:|:|
Db 93 SSFYFGMDV 102
```

```
RESULT 10
US-11-017-550-42
Sequence 42, Application US/11017550
Publication No. US20050250183A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
```

APPLICANT: Anderson, John C
APPLICANT: Chiu, Jason
APPLICANT: Liu, David R
APPLICANT: Magliery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Mehl, Ryan A
APPLICANT: Pastinak, Miro
APPLICANT: Santoro, Stephen W
APPLICANT: Zhang, Zhilwen
TITLE OF INVENTION: In vivo incorporation of unnatural amino acids
FILE REFERENCE: 34-00120US
CURRENT APPLICATION NUMBER: US/11/017,550
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/126,927
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 306
TYPE: PRT
ORGANISM: Methanococcus jannaschii
US-11-017-550-42

Query Match 60.0%; Score 36; DB 7; Length 306;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 TYYFGADV 11
DB 158 TYYAGVDV 166

RESULT 11
US-10-639-799-112
Sequence 112, Application US/10839799
Publication No. US20050249726A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/839,799
FILING DATE: 06-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,265
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-839-799-112

Query Match 58.3%; Score 35; DB 1; Length 87;
Best Local Similarity 75.0%; Pred. No. 1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LATYYFG 8
DB 72 LATYCFG 79

RESULT 12
US-10-721-763-29
Sequence 29, Application US/10721763
Publication No. US20050249729A1
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
FILE REFERENCE: PH-1573-PCT
CURRENT APPLICATION NUMBER: US/10/721,763
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: JP2001-150213
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: JP2001-243040
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: JP2001-314489
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-721-763-29

Query Match 58.3%; Score 35; DB 1; Length 145;
Best Local Similarity 71.4%; Pred. No. 1.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 YFYGADV 11
DB 128 YYYGADV 134

RESULT 13
US-10-721-763-25
Sequence 25, Application US/10721763
Publication No. US20050249729A1
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
FILE REFERENCE: PH-1573-PCT
CURRENT APPLICATION NUMBER: US/10/721,763
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: JP2001-150213
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: JP2001-243040
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: JP2001-314489
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
US-10-721-763-25

Query Match 58.3%; Score 35; DB 1; Length 154;
Best Local Similarity 71.4%; Pred. No. 1.8;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 YYYFGLDV 11
||:||||
Db 135 YYYGMDV 141

RESULT 14
US-11-017-550-37
Sequence 37, Application US/11017550
Publication No. US20050250183A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Anderson, John C
APPLICANT: Chin, Jason
APPLICANT: Liu, David R
APPLICANT: Magliery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Mehl, Ryan A
APPLICANT: Pastrnak, Miro
APPLICANT: Sanctoro, Stephen W
APPLICANT: Zhang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/11/017,550
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/126,927
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 306
TYPE: PRT
ORGANISM: Mechanococcus jannaschii
US-11-017-550-37

Query Match 55.0%; Score 33; DB 7; Length 306;
Best Local Similarity 62.5%; Pred. No. 8;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
||:||||
Db 159 YYYGMDV 166

RESULT 15
US-11-022-562-211
Sequence 211, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Rupprecht, Ruth M.
APPLICANT: Shieong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DEN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322

PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 211
LENGTH: 2280
TYPE: PRT
ORGANISM: Hepatitis C Virus
US-11-022-562-211

Query Match 55.0%; Score 33; DB 7; Length 2280;
Best Local Similarity 70.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 ATYYFGLDV 11
||:||||
Db 1414 AVAYYRGLDV 1423

Search completed: November 21, 2005, 12:33:51
Job time : 0.301465 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 18.7436 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-156
Perfect score: 81
Sequence: 1 WVRQAPGKLEWVA 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	81	100.0	14 2 AAR97326	Aar97326 Humanised
2	81	100.0	14 5 Aa017610	Aa017610 Human PAP
3	81	100.0	14 7 ABO33880	Ab033880 Anti-GPI-
4	81	100.0	14 7 AD120633	Ad120633 HPR2 prot
5	81	100.0	14 8 ADR38742	Adr38742 Mouse hea
6	81	100.0	14 8 ADR38754	Adr38754 Mouse hea
7	81	100.0	14 8 ADR38738	Adr38738 Mouse hea
8	81	100.0	14 8 ADR38762	Adr38762 Mouse hea
9	81	100.0	14 8 ADR38766	Adr38766 Mouse hea
10	81	100.0	14 8 ADR38766	Adr38766 Mouse hea
11	81	100.0	14 8 ADR38758	Adr38758 Mouse hea
12	81	100.0	14 8 ADR38750	Adr38750 Mouse hea
13	81	100.0	14 9 ADW96723	Adw96723 Anti-EGFR
14	81	100.0	14 9 ADW96723	Adw96723 Anti-EGFR
15	81	100.0	14 9 ADW80308	Adw80308 Human ant
16	81	100.0	14 9 ADM80285	Adm80285 Human ant
17	81	100.0	14 9 ADY31370	Ady31370 Human ant
18	81	100.0	14 9 ADY31373	Ady31373 Human ant
19	81	100.0	14 9 ADY31400	Ady31400 Human ant
20	81	100.0	14 9 ADZ35836	Adz35836 Anti-gluc
21	81	100.0	14 9 ABA21477	Aba21477 Human ant
22	81	100.0	17 9 ADY31505	Ady31505 Human ant
23	81	100.0	17 9 ADY31532	Ady31532 Human ant
24	81	100.0	17 9 ADY31502	Ady31502 Human ant

25	81	100.0	19 2 AAW94736	Aaw94736 Anti-Strap
26	81	100.0	44 8 ADU87725	Adu87725 Human hea
27	81	100.0	58 9 AEC20858	Aec20858 Human var
28	81	100.0	61 2 AAR76975	Aar76975 HSV-neutr
29	81	100.0	62 2 AAR76976	Aar76976 HSV-neutr
30	81	100.0	66 6 ABUS6837	Abus6837 BONT/A Hc
31	81	100.0	66 6 ABUS6866	Abus6866 BONT/A Hc
32	81	100.0	82 8 ADL35113	Adl35113 Humanised
33	81	100.0	82 8 ADL35115	Adl35115 Humanised
34	81	100.0	82 8 ADL35112	Adl35112 Murine an
35	81	100.0	82 8 ADL35114	Adl35114 Humanised
36	81	100.0	82 8 ADL35117	Adl35117 Humanised
37	81	100.0	82 8 ADL35116	Adl35116 Humanised
38	81	100.0	82 9 ABA21573	Aba21573 Human Ig
39	81	100.0	87 8 ADU87732	Adu87732 Amino aci
40	81	100.0	89 6 AAR35911	Aar35911 Human DP5
41	81	100.0	91 9 ADW97148	Adw97148 Human IL-
42	81	100.0	92 9 ADW97150	Adw97150 Human IL-
43	81	100.0	93 6 ABO27274	Ab027274 Human Hum
44	81	100.0	93 9 ADW97147	Adw97147 Human IL-
45	81	100.0	93 9 ADW97179	Adw97179 Human IL-

ALIGNMENTS

RESULT 1
AAR97326
ID AAR97326 standard; peptide; 14 AA.

AC AAR97326;
DT 15-OCT-1996 (first entry)

DE Humanised monoclonal antibody heavy chain framework region.

KM Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW Complementary determining region; anti-carcinoma/embryonic antigen; CEA;
KM diagnosis; imaging; therapy; immune response.

XX Homo sapiens.

XX W09611013-AL.

XX 18-APR-1996.

XX 28-SEP-1995; 95WO-US011964.

XX 05-OCT-1994; 94US-00318157.

XX (IMMU-) IMMUNOMEDICS INC.

XX Hansen HJ, Armour KL;

XX WPI, 1996-209653/21.

PT New humanised anti-CEA monoclonal antibody - having engrafted murine
CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.

XX Claim 7, Page 39; 62pp; English.

XX New humanised monoclonal antibodies (MAbs) comprising the complementary
determining regions (CDRs) of a parental murine class III anti-
carcinoembryonic (CEA) Mab engrafted to the framework regions (FRs) of a
heterologous antibody which can be derived from any species including
human, retain the anti-CEA binding specificity of the parental murine Mab
but are less immunogenic in a human subject than the parental murine Mab
humanised antibodies can be used in diagnosis, imaging and therapy of CEA
-producing cancers and patients receiving the humanised antibodies and
conjugates show improved therapeutic results, decreased immune responses
and decreased immune-mediated adverse effects compared to the parent
antibody. This sequence corresponds to the second framework region of the
heavy chain of the humanised Mab. See AAR97313-97333

XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLSEWVA 14
Db 1 WVRQAPGKGLSEWVA 14

RESULT 2
AA017610
ID AA017610 standard; peptide; 14 AA.

AC AA017610;

DT 08-AUG-2002 (first entry)

DE Human PAPalpa specific VL region from VH50 FR2 peptide.

XX Human; PAPalpa; fibroblast activating protein alpha; antibody; Ab;
KM gene therapy; cancer; wound healing; inflammation; cytostatic.

XX Homo sapiens.

OS WC000168708-A2.

PN WC000168708-A2.

XX 20-SEP-2001.

PF 16-MAR-2001; 2001WO-EP004716.

XX 17-MAR-2000; 2000DE-01013286.

PR 11-SEP-2000; 2000GB-00022216.

XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.

XX Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Merzmann M;

PI Schmidt A;

XX WPI; 2002-041180/05.

DR N-PSDB; AAL46555.

XX New human humanized antibody that specifically binds to fibroblasts

PT activating protein alpha, useful for treating cancer or tumor, and for

PT imaging tumors associated with activated stromal fibroblasts, e.g. lung

PT or breast cancer.

PS Disclosure; Fig 6C; 109pp; English.

XX The present invention relates to a human or humanised antibody (Ab) which

CC specifically binds to fibroblast activating protein alpha (FAPalpa). The

CC antibodies are useful for preparing a composition for the treatment of

CC cancer, and for imaging tumours associated with activated stromal

CC fibroblasts, such as colorectal cancer, non-small-cell lung cancer,

CC breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder

CC cancer, pancreatic cancer and metastatic brain cancer, and diseases

CC associated with the same, such as inflammation and wound healing. The

CC present sequence is a peptide described in the exemplification of the

CC invention

XX Sequence 14 AA;

Query Match 100.0%; Score 81; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLSEWVA 14
Db 1 WVRQAPGKGLSEWVA 14

RESULT 3
AB033890

ID AB033890 standard; peptide; 14 AA.

XX AB033890;

DT 18-SEP-2003 (first entry)

XX Anti-GPI-antibody heavy chain framework region #8.

XX Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;

KM anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;

KM autoimmune disease; rheumatoid arthritis; heavy chain variable region;

XX VH; framework region.

OS Homo sapiens.

PN US2002146753-A1.

XX 10-OCT-2002.

PF 06-APR-2001; 2001US-00828708.

XX 06-APR-2001; 2001US-00828708.

XX (DITZEL) DITZEL H.

PA (BURTON) BURTON D R.

PA (SCHALLER) SCHALLER M.

XX Ditzel H, Burton DR, Schaller M;

XX WPI; 2003-521517/49.

XX Immunopolypeptide for diagnosis and treatment of human autoimmune

PT disease, e.g., human rheumatoid arthritis; comprises a polypeptide that

PT binds to human glucose-6-phosphate isomerase.

XX Claim 6; Fig 4B; 47pp; English.

XX The invention describes an immunopolypeptide comprising a polypeptide

CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and

CC compositions are used for diagnosis and treatment of human autoimmune

CC disease, e.g., human rheumatoid arthritis. This is the amino acid

CC sequence of human anti-GPI-antibody heavy chain variable region framework

CC region

XX Sequence 14 AA;

QY 1 WVRQAPGKGLSEWVA 14

Db 1 WVRQAPGKGLSEWVA 14

RESULT 4
AD120633

ID AD120633 standard; protein; 14 AA.

XX AD120633;

XX 22-APR-2004 (first entry)

XX HFR2 protein.

XX immunoglobulin molecule; heavy chain framework region; HFR1; HFR2; HFR3;

KM HFR4; tumour imaging; protein chips assay; light chain framework region;

XX LFR.

XX Synthetic.

PN WO2003025124-A2.
 XX 27-MAR-2003.
 PD 13-SEP-2002, 2002WO-US029003.
 PF 14-SEP-2001, 2001US-0318904P.
 PR (FRAU-) FRAUNHOFER INST MOLEKULARBIOLOGIE & ANGE.
 XX Zhang MY, Schillberg S, Zimmermann S, Di Fiore S, Emans N;
 PI Fischer R;
 DR WPI: 2003-371805/35.
 N-PSDB; ADI20654, ADI20663, ADI20672.
 PT New immunoglobulin molecule, useful in therapeutic or diagnostic assays
 PT comprising ELISA, phage display, tumor imaging or protein chips assay or
 PT in screening assays for detecting molecules that bind to the
 PT immunoglobulin molecule.
 XX
 PS Claim 7; SEQ ID NO 2; 198pp; English.
 CC The present invention relates to an immunoglobulin molecule comprising of
 CC one or more heavy chain framework regions comprising HFR1, HFR2, HFR3 or
 CC HFR4 and one or more light chain framework regions comprising LFR1, LFR2,
 CC LFR3 or LFR4; and complementarily determining regions (CDRs) comprising
 CC CDR-H1, CDR-H2, CDR-H3 and/or CDR-L1, CDR-L2 or CDR-L3. The immunoglobulin
 CC is useful in therapeutic or diagnostic assays comprising ELISA, phage
 CC display, tumor imaging or protein chips assay. Further, the
 CC immunoglobulin is useful in screening assays for detecting molecules that
 CC bind to the immunoglobulin molecule. The present sequence represents a
 CC chain framework region.
 CC
 SO Sequence 14 AA;
 Query Match 100.0%; Score 81; DB 7; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WVRQAPGKGLWVA 14
 DB 1 WVRQAPGKGLWVA 14
 RESULT 5
 ADR38742
 ID ADR38742 standard; peptide; 14 AA.
 XX ADR38742;
 AC
 XX 02-DEC-2004 (first entry)
 DT
 XX Mouse heavy chain anti-BONT-antibody framework 2 seqid 144.
 DE
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW framework 2.
 KM
 XX Mus sp.
 OS
 XX US2004175385-A1.
 PN
 XX 09-SEP-2004.
 PD
 XX 01-AUG-2003, 2003US-00632706.
 PF
 XX 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 PA (REGC) UNIV CALIFORNIA.
 XX

PI Marks JD, Amersdorfer P;
 XX WPI: 2004-652009/63.
 DR
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 PT
 XX Example 4; SEQ ID NO 144; 110pp; English.
 PS
 XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC 825, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BONT-antibody framework region 2.
 CC
 SO Sequence 14 AA;
 Query Match 100.0%; Score 81; DB 8; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WVRQAPGKGLWVA 14
 DB 1 WVRQAPGKGLWVA 14
 RESULT 6
 ADR38754
 ID ADR38754 standard; peptide; 14 AA.
 XX ADR38754;
 AC
 XX 02-DEC-2004 (first entry)
 DT
 XX Mouse heavy chain anti-BONT-antibody framework 2 seqid 156.
 DE
 XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW framework 2.
 KM
 XX Mus sp.
 OS
 XX US2004175385-A1.
 PN
 XX 09-SEP-2004.
 PD
 XX 01-AUG-2003, 2003US-00632706.
 PF
 XX 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 PA
 XX

XX	(REGC) UNIV CALIFORNIA.
PT	Marks JD, Ameredorfer P;
XX	
DR	WPI; 2004-652009/63.
XX	
PT	New isolated antibody that neutralizes botulinum neurotoxin type A,
PT	useful for diagnosing botulism or for treating pathologies associated
PT	with botulinum neurotoxin poisoning.
XX	
PS	Example 4; SEQ ID NO 156; 110pp; English.
XX	
CC	The invention describes an isolated antibody (I) that specifically binds
CC	to an epitope specifically bound by an antibody expressed by a specific
CC	clone where (I) binds to and neutralizes botulinum neurotoxin type A
CC	(BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC	specifically bound by an antibody expressed by a clone chosen from clone
CC	S25, C25, C39, ICG, 3012, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC	3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
CC	neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC	comprising BONT/A neutralising epitope having an epitope that is
CC	specifically bound by an antibody expressed by clones as mentioned in (I)
CC	; producing (I); and a composition (III) comprising several anti-
CC	-botulinum neurotoxin antibodies, where each antibody is specific for a
CC	different epitope of a botulinum neurotoxin and the combination of
CC	antibodies shows greater toxin neutralisation than the single antibodies
CC	in surplus. The following are disclosed: a pharmaceutical composition
CC	comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC	BONT/A antibody and for neutralising a botulinum neurotoxin which
CC	involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC	specific for a different epitope of the botulinum neurotoxin and the
CC	combination of antibodies shows greater toxin neutralisation than the
CC	single antibodies in surplus. (I) is useful for diagnosing the botulism
CC	or for treating pathologies associated with botulinum neurotoxin
CC	poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC	enables rapid detection or diagnosis of botulism. This is the amino acid
CC	sequence of mouse heavy chain anti-BONT-antibody framework region 2.
XX	
XX	Sequence 14 AA:
QY	Query Match 100.0%; Score 81; DB 8; Length 14;
DB	Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Match	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
DB	1 WVRQAPGKGLMYA 14 1 WVRQAPGKGLMYA 14
RESULT 7	
ID	ADR38738
AD	ADR38738 standard; peptide; 14 AA.
XX	
AC	ADR38738;
DT	02-DEC-2004 (first entry)
XX	
DE	Mouse heavy chain anti-BONT-antibody framework 2 seqid 140.
XX	
KM	antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KM	BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KM	toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KM	framework 2.
OS	Mus sp.
XX	
FN	US2004175385-A1.
PD	09-SEP-2004.
PF	01-AUG-2003; 2003US-00632706.
PR	31-AUG-1998; 98US-00144886.

XX	01-AUG-2002; 2002US-0400721P.
XX	(REGC) UNIV CALIFORNIA.
PA	
P1	Marks JD, Amersdorfer P;
DR	WPI, 2004-652009/63.
XX	
PT	New isolated antibody that neutralizes botulinum neurotoxin type A,
PT	useful for diagnosing botulism or for creating pathologies associated
PT	with botulinum neurotoxin poisoning.
XX	
PS	Example 4; SEQ ID NO 140; 110pp; English.
CC	The invention describes an isolated antibody (I) that specifically binds
CC	to an epitope specifically bound by an antibody expressed by a specific
CC	clone where (I) binds to and neutralises botulinum neurotoxin type A
CC	(BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC	specifically bound by an antibody expressed by a clone chosen from clone
CC	S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, MR1(V), MR1(T), 3-1,
CC	3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC	neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC	comprising BoNT/A neutralising epitope having an epitope that is
CC	specifically bound by an antibody expressed by clones as mentioned in (I)
CC	; producing (I); and a composition (III) comprising several anti-
CC	botulinum neurotoxin antibodies, where each antibody is specific for a
CC	different epitope of a botulinum neurotoxin and the combination of
CC	antibodies shows greater toxin neutralisation than the single antibodies
CC	in surplus. The following are disclosed: a pharmaceutical composition
CC	comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC	BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC	involves contracting neurotoxin with (I) in surplus, where each of (I) is
CC	specific for a different epitope of the botulinum neurotoxin and the
CC	combination of antibodies shows greater toxin neutralisation than the
CC	single antibodies in surplus. (II) is useful for diagnosing the botulism
CC	or for treating pathologies associated with botulinum neurotoxin
CC	poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC	enables rapid detection or diagnosis of botulism. This is the amino acid
CC	sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX	
SQ	Sequence 14 AA;
	Query Match 100.0%; Score 81; DB 8; Length 14;
	Best Local Similarity 100.0%; Pred. NO. 3.2e-05; Indels 0; Gaps 0;
	Matches 14; Conservative 0; Mismatches 0;
OY	1 WVROAPGGKLEWVA 14 1 WVRQAPKGLEWVA 14
DB	
RESULT 8	
ADNR38762	
ID	ADR38762 standard; peptide; 14 AA.
AC	ADR38762;
XX	
DT	02-DEC-2004 (first entry)
DE	Mouse heavy chain anti-BoNT-antibody framework 2 seqid 164.
XX	
KV	antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW	BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KX	toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain; framework 2.
XX	
OS	Mus sp.
XX	
PN	US2004175385-A1.
XX	
PD	09-SEP-2004.
XX	
PF	01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-0014486.
 PR 01-AUG-2002; 2002US-0400721P.
 XX (REGC) UNIV CALIFORNIA.
 PA Marks JD, Amerdorfer P;
 PI WPI; 2004-652009/63.
 XX
 XX
 DR WPI; 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX
 XX

Example 4; SEQ ID NO 164; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.

XX Sequence 14 AA;

SO Query Match 100.0%; Score 81; DB 8; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKLEWVA 14
 |||||
 DB 1 WVRQAPGKLEWVA 14

RESULT 9
 ADR38746

ID ADR38746 standard; peptide; 14 AA.

XX ADR38746;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 148.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;

KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KM framework 2.

OS Mus sp.

XX US2004175385-A1.

PN 09-SEP-2004.

PD

XX 01-AUG-2003; 2003US-00632706.

PF 31-AUG-1998; 98US-0014486.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

PA Marks JD, Amerdorfer P;

PI WPI; 2004-652009/63.

XX

DR WPI; 2004-652009/63.

XX

PT New isolated antibody that neutralizes botulinum neurotoxin type A,

PT useful for diagnosing botulism or for treating pathologies associated

PT with botulinum neurotoxin poisoning.

XX

Example 4; SEQ ID NO 148; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.

XX Sequence 14 AA;

SO Query Match 100.0%; Score 81; DB 8; Length 14;

Best Local Similarity 100.0%; Pred. No. 3.2e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKLEWVA 14
 |||||
 DB 1 WVRQAPGKLEWVA 14

RESULT 10
 ADR38766

ID ADR38766 standard; peptide; 14 AA.

XX ADR38766;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 168.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;

KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KM framework 2.

OS Mus sp.

XX US2004175385-A1.

PN

```

XX PD 09-SEP-2004.
XX PF 01-AUG-2003; 2003US-00632706.
XX PR 31-AUG-1998; 98US-00144886.
XX PR 01-AUG-2002; 2002US-0400721P.
XX (REGC ) UNIV CALIFORNIA.
XX PA Marks JD, Amersdorfer P;
XX PI WPI; 2004-652009/63.
XX DR
XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.
XX PS Example 4; SEQ ID NO 168; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BONT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BONT-antibody framework region 2.
XX
SQ Sequence 14 AA;
XX
Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKGLMWYA 14
DB 1 WVRQAPGKGLMWYA 14

```

```

XX XX US2004175385-A1.
XX PN
XX PD 09-SEP-2004.
XX PF 01-AUG-2003; 2003US-00632706.
XX PR 31-AUG-1998; 98US-00144886.
XX PR 01-AUG-2002; 2002US-0400721P.
XX (REGC ) UNIV CALIFORNIA.
XX PA Marks JD, Amersdorfer P;
XX PI WPI; 2004-652009/63.
XX DR
XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.
XX PS Example 4; SEQ ID NO 160; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BONT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BONT-antibody framework region 2.
XX
SQ Sequence 14 AA;
XX
Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKGLMWYA 14
DB 1 WVRQAPGKGLMWYA 14

```

```

RESULT 11
ADR38758
ID ADR38758 standard; peptide; 14 AA.
XX
AC ADR38758;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BONT-antibody framework 2 segid 160.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
MS Mus sp.

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RESULT 12
ADR38750
ID ADR38750 standard; peptide; 14 AA.
XX
AC ADR38750;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BONT-antibody framework 2 segid 152.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.

```

XX Mus sp.
 XX US2004175385-A1.
 XX
 XX 09-SEP-2004.
 XX
 XX 01-AUG-2003; 2003US-00632706.
 XX
 XX 31-AUG-1998; 98US-00144886.
 XX 01-AUG-2002; 2002US-0400721P.
 XX (R8GC) UNIV CALIFORNIA.
 XX
 XX Marks JD, Amersdorfer P;
 XX WPI; 2004-652009/63.
 XX
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 XX useful for diagnosing botulism or for treating pathologies associated
 XX with botulinum neurotoxin poisoning.
 XX
 XX Example 4; SEQ ID NO 152; 110pp; English.
 XX
 XX The invention describes an isolated antibody (I) that specifically binds
 XX to an epitope specifically bound by an antibody expressed by a specific
 XX clone where (I) binds to and neutralizes botulinum neurotoxin type A
 XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 XX specifically bound by an antibody expressed by a clone chosen from clone
 XX 525, C35, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 XX 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 XX comprising BONT/A neutralising epitope having an epitope that is
 XX specifically bound by an antibody expressed by clones as mentioned in (I)
 XX ; producing (I); and a composition (III) comprising several anti-
 XX botulinum neurotoxin antibodies, where each antibody is specific for a
 XX different epitope of a botulinum neurotoxin and the combination of
 XX antibodies shows greater toxin neutralisation than the single antibodies
 XX in surplus. The following are disclosed: a pharmaceutical composition
 XX comprising (I); and a kit comprising (I). (I) is useful for neutralising
 XX BONT/A antibody and for neutralising a botulinum neurotoxin which
 XX involves contacting neurotoxin with (I) in surplus, where each of (I) is
 XX specific for a different epitope of the botulinum neurotoxin and the
 XX combination of antibodies shows greater toxin neutralisation than the
 XX single antibodies in surplus. (I) is useful for diagnosing the botulism
 XX or for treating pathologies associated with botulinum neurotoxin
 XX poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 XX enables rapid detection or diagnosis of botulism. This is the amino acid
 XX sequence of mouse heavy chain anti-BONT-antibody framework region 2.
 XX
 XX Sequence 14 AA;
 XX
 XX Query Match 100.0%; Score 81; DB 8; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 WYRQAPGKGLBMYA 14
 XX | | | | | | | | | | | | | |
 XX DB 1 WYRQAPGKGLBMYA 14
 XX
 XX RESULT 13
 XX ADM96736
 XX ID ADM96736 standard; peptide; 14 AA.
 XX AC ADM96736;
 XX DT 21-APR-2005 (first entry)
 XX
 XX Anti-EGFRvIII antibody 13.1.2 VH peptide #3.
 XX
 XX Monoclonal antibody; diagnosis; therapy; cancer; tumor; carcinoma;
 XX glioma; neoplasm; cytostatic; epidermal growth factor receptor;
 XX

KM heavy chain variable region.
 XX Homo sapiens.
 XX OS
 XX WO2005012479-A2.
 XX
 XX 10-FEB-2005.
 XX
 XX 25-JUN-2004; 2004WO-US020564.
 XX
 XX 27-JUN-2003; 2003US-0483145P.
 XX 26-NOV-2003; 2003US-0525570P.
 XX 15-APR-2004; 2004US-0562453P.
 XX (ABGE-) ABGENIX INC.
 XX
 XX Weber R, Feng X, Foord O, Green L, Gudae J, Keyt B, Liu Y,
 XX Rathnaswami P, Raya R, Yang XD, Corvalan J, Foltz I, Jia X,
 XX Kang J, King CT, Klakamp SL, Su QY;
 XX WPI; 2005-142884/15.
 XX
 XX New human monoclonal antibodies directed against type III deletion
 XX mutants of epidermal growth factor receptor (EGFRvIII), useful for
 XX diagnosing, preventing or treating diseases associated with EGFRvIII
 XX expression, e.g. cancer.
 XX
 XX Example 17; SEQ ID NO 122; 207pp; English.
 XX
 XX The invention relates to an isolated human monoclonal antibody, or its
 XX variant, directed against deletion mutants of epidermal growth factor
 XX receptor, particularly to the type III deletion mutant (EGFRvIII). Also
 XX included are a hybridoma cell line producing the above antibody, a
 XX transformed cell comprising a gene encoding the antibody, an isolated
 XX polynucleotide molecule comprising a nucleotide sequence encoding a heavy
 XX or light chain amino acid sequence (or its fragment), an article of
 XX manufacture (comprising a container, a composition contained in the
 XX container, and a package insert or label indicating that the composition
 XX can be used to treat cancer characterized by the expression of EGFRvIII,
 XX where the composition comprises the antibody cited above), an assay kit
 XX for the detection of EGFRvIII in mammalian tissues or cells (to screen
 XX for lung, colon, gastric, renal, prostate or ovarian carcinomas, the
 XX EGFRvIII being an antigen expressed by epithelial cancers, the kit
 XX comprising an antibody that binds the antigen protein and means for
 XX indicating the reaction of the antibody with the antigen, if present), a
 XX purified protein variant of EGFRvIII, selecting variants of antibodies to
 XX EGFRvIII, making antibody variants to EGFRvIII and killing a targeted
 XX cell. The composition and methods are useful for diagnosing, preventing
 XX or treating diseases associated with the expression of EGFRvIII, such as
 XX cancer, gliomas, tumors and carcinomas. The present sequence is a peptide
 XX derived from a VH region of an anti-EGFRvIII antibody of the invention
 XX used to determine the antibody structure.
 XX
 XX Sequence 14 AA;
 XX
 XX Query Match 100.0%; Score 81; DB 9; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 WYRQAPGKGLBMYA 14
 XX | | | | | | | | | | | | | |
 XX DB 1 WYRQAPGKGLBMYA 14
 XX
 XX RESULT 14
 XX ADM96723
 XX ID ADM96723 standard; peptide; 14 AA.
 XX AC ADM96723;
 XX DT 21-APR-2005 (first entry)
 XX

DE Anti-EGFRvIII antibody 131 VH peptide #3.
XX Monoclonal antibody; diagnosis; therapy; cancer; tumor; carcinoma;
KW glioma; neoplasm; cytostatic; epidermal growth factor receptor;
XX heavy chain variable region.
XX Homo sapiens.
PN NC02005012479-A2.
XX
XX 10-FEB-2005.
PD
XX 25-JUN-2004; 2004MO-US020564.
PF
XX 27-JUN-2003; 2003JUS-0483145P.
PR 26-NOV-2003; 2003JUS-0525570P.
PR 15-APR-2004; 2004US-0562453P.
XX
XX (ABGE-) ABGENIX INC.
PA
PI Weber R, Feng X, Foord O, Green L, Gudas J, Keyt B, Liu Y;
PI Rathanaswami P, Raya R, Yang XD, Corvalan J, Foltz I, Jia X;
PI Kang J, King CT, Klakamp SL, Su QJ;
XX WPI; 2005-142884/15.
DR
XX
XX New human monoclonal antibodies directed against type III deletion
PT mutants of epidermal growth factor receptor (EGFRvIII), useful for
PT diagnosing, preventing or treating diseases associated with EGFRvIII
PT expression, e.g. cancer.
XX
XX
XX Example 16; SEQ ID NO 109; 207pp; English.
XX
XX The invention relates to an isolated human monoclonal antibody, or its
CC variant, directed against deletion mutants of epidermal growth factor
CC receptor, particularly to the type III deletion mutant (EGFRvIII). Also
CC included are a hybridoma cell line producing the above antibody, a
CC transformed cell comprising a gene encoding the antibody, inhibiting cell
CC proliferation associated with the expression of EGFRvIII, an isolated
CC polynucleotide molecule comprising a nucleotide sequence encoding a heavy
CC or light chain amino acid sequence (or its fragment), an article of
CC manufacture (comprising a container, a composition contained in the
CC container, and a package insert or label indicating that the composition
CC can be used to treat cancer characterized by the expression of EGFRvIII,
CC where the composition comprises the antibody cited above), an assay kit
CC for the detection of EGFRvIII in mammalian tissues or cells (to screen
CC for lung, colon, gastric, renal, prostate or ovarian carcinomas, the
CC EGFRvIII being an antigen expressed by epithelial cancers, the kit
CC comprising an antibody that binds the antigen protein and means for
CC indicating the reaction of the antibody with the antigen, if present), a
CC purified protein variant of EGFRvIII, selecting variants of antibodies to
CC EGFRvIII, making antibody variants to EGFRvIII and killing a targeted
CC cell. The composition and methods are useful for diagnosing, preventing
CC or treating diseases associated with the expression of EGFRvIII, such as
CC cancer, gliomas, tumors and carcinomas. The present sequence is a peptide
CC derived from a VH region of an anti-EGFRvIII antibody of the invention
CC used to determine the antibody structure.
XX
XX
SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 81; DB 9; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWVA 14
|||
Db 1 WVRQAPGKGLWVA 14

RESULT 15
ADM80308
ID ADM80308 standard; peptide; 14 AA.
XX

AC ADM80308;
XX
XX 21-APR-2005 (first entry)
DT
XX
XX Human anti-EGFRvIII antibody 13.1.2 VH peptide - SEQ ID 122.
DE
XX cell death; monoclonal antibody; toxin; cytostatic; cancer; neoplasm;
KW lung tumor; colon tumor; stomach tumor; renal tumor; prostatic cancer;
KW breast tumor; ovary tumor; epidermal growth factor receptor; EGFRvIII;
XX heavy chain variable region.
XX
XX Homo sapiens.
OS
XX
XX NC02005010151-A2.
PN
XX
XX 03-FEB-2005.
PD
XX
XX 25-JUN-2004; 2004MO-US020295.
PF
XX
XX 27-JUN-2003; 2003JUS-0483145P.
PR 26-NOV-2003; 2003JUS-0525570P.
PR 15-APR-2004; 2004US-0562453P.
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Weber R, Feng X, Foord O, Green L, Gudas J, Keyt B, Liu Y;
PI Rathanaswami P, Raya R, Yang XD, Corvalan J, Foltz I, Jia X;
PI Kang J, King CT, Klakamp SL, Su QJ;
XX WPI; 2005-123139/13.
DR
XX
XX New isolated antibody that binds to epidermal growth factor receptor type
PT III mutant EGFRvIII and being conjugated to therapeutic agent such as
PT toxin, useful for inhibiting cell proliferation associated with
PT expression of EGFRvIII.
XX
XX Example 18; SEQ ID NO 122; 233pp; English.
XX
XX The invention relates to a novel method for killing a target cell. The
CC method comprises contacting the cell with an isolated antibody or its
CC fragment that binds to epidermal growth factor receptor type III deletion
CC mutant (EGFRvIII), the antibody being conjugated to a therapeutic agent,
CC which is a toxin chosen from ABPP, MMAE, AURISTATIN B, DM-1 and ZAP, and
CC where the antibody comprises a heavy chain amino acid sequence chosen
CC from antibodies 13.1.2, 131, 170, 150, 085, 250. EGFR variants are caused
CC by gene rearrangement accompanied by gene amplification. Eight major
CC variants of EGFR are known. EGFRvIII, which is the most commonly
CC occurring variant of EGFR in human cancers, comprises a 267 aa in-frame
CC deletion in the extracellular domain. The method of the invention
CC demonstrates cytostatic activity and may be useful for inhibiting cell
CC proliferation associated with the expression of EGFRvIII or for
CC inhibiting cell proliferation of cells expressing EGFRvIII. As such the
CC method may be utilized, in vivo, on a mammal e.g. human, suffering from
CC an epithelial cell cancer such as lung, colon, gastric, renal, prostate,
CC breast, glioblastoma or ovarian carcinoma. The current sequence is that
CC of a human anti-epidermal growth factor receptor type III variant
CC (EGFRvIII) antibody 13.1.2 heavy chain variable region peptide of the
CC invention.
XX
XX
SQ Sequence 14 AA;
XX
XX Query Match 100.0%; Score 81; DB 9; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLWVA 14
|||
Db 1 WVRQAPGKGLWVA 14

Search completed: November 21, 2005, 12:20:01
Job time : 19.7436 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 3.41026 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-156
Perfect score: 81
Sequence: 1 WVRQAPGKLEWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	81	100.0	94 2 PL0120	Ig heavy chain V-I
2	81	100.0	96 2 PH0873	Ig heavy chain V-I
3	81	100.0	97 2 S44115	Ig heavy chain V-I
4	81	100.0	97 2 PH0872	Ig heavy chain V-I
5	81	100.0	98 2 PL0116	Ig heavy chain V-I
6	81	100.0	98 2 S29543	Ig heavy chain V-I
7	81	100.0	98 2 PL0123	Ig heavy chain V-I
8	81	100.0	98 2 S29546	Ig heavy chain V-I
9	81	100.0	99 2 S20765	Ig heavy chain V-I
10	81	100.0	100 2 S26462	Ig heavy chain V-I
11	81	100.0	101 2 B42575	Ig heavy chain V-I
12	81	100.0	108 2 PH1642	Ig heavy chain V-I
13	81	100.0	109 2 PH1646	Ig heavy chain V-I
14	81	100.0	109 2 PH1644	Ig heavy chain V-I
15	81	100.0	110 2 PH1655	Ig heavy chain V-I
16	81	100.0	110 2 PH1092	Ig heavy chain V-I
17	81	100.0	110 2 PH1091	Ig heavy chain V-I
18	81	100.0	111 2 PH1643	Ig heavy chain V-I
19	81	100.0	111 2 PH1645	Ig heavy chain V-I
20	81	100.0	113 2 S57440	Ig heavy chain V-I
21	81	100.0	113 2 S57441	Ig heavy chain V-I
22	81	100.0	113 2 S38490	Ig heavy chain V-I
23	81	100.0	114 2 PH1658	Ig heavy chain V-I
24	81	100.0	114 2 PH1657	Ig heavy chain V-I
25	81	100.0	114 2 S46390	Ig heavy chain V-I
26	81	100.0	114 2 S46391	Ig heavy chain V-I
27	81	100.0	114 2 S46392	Ig heavy chain V-I
28	81	100.0	114 2 S36280	Ig heavy chain V-I
29	81	100.0	115 2 S36284	Ig heavy chain V-I

30	81	100.0	115 2 S57445	Ig heavy chain V-I
31	81	100.0	115 2 S36267	Ig heavy chain V-I
32	81	100.0	116 1 M3H0U1	Ig heavy chain V-I
33	81	100.0	117 1 G1H0W5	Ig heavy chain V-I
34	81	100.0	117 2 S17079	Ig heavy chain V-I
35	81	100.0	117 2 S36270	Ig heavy chain V-I
36	81	100.0	117 2 S78486	Ig heavy chain V-I
37	81	100.0	118 2 S31677	Ig heavy chain V-I
38	81	100.0	118 2 PH1660	Ig heavy chain V-I
39	81	100.0	118 2 PH1662	Ig heavy chain V-I
40	81	100.0	118 2 S31116	Ig heavy chain V-I
41	81	100.0	119 1 G1H0N1	Ig heavy chain V-I
42	81	100.0	119 1 M3H0U1	Ig heavy chain V-I
43	81	100.0	119 1 M3H0U1	Ig heavy chain V-I
44	81	100.0	119 2 S31111	Ig heavy chain V-I
45	81	100.0	119 2 A27630	Ig heavy chain pre

ALIGNMENTS

RESULT 1
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C/Accession: PL0120
R/Bird, J.; Galli, N.; Link, M.; Stiles, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A/Reference number: PL0116, MUID:88286083, PMID:2840480
A/Accession: PL0120
A/Molecule type: mRNA
A/Residues: 1-94 <BIR>
A/Cross-references: UNIPROT:Q8WUK1, UNIPROT:Q9UNJ3, UNIPARC:UPI0000176A2C
A/Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A/Note: The sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f
C/Superfamily: Immunoglobulin homology
C/Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F/31-35/Region: complementarity-determining 1
F/49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. NO. 4.6e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKLEWVA 14
DB 36 WVRQAPGKLEWVA 49

RESULT 2
PH0873
Ig heavy chain V region (anti-DNA, I-2a) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
C/Accession: PH0873
R/Mahleiner-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A/Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.
A/Reference number: PH0863, MUID:92078875, PMID:1660528
A/Accession: PH0873
A/Molecule type: DNA
A/Residues: 1-96 <MAN>
A/Cross-references: UNIPARC:UPI0000176C02
A/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/14-96/Domain: immunoglobulin homology <IMM>
F/30-35/Region: complementarity-determining 1
F/49-66/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 96;

Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | |
Db 35 WVRQAPGKGLWVA 48

RESULT 3

S4415

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C/Accession: S4415

R/Hawkins, R.B.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

Submitted to the EMBL Data Library, March 1994

A/Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable r

A/Reference number: S44105

A/Accession: S4415

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-97 <MAN>

A/Cross-references: UNIPARC:UPI000011662B; EMBL:Z31384; NID:G472969; PIDN:CAA8359.1; PI

C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 81; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 4

PH0872

Ig heavy chain V region (anti-DNA, III-3R) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004

C/Accession: PH0872

R/Mahleimer-Lory, A.; Katz, J.B.; Pillingner, M.; Ghoseain, C.; Smith, A.; Diamond, B.

J. Exp. Med. 174, 1639-1652, 1991

A/Title: Molecular characterization of antibodies bearing an anti-DNA-associated idiotype

A/Reference number: PH0862; MUID:92078875; PMID:1660528

A/Accession: PH0872

A/Molecule type: DNA

A/Residues: 1-97 <MAN>

A/Cross-references: UNIPROT:Q9ULB6; UNIPARC:UPI0000176C04

A/Note: a "G" was inserted at the position of between 72nd and 73rd of the DNA sequence

C/Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/14-97/Domain: immunoglobulin homology <IMM>

F/30-35/Region: complementarity-determining 1

F/49-66/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | |
Db 35 WVRQAPGKGLWVA 48

RESULT 5

Ig heavy chain V-III region (AW-Vx) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999

C/Accession: PL0116; S26892

R/Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A/Reference number: PL0116; MUID:88286083; PMID:2840480

A/Accession: PL0116

A/Molecule type: mRNA

A/Residues: 1-98 <BIR>

A/Cross-references: UNIPARC:UPI0000031F3A

A/Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL

A/Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement fr

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885; MUID:93021117; PMID:1404388

A/Accession: S26892

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Cross-references: UNIPARC:UPI0000031F3A; EMBL:Z12349; NID:G32918; PIDN:CAA78219.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

F/31-35/Region: complementarity-determining 1

F/49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 6

S29543

Ig heavy chain V region (COS 3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999

C/Accession: S29543

R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.

Submitted to the EMBL Data Library, October 1992

A/Reference number: S29543

A/Accession: S29543

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Cross-references: UNIPARC:UPI000011649C; EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | | | | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 7

PL0123

Ig heavy chain V-III region (TD-Vr) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999

C/Accession: PL0123; S26897

R/Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A/Reference number: PL0116; MUID:88286083; PMID:2840480

A/Accession: PL0123

A/Molecule type: mRNA

A/Residues: 1-98 <BIR>

A/Cross-references: UNIPARC:UPI0000116413

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
 A:Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117; PMID:1404388
 A:Accession: S26897
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 A:Cross-references: UNIPARC:UPI0000116413; EMBL:Z12354; NID:G32930; PIDN:CAA78224.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14
 |||||
 Db 36 WVRQAPGKGLWVA 49

RESULT 8

IG heavy chain V region (COS-8 / DP-46) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S29546; S26888
 R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S29543
 A:Accession: S29546
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 A:Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PID
 A:Note: designated COS-8
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germ-line V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117; PMID:1404388
 A:Accession: S26888
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <TOM>
 A:Cross-references: UNIPARC:UPI000002DD16; EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID
 A:Note: designated DP-46
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14
 |||||
 Db 36 WVRQAPGKGLWVA 49

RESULT 9

IG heavy chain V region - human

C:Species: Homo sapiens (man)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C:Accession: S20765
 R:Mortari, F.; Wang, J.; Schroeder, H.W.
 submitted to the EMBL Data Library, April 1992
 A:Description: Analysis of human cord blood Ig heavy chain IGA and IGG repertoire.
 A:Reference number: S20764

A:Accession: S20765
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-99 <MO>
 A:Cross-references: UNIPARC:UPI0000116387; EMBL:Z11943; NID:G33858; PIDN:CAA78000.1; PID:
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 81; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14
 |||||
 Db 12 WVRQAPGKGLWVA 25

RESULT 10

IG heavy chain V region - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
 C:Accession: S26462
 R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991
 A:Reference number: S26459
 A:Accession: S26462
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-100 <KAN>
 A:Cross-references: UNIPARC:UPI0000176E5E; EMBL:X59104; NID:G51920; PID:G51921
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14
 |||||
 Db 28 WVRQAPGKGLWVA 41

RESULT 11

IG heavy chain V region (anti-angiotensin II) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: B42575
 R:Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.
 Science 257, 528-531, 1992
 A:Title: Recognition of angiotensin II antibodies at different levels of an idiotypic re
 A:Reference number: A42575; MUID:92342952; PMID:1636087
 A:Accession: B42575
 A:Molecule type: mRNA
 A:Residues: 1-101 <GAR>
 A:Cross-references: UNIPARC:UPI00001153E9; GJ:S40679; NID:G252098; PIDN:AAB32669.1; PID:G
 A:Experimental source: BALB/c mice, myeloma cell line NS-1
 A:Note: sequence extracted from NCBI backbone (NCBIN:109337, NCBID:109338)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:7-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 5e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLWVA 14
 |||||
 Db 28 WVRQAPGKGLWVA 41

RESULT 12

PH1642
Ig heavy chain V region (clone 5A10) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C/Accession: PH1642
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1642
A/Molecule type: mRNA
A/Residues: 1-108 <HIL>
A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B78
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14
|||||

DB 28 WVRQAPGKGLWYA 41

RESULT 13

PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C/Accession: PH1646
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1646
A/Molecule type: mRNA
A/Residues: 1-109 <HIL>
A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B7C
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14
|||||

DB 28 WVRQAPGKGLWYA 41

RESULT 14

PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C/Accession: PH1644
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1644
A/Molecule type: mRNA
A/Residues: 1-109 <HIL>
A/Cross-references: UNIPROT:Q9UL93; UNIPARC:UPI0000176B7A
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14
|||||

DB 28 WVRQAPGKGLWYA 41

RESULT 15

PH1655
Ig heavy chain V region (clone 2B8) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH1655
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1655
A/Molecule type: mRNA
A/Residues: 1-110 <HIL>
A/Cross-references: UNIPARC:UPI0000176BDC
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWYA 14
|||||

DB 28 WVRQAPGKGLWYA 41

Search completed: November 21, 2005, 12:22:15
Job time : 4.41026 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 20.7179 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-156
Perfect score: 81
Sequence: 1 WVRQAPGKGLWVA 14

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	81	100.0	Q9ULB6_HUMAN	Q9ULB6 homo sapien
2	81	100.0	Q9UL90_HUMAN	Q9UL90 homo sapien
3	81	100.0	HV3T_HUMAN	P01781 homo sapien
4	81	100.0	Q9UL53_HUMAN	Q9UL53 homo sapien
5	81	100.0	HV3O_HUMAN	P01776 homo sapien
6	81	100.0	HV3M_HUMAN	P01770 homo sapien
7	81	100.0	HV3N_HUMAN	P01775 homo sapien
8	81	100.0	HV3J_HUMAN	P01771 homo sapien
9	81	100.0	Q9UL84_HUMAN	Q9UL84 homo sapien
10	81	100.0	HV3K_HUMAN	P01772 homo sapien
11	81	100.0	HV01_RAT	P01805 rattus norv
12	81	100.0	Q65ZC9_HUMAN	Q65ZC9 homo sapien
13	81	100.0	Q6N093_HUMAN	Q6N093 homo sapien
14	81	100.0	Q6P6C4_HUMAN	Q6P6C4 homo sapien
15	81	100.0	Q6R1A4_HUMAN	Q6R1A4 homo sapien
16	81	100.0	Q6R1A4_MOUSE	Q6R1A4 mus musculu
17	81	100.0	Q6P055_HUMAN	Q6P055 homo sapien
18	81	100.0	Q6P181_HUMAN	Q6P181 homo sapien
19	81	100.0	Q6MZX9_HUMAN	Q6MZX9 homo sapien
20	81	100.0	Q6ZVX0_HUMAN	Q6ZVX0 homo sapien
21	81	100.0	Q6P195_HUMAN	Q6P195 homo sapien
22	81	100.0	Q8WTK1_HUMAN	Q8WTK1 homo sapien
23	81	100.0	Q4T5S4_TETNG	Q4T5S4 tetraodon n
24	80	98.8	Q4S2P9_TETNG	Q4S2P9 tetraodon n
25	80	98.8	Q6B6V3_RABIT	Q6B6V3 oryctolagus
26	80	98.8	Q6B6W5_RABIT	Q6B6W5 oryctolagus
27	80	98.8	Q6B6S4_RABIT	Q6B6S4 oryctolagus
28	80	98.8	Q6B6S7_RABIT	Q6B6S7 oryctolagus
29	80	98.8	Q4T5M5_TETNG	Q4T5M5 tetraodon n
30	80	98.8	HV3L_HUMAN	P01773 homo sapien
31	80	98.8		

ALIGNMENTS

RESULT 1			
ID	Q9ULB6_HUMAN	PRELIMINARY;	PRT; 95 AA.
AC	Q9ULB6		
DT	01-MAY-2000 (TRENBLREL.13, Created)		
DT	01-MAY-2000 (TRENBLREL.13, Last sequence update)		
DT	01-MAR-2004 (TRENBLREL.26, Last annotation update)		
DS	Immunoglobulin heavy chain (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Tange Y., Kayano H.;		
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed:1660528;		
RA	Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A., Diamond B.;		
RT	"Molecular characteristics of antibodies bearing an anti-DNA-associated idotype."		
RT	J. Exp. Med. 174:1639-1652(1991).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed:7679990;		
RA	Griffiths A.D., Malmqvist M., Marks J.D., Bye J.M., Embleton M.J., Hughes-Jones N.C.;		
RT	"Human anti-self antibodies with high specificity from phage display libraries."		
RT	EMBO J. 12:725-734(1993).		
RL	EMBL, AB035268; BAAB7067.1; -, Genomic DNA.		
DR	PIR; PH0872; PH0872.		
DR	PIR; S36280; S36280.		
DR	HSSP; P01820; I67J.		
DR	InterPro; IPR007110; IG-1-like.		
DR	InterPro; IPR003596; IG_v.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS50835; IG_LIKE; 1.		
FT	NON_TER 1		
FT	NON_TER 1		
SQ	SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;		
Query Match			
Best Local Similarity 100.0%; Pred. No. 2.6e-05; Length 95;			
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 WVRQAPGKGLWVA 14		
Db			
	35 WVRQAPGKGLWVA 48		

32	80	98.8	124	2	Q9N0M4_RABIT	Q9N0M4 oryctolagus
33	80	98.8	124	2	Q9N0M6_RABIT	Q9N0M6 oryctolagus
34	80	98.8	479	2	Q5P0K9_RAT	Q5P0K9 rattus norv
35	80	98.8	480	2	Q6N094_HUMAN	Q6N094 homo sapien
36	78	96.3	104	2	Q9UL87_HUMAN	Q9UL87 homo sapien
37	78	96.3	112	2	Q9HCC1_HUMAN	Q9HCC1 homo sapien
38	78	96.3	112	2	Q9UGP3_HUMAN	Q9UGP3 homo sapien
39	78	96.3	116	1	HV3R_HUMAN	P01779 homo sapien
40	78	96.3	117	1	HV01_CAICR	P01813 caiman croc
41	78	96.3	117	1	HV3C_CARAU	P19180 carassius a
42	78	96.3	117	1	HV3C_HUMAN	P01764 homo sapien
43	78	96.3	118	2	Q9UL51_HUMAN	Q9UL51 homo sapien
44	78	96.3	121	2	Q9UL71_HUMAN	Q9UL71 homo sapien
45	78	96.3	147	2	Q9Y509_HUMAN	Q9Y509 homo sapien

```

RESULT 2
Q9UL90 HUMAN PRELIMINARY, PRT, 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NCBIOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NCBIOTIDE SEQUENCE.
RX PubMed=1730252;
RA Rasphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -, mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 100.0%; Score 81; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
Db 36 WVRQAPGKGLWVA 49

RESULT 3
HV3T HUMAN STANDARD, PRT, 116 AA.
ID HV3T HUMAN
AC P01781;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region GAL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75059123; PubMed=4803843;
RA Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT "The primary structure of a monoclonal Igm-immunoglobulin
RT (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT type), subgroup H III. Architecture of the complete Igm-molecule.";

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RL Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN [2]
RP SEQUENCE REVISION TO 28-33.
RA Hilschmann N.;
RL Submitted (JUN-1975) to the PIR data bank.
CC -1- MISCELLANEOUS: This mu chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02064; M3HUGL.
DR HSSP; P01772; 2FB4.
DR SMR; P01781; 1-116.
DR GO; GO:0005576; Extracellular region; NAS.
DR GO; GO:0003823; Antigen binding; NAS.
DR GO; GO:0006955; P-immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin domain;
KV Immunoglobulin V region.
FT DOMAIN 1 112
FT NON_TER 116
SQ SEQUENCE 116 AA; 12731 MW; 2C67CA9A9AAA1282 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
Db 36 WVRQAPGKGLWVA 49

RESULT 4
Q9UL93 HUMAN PRELIMINARY, PRT, 116 AA.
ID Q9UL93
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NCBIOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NCBIOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Opliger I.R., Mannik M., Sasse E.H.;
RT "The structural basis of germ-line-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336(1993).
RN [3]
RP NCBIOTIDE SEQUENCE.
RX PubMed=2840480;
RA Bird J., Galili N., Link M., Stites D., Sklar J.;

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RT "Continuing rearrangement but absence of somatic hypermutation in
 RT immunoglobulin genes of human B cell precursor leukemia.";
 RL J. Exp. Med. 168:229-245 (1988).
 DR EMBL: AF035021; AAC56257.1; -, mRNA.
 DR PIR: PH1644; PH1644.
 DR PIR: P0120; P0120.
 DR HSSP: P01772; 2FB4.
 DR SMR: Q9UL93; 1-116.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 FT NON TER 1 116
 FT NON TER 1 116
 SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKLEWVA 14
 |||||
 DB 35 WVRQAPGKLEWVA 48

RESULT 5
 HV30 HUMAN STANDARD; PRT; 117 AA.
 AC P01776;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-II region WAS.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=74142702; PubMed=4522793;
 RA Capra J.D., Kehoe J.M.;
 RT "Variable region sequences of five human immunoglobulin heavy chains
 RT of the VH3 subgroup: definitive identification of four heavy chain
 RT hypervariable regions."
 RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
 CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
 CC protein.
 CC -1- SIMILARITY: Contains 1 Ig-1like (immunoglobulin-like) domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC removed.
 CC PIR: A02059; GIH0WS.
 DR HSSP: P01772; 2FB4.
 DR GO: GO:0005576; C:extracellular region; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DOMAIN 1 112
 FT NON TER 1 117
 FT NON TER 1 117
 SQ SEQUENCE 117 AA; 13091 MW; 201DEF0E1E53D9BF CRC64;

Query Match 100.0%; Score 81; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKLEWVA 14
 |||||
 DB 36 WVRQAPGKLEWVA 49

RESULT 6
 HV31 HUMAN STANDARD; PRT; 119 AA.
 ID HV31 HUMAN STANDARD; PRT; 119 AA.
 AC P01770;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-II region NIE.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=77070269; PubMed=826475;
 RA Ponstingl H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic
 RT peptides of the H-chain, alignment of the tryptic peptides and
 RT discussion of the complete structure."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Drexler L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein NIE). I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges."
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
 CC protein.
 CC -1- SIMILARITY: Contains 1 Ig-1like (immunoglobulin-like) domain.
 CC -----
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 CC removed.
 CC PIR: A91668; GIH0NI.
 DR HSSP: P01772; 2FB4.
 DR SMR: P01770; 1-119.
 DR GO: GO:0005576; C:extracellular region; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-1like.
 DR InterPro: IPR003596; IG_V.
 DR SMART: SM00406; IGV: 1.
 DR PROSITE: PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region; Pyroliidone carboxylic acid.
 FT DOMAIN 1 112
 FT MOD RES 1 112
 FT DISULFID 22 96
 FT NON TER 119 119
 FT NON TER 119 119
 SQ SEQUENCE 119 AA; 13243 MW; C96935A6B55B165B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKLEWVA 14
 |||||
 DB 36 WVRQAPGKLEWVA 49

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RESULT 7
HV3M HUMAN STANDARD; PRT; 119 AA.
ID HV3M HUMAN
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT VARIANT 54 54
FT VARIAT
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12954 MW; 2R018AF4DCBE2610 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 WVRQAPGKGLWVA 14
DB 36 WVRQAPGKGLWVA 49

RESULT 8
HV3M HUMAN STANDARD; PRT; 119 AA.
ID HV3M HUMAN
AC P01775;
DT 21-JUL-1986 (Rel. 01, Created)
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT VARIANT 54 54
FT VARIAT
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12954 MW; 2R018AF4DCBE2610 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 WVRQAPGKGLWVA 14
DB 36 WVRQAPGKGLWVA 49

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OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12858 MW; D6338098794DCFB5 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 WVRQAPGKGLWVA 14
DB 36 WVRQAPGKGLWVA 49

RESULT 9
HV3J HUMAN STANDARD; PRT; 121 AA.
ID HV3J HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
RT "Structure of antibodies with shared idiotypic: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins."
DR GO:0003823; F:antigen binding; NAS.
DR GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 112
FT NON TER 119 119
SQ SEQUENCE 119 AA; 12858 MW; D6338098794DCFB5 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 119;
Best local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 WVRQAPGKGLWVA 14
DB 36 WVRQAPGKGLWVA 49

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DR PIR; A02054; GIHUKL.
DR HSSP; P01772; 2PB4.
DR SMR; P01771; 2-121.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;

Query Match 100.0%; Score 81; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYRQAPGKLEWVA 14
DB 36 WYRQAPGKLEWVA 49

RESULT 10
Q9UL84_HUMAN PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TRENBLREL. 13; Created)
DT 01-MAY-2000 (TRENBLREL. 13; Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25; Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR HSSP; P01772; 2PB4.
DR EMBL; AF035030; AAD56266.1; -; mRNA.
DR SMR; Q9UL84; 1-122.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 121 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D4136545B8 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WYRQAPGKLEWVA 14
DB 36 WYRQAPGKLEWVA 49

RESULT 11
HY3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;

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DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hillechmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguerite M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR PIR; A02055; GIHUKL.
DR PDB; 2PB4; X-ray; H=2-126.
DR PDB; 2IG2; X-ray; H=2-126.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1
FT DISULFID 22 96
FT DISULFID 105 110
FT NON_TER 126 126
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT STRAND 41 42
FT TURN 45 51
FT STRAND 53 54
FT TURN 58 60
FT STRAND 62 64
FT HELIX 65 65
FT STRAND 66 67
FT TURN 68 73
FT STRAND 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

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Query Match 100.0%; Score 81; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
 |||||
 Db 36 WVRQAPGKGLEWVA 49

RESULT 12

HV01 RAT STANDARD; PRT; 142 AA.
 AC P01805;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region IR2 precursor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RX NCBIOTIDE SEQUENCE.
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Petersson U., Engstrom A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 E.";
 RL Nucleic Acids Res. 10:6041-6049 (1982).
 CC -1- MISCELLANEOUS: The mRNA was isolated from an IGH-secreting
 immunocytoma that arises spontaneously in LOU/C/MuL rats.
 CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

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 CC PIR; A02075; EVRTR2.
 DR HSP; P01789; IMCP.
 DR SMR; P01805; 20-141.
 DR Ensembl; ENSRN000000031589; Rattus norvegicus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; Ig_Like; 1.
 DR PROSITE; PS50835; Ig_Like; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 142 Ig heavy chain V region IR2.
 FT DOMAIN 20 133 Ig-like.
 FT NON TER 142 142
 SQ SEQUENCE 142 AA; 16024 MW; D82956CFE745DF3B CRC64;

Query Match 100.0%; Score 81; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
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 Db 55 WVRQAPGKGLEWVA 68

RESULT 13

065ZC9 HUMAN PRELIMINARY; PRT; 240 AA.
 AC 065ZC9;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Single-chain Fv (Fragment).
 GN Name=scfv;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C1q/7;
 RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diadotides.";
 RL Nat. Biotechnol. 15:629-631 (1997).
 DR EMBL; Y13056; CAA73499.1; -; mRNA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00406; Ig; 2.
 DR PROSITE; PS50835; Ig_Like; 2.
 FT NON TER 1 1
 FT NON TER 240 240
 SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645FE4B373 CRC64;

Query Match 100.0%; Score 81; DB 2; Length 240;
 Best Local Similarity 100.0%; Pred. No. 6.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
 |||||
 Db 36 WVRQAPGKGLEWVA 49

RESULT 14

06N093 HUMAN PRELIMINARY; PRT; 417 AA.
 ID 06N093;
 AC 06N093;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp668I04196 (Fragment).
 GN Name=DKFZp668I04196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oanger A.,
 RA Fodor G., Han W., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640623; CAA5777.1; -; mRNA.
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; Ig; 1.
 DR PROSITE; PS50835; Ig_Like; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1 1
 FT NON TER 417 417
 SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;

Query Match 100.0%; Score 81; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLEWVA 14
| | | | | | | | | |
DB 8 WVRQAPGKGLEWVA 21

RESULT 15

06P6C4 HUMAN PRELIMINARY; PRT; 465 AA.
AC 06P6C4
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Raye J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splicein.
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAH62335.1; -, mRNA.
DR HSSP; P01661; IADQ.
DR SMR; 06P6C4; 20-465.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-sect; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS50290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD9348ADC37E6D CRC64;

Query Match 100.0%; Score 81; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WVRQAPGKGLEWVA 14
| | | | | | | | | |
DB 55 WVRQAPGKGLEWVA 68

Search completed: November 21, 2005, 12:04:10
Job time : 21.7179 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 ; Search time 5.28205 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-156

Perfect score: 81

Sequence: 1 WVRQAPGKGLWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/pdata/1/1aa/5-COMB.pep.*
2: /cgn2_6/pdata/1/1aa/6-COMB.pep.*
3: /cgn2_6/pdata/1/1aa/H-COMB.pep.*
4: /cgn2_6/pdata/1/1aa/PCUS-COMB.pep.*
5: /cgn2_6/pdata/1/1aa/BB-COMB.pep.*
6: /cgn2_6/pdata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	14	1	US-08-318-157B-33 Sequence 33, Appl
2	81	100.0	14	2	US-09-534-717-645 Sequence 644, App
3	81	100.0	89	2	US-09-534-717-646 Sequence 645, App
4	81	100.0	95	2	US-09-534-717-647 Sequence 646, App
5	81	100.0	98	1	US-08-211-202-118 Sequence 647, App
6	81	100.0	98	1	US-07-942-245-37 Sequence 648, App
7	81	100.0	98	2	US-10-194-975-15 Sequence 649, App
8	81	100.0	98	2	US-10-194-975-23 Sequence 650, App
9	81	100.0	98	2	US-10-194-975-25 Sequence 651, App
10	81	100.0	98	2	US-10-194-975-26 Sequence 652, App
11	81	100.0	98	2	US-09-534-717-624 Sequence 653, App
12	81	100.0	98	2	US-09-534-717-625 Sequence 654, App
13	81	100.0	98	2	US-09-534-717-626 Sequence 655, App
14	81	100.0	98	2	US-09-534-717-627 Sequence 656, App
15	81	100.0	98	2	US-09-534-717-628 Sequence 657, App
16	81	100.0	98	2	US-09-534-717-629 Sequence 658, App
17	81	100.0	98	2	US-09-534-717-630 Sequence 659, App
18	81	100.0	98	2	US-09-534-717-631 Sequence 660, App
19	81	100.0	98	2	US-09-534-717-632 Sequence 661, App
20	81	100.0	98	2	US-09-534-717-633 Sequence 662, App
21	81	100.0	98	2	US-09-534-717-634 Sequence 663, App
22	81	100.0	98	2	US-09-534-717-635 Sequence 664, App
23	81	100.0	98	2	US-09-534-717-636 Sequence 665, App
24	81	100.0	98	2	US-09-534-717-637 Sequence 666, App
25	81	100.0	98	2	US-09-534-717-640 Sequence 667, App
26	81	100.0	98	2	US-09-534-717-641 Sequence 668, App
27	81	100.0	98	2	US-09-534-717-642 Sequence 669, App

28	81	100.0	98	2	US-09-534-717-644 Sequence 644, App
29	81	100.0	98	2	US-09-534-717-645 Sequence 645, App
30	81	100.0	98	2	US-09-534-717-646 Sequence 646, App
31	81	100.0	98	2	US-09-534-717-647 Sequence 647, App
32	81	100.0	98	2	US-09-534-717-648 Sequence 648, App
33	81	100.0	98	2	US-09-534-717-649 Sequence 649, App
34	81	100.0	98	2	US-09-534-717-650 Sequence 650, App
35	81	100.0	98	2	US-09-534-717-651 Sequence 651, App
36	81	100.0	98	2	US-09-534-717-652 Sequence 652, App
37	81	100.0	98	2	US-09-534-717-653 Sequence 653, App
38	81	100.0	98	2	US-09-534-717-654 Sequence 654, App
39	81	100.0	98	2	US-09-534-717-655 Sequence 655, App
40	81	100.0	98	2	US-09-534-717-656 Sequence 656, App
41	81	100.0	98	2	US-09-534-717-657 Sequence 657, App
42	81	100.0	98	2	US-10-330-613A-61 Sequence 61, Appl
43	81	100.0	98	2	US-10-330-613A-62 Sequence 62, Appl
44	81	100.0	100	2	US-09-840-459-35 Sequence 35, Appl
45	81	100.0	100	2	US-09-497-625A-35 Sequence 35, Appl

ALIGNMENTS

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RESULT 1
US-08-318-157B-33
; Sequence 33, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28, 665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
US-08-318-157B-33

Query Match 100.0% Score 81; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14
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RESULT 2
US-09-253-794-33
; Sequence 33, Application US/09253794
; Patent No. 6676924
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CERA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-253-794-33

Query Match 100.0%; Score 81; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2,9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
Db 1 WVRQAPGKGLWVA 14

RESULT 3
US-09-472-087-72
; Sequence 72, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEYER, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALLAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PPI
; CURRENT APPLICATION NUMBER: US/09/472,087
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; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 72
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-72

Query Match 100.0%; Score 81; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 2,2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
Db 27 WVRQAPGKGLWVA 40

RESULT 4
US-09-534-717-653
; Sequence 653, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfield et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 653
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-653

Query Match 100.0%; Score 81; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2,4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
Db 36 WVRQAPGKGLWVA 49

RESULT 5
US-08-211-202-118
; Sequence 118, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Reneerus Jacobus Matheus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPER, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3866
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-118

Query Match 100.0%; Score 81; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WVRQAPGKGLWVA 14
|||||
Db 36 WVRQAPGKGLWVA 49

RESULT 6

US-07-942-245-37
Sequence 37, Application US/07942245
Patent No. 5639641

GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSER: Sughrie, Mion, Zinn, Macpeak & Seas
CITY: 2100 Pennsylvania Avenue, N.W.
STATE: Washington
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992

CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-37

Query Match 100.0%; Score 81; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WVRQAPGKGLWVA 14
|||||
Db 36 WVRQAPGKGLWVA 49

RESULT 7

US-10-194-975-15
Sequence 15, Application US/10194975
Patent No. 6881557

GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT FILING DATE: 2002-10-10/194,975
PRIOR APPLICATION NUMBER: US/10/194,975
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-15

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 WVRQAPGKGLWVA 14
|||||
Db 36 WVRQAPGKGLWVA 49

RESULT 8

US-10-194-975-23
Sequence 23, Application US/10194975
Patent No. 6881557

GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT FILING DATE: 2002-10-10/194,975
PRIOR APPLICATION NUMBER: US/10/194,975
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 23
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-194-975-23

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKGLWVA 14
| | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 9
US-10-194-975-24
; Sequence 24, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Focote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 10
US-10-194-975-25
; Sequence 25, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Focote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-25

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 11
US-10-194-975-26
; Sequence 26, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Focote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-26

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 12
US-09-534-717-624
; Sequence 624, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-624

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
| | | | |
Db 36 WVRQAPGKGLWVA 49

RESULT 13
US-09-534-717-625
; Sequence 625, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-625

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 WVRQAPGKGLEWVA 14
 |||||
 Db 36 WVRQAPGKGLEWVA 49

RESULT 14

US-09-534-717-626
 ; Sequence 626, Application US/09534717
 ; Patent No. 6914128
 ; GENERAL INFORMATION:
 ; APPLICANT: Jochen, Salfeld et al.
 ; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
 ; FILE REFERENCE: BBI-093CP
 ; CURRENT APPLICATION NUMBER: US/09/534,717
 ; CURRENT FILING DATE: 2000-03-24
 ; EARLIER APPLICATION NUMBER: 60/126,603
 ; EARLIER FILING DATE: March 25, 1999
 ; NUMBER OF SEQ ID NOS: 675
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 626
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-534-717-626

Query Match 100.0%; Score 81; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14
 |||||
 Db 36 WVRQAPGKGLEWVA 49

RESULT 15

US-09-534-717-627
 ; Sequence 627, Application US/09534717
 ; Patent No. 6914128
 ; GENERAL INFORMATION:
 ; APPLICANT: Jochen, Salfeld et al.
 ; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
 ; FILE REFERENCE: BBI-093CP
 ; CURRENT APPLICATION NUMBER: US/09/534,717
 ; CURRENT FILING DATE: 2000-03-24
 ; EARLIER APPLICATION NUMBER: 60/126,603
 ; EARLIER FILING DATE: March 25, 1999
 ; NUMBER OF SEQ ID NOS: 675
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 627
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-534-717-627

Query Match 100.0%; Score 81; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 2.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLEWVA 14
 |||||
 Db 36 WVRQAPGKGLEWVA 49

Search completed: November 21, 2005, 12:07:38
 Job time : 5.28305 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 ; Search time 17.3333 Seconds
(without alignments)
337.478 Million cell updates/sec

Title: US-10-632-706-156
Perfect score: 81
Sequence: 1 WVRQAPKGLMWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	81	100.0	14 3 US-09-253-794-33	Sequence 33, App1
2	81	100.0	14 3 US-09-828-708-64	Sequence 64, App1
3	81	100.0	14 4 US-10-632-706-140	Sequence 140, App
4	81	100.0	14 4 US-10-632-706-144	Sequence 144, App
5	81	100.0	14 4 US-10-632-706-148	Sequence 148, App
6	81	100.0	14 4 US-10-632-706-152	Sequence 152, App
7	81	100.0	14 4 US-10-632-706-156	Sequence 156, App
8	81	100.0	14 4 US-10-632-706-160	Sequence 160, App
9	81	100.0	14 4 US-10-632-706-164	Sequence 164, App
10	81	100.0	14 4 US-10-632-706-168	Sequence 168, App
11	81	100.0	14 5 US-10-788-625-6	Sequence 6, App1
12	81	100.0	14 5 US-10-489-328-2	Sequence 2, App1
13	81	100.0	14 5 US-10-923-068-202	Sequence 202, App
14	81	100.0	14 5 US-10-923-068-205	Sequence 205, App
15	81	100.0	14 5 US-10-923-068-232	Sequence 232, App
16	81	100.0	14 5 US-10-877-773-109	Sequence 109, App
17	81	100.0	14 5 US-10-877-773-122	Sequence 122, App
18	81	100.0	14 5 US-10-877-774-109	Sequence 109, App
19	81	100.0	14 5 US-10-877-774-122	Sequence 122, App
20	81	100.0	14 5 US-10-630-009-64	Sequence 64, App1
21	81	100.0	14 5 US-10-755-382-33	Sequence 33, App1
22	81	100.0	14 5 US-10-984-960A-41	Sequence 41, App1
23	81	100.0	14 5 US-10-923-068-334	Sequence 334, App
24	81	100.0	17 5 US-10-923-068-337	Sequence 337, App
25	81	100.0	17 5 US-10-923-068-364	Sequence 364, App
26	81	100.0	44 5 US-10-842-011-39	Sequence 39, App1
27	81	100.0	82 4 US-10-230-880-118	Sequence 118, App

28	81	100.0	82 4 US-10-230-880-119	Sequence 119, App
29	81	100.0	82 4 US-10-230-880-120	Sequence 120, App
30	81	100.0	82 4 US-10-230-880-121	Sequence 121, App
31	81	100.0	82 4 US-10-230-880-122	Sequence 122, App
32	81	100.0	82 4 US-10-230-880-123	Sequence 123, App
33	81	100.0	87 5 US-10-788-625-90	Sequence 90, App1
34	81	100.0	87 5 US-10-842-011-45	Sequence 45, App1
35	81	100.0	89 5 US-10-612-497-72	Sequence 72, App1
36	81	100.0	89 5 US-10-776-649-72	Sequence 72, App1
37	81	100.0	93 3 US-09-910-483-39	Sequence 39, App1
38	81	100.0	93 3 US-09-910-483-45	Sequence 45, App1
39	81	100.0	95 4 US-10-363-204-89	Sequence 89, App1
40	81	100.0	95 4 US-10-363-204-91	Sequence 91, App1
41	81	100.0	95 5 US-10-884-830-653	Sequence 653, App
42	81	100.0	98 3 US-09-948-939-15	Sequence 15, App1
43	81	100.0	98 3 US-09-948-939-21	Sequence 21, App1
44	81	100.0	98 4 US-10-194-975-15	Sequence 15, App1
45	81	100.0	98 4 US-10-194-975-23	Sequence 23, App1

ALIGNMENTS

RESULT 1
US-09-253-794-33
Sequence 33, Application US/09253794
Patent No. US20020018750A1
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/POCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-253-794-33
Query Match 100.0%; Score 81; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

RESULT 2

US-09-828-708-64
Sequence 64, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their particl
TITLE OF INVENTION: Autoimmune disease
FILE REFERENCE: 1361.0050S1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 64
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-64

Query Match 100.0%; Score 81; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

RESULT 3

US-10-632-706-140
Sequence 140, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 140
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-140

Query Match 100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

RESULT 4

US-10-632-706-144

Sequence 144, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:

APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 144
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-144

Query Match 100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

RESULT 5

US-10-632-706-148
Sequence 148, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 148
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-148

Query Match 100.0%; Score 81; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
DB 1 WVRQAPGKGLWVA 14

RESULT 6

US-10-632-706-152
Sequence 152, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:

RESULT 10
 US-10-632-706-168
 ; Sequence 168, Application US/10632706
 ; Publication No. US20040175385A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MARKS, JAMES D.
 ; APPLICANT: AMERSDORFER, PETER
 ; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
 ; TITLE OF INVENTION: NEUROTOXINS
 ; FILE REFERENCE: 407T-895120US
 ; CURRENT APPLICATION NUMBER: US/10/632,706

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1  CURRENT FILING DATE: 2003-08-01
2  PRIOR APPLICATION NUMBER: US 60/400,721
3  PRIOR FILING DATE: 2002-08-01
4  PRIOR APPLICATION NUMBER: US 09/144,806
5  PRIOR FILING DATE: 1998-08-31
6  NUMBER OF SEQ ID NOS: 278
7  SOFTWARE: PatentIn version 3.2
8  SEQ ID NO 168
9  LENGTH: 14
10 TYPE: prt
11 ORGANISM: Artificial
12 FEATURES:
13 OTHER INFORMATION: single chain antibody fragment
14 US-10-632-706-168

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Query Match	100.0%	Score 81	DB 4	Length 14
Best Local Similarly	100.0%	Pred. NO.	1.5e-05	
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY      1 WVRQAPGKGLEWVA 14
         |||||
Db      1 WVRQAPGKGLEWVA 14
```

```

RESULT 11
US-10-788-625--6
Sequence 6, Application US/10788625
Publication No. US2004026068A1
GENERAL INFORMATION:
APPLICANT: Teurushita, Naoya
APPLICANT: Kumar, Shankar
APPLICANT: Vasquez, Maximiliano
TITLE OR INVENTION: Humanized Chicken Antibodies
FILE REFERENCE: 05882.0044.NPUS02
CURRENT APPLICATION NUMBER: US/10/788,625
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-788-625--6

```

Query Match	100.0%	Score 81;	DB 5;	length 14;
Best Local Similarity	100.0%	Pred. No. 1.3e-05;		
Matches 14; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	WVRQAPGKGLEWVA	14
Dd	1	WVRQAPGKGLEWVA	14

RESULT 12
 US-10-489-328-2
 Sequence 2, Application US/10489328
 Publication No. US20050037420A1
 GENERAL INFORMATION:
 APPLICANT: Fraunhofer -Gesellschaft zur Förderung der angewandten
 Forschung e.V.
 APPLICANT: ZHANG, Mei Yun
 APPLICANT: SCHILLBERG, Stefan
 APPLICANT: ZIMMERMANN, Sabine
 APPLICANT: DI FIORE, Stefano
 APPLICANT: EMANS, Neil
 APPLICANT: FISCHER, Rainer
 TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Methods
 TITLE OF INVENTION: Of Making and Using
 FILE REFERENCE: FRAU-202.105
 CURRENT APPLICATION NUMBER: US/10/489,328
 CURRENT FILING DATE: 2004-03-11
 PRIOR APPLICATION NUMBER: PCT/US02/29003
 PRIOR FILING DATE: 2002-09-13

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1 PRIOR APPLICATION NUMBER: 60/318,904
2 PRIOR FILING DATE: 2001-09-14
3 NUMBER OF SEQ ID NOS: 84
4 SOFTWARE: Patentin version 3.2
5 SEQ ID NO 2
6 LENGTH: 14
7 TYPE: PRT
8 ORGANISM: Artificial Sequence
9 FEATURE:
10 OTHER INFORMATION: This is a heavy chain framework region 2 (HFR2)
11 US-10-489-328-2

```

Query Match	100.0%	Score 81	DB 5	Length 14
Best Local Similarity	100.0%	Pred. No.	1.5e-05	
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	WVRQAPGKGLEWVA	14
Db	1	WVRQAPGKGLEWVA	14

```

RESULT 13
US-10-923-068-202
  Sequence 202, Application US/10923068
  Publication No. US20050042664A1
  GENERAL INFORMATION:
  APPLICANT: Wu, Herren
  APPLICANT: Dall'Aquila, William
  APPLICANT: Damschroder, Melissa
  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
  FILE REFERENCE: A8600US
  CURRENT APPLICATION NUMBER: US/10/923,068
  CURRENT FILING DATE: 2004-08-20
  NUMBER OF SEQ ID NOS: 518
  SOFTWARE: FastSeq for Windows Version 4.0
  SEQ ID NO 202
  LENGTH: 14
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-923-068-202

```

Query Match	100.0%	Score 81	DB 5	Length 14
Best Local Similarity	100.0%	Pred. No.	1.5e-05	
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 WVRQAPGKGLEWVA 14
|||
Db 1 WVRQAPGKGLEWVA 14

```

RESULT 14
US-10-923-068-205
  Sequence 205, Application US/10923068
  Publication No. US20050042654A1
  GENERAL INFORMATION:
  APPLICANT: Wu, Heren
  APPLICANT: Dai, Aquna, William
  APPLICANT: Damschroder, Melissa
  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
  FILE REFERENCE: A860005
  CURRENT APPLICATION NUMBER: US/10/923,068
  CURRENT FILING DATE: 2004-08-20
  NUMBER OF SEQ ID NOS: 518
  SOFTWARE: FastSeq for Windows Version 4.0
  SEQ ID NO 205
  LENGTH: 14
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-923-068-205

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Query Match	100.0%	Score 81, DB 5, Length 14,
Best Local Similarly	100.0%	Pred. No. 1.5e-05,
Matches 14, Conservative	0,	Mismatches 0, Indels 0, Gaps 0

OY 1 WVRQAPGKLEWVA 14
 |||||
 DB 1 WVRQAPGKLEWVA 14

RESULT 15
 US-10-923-068-232
 ; Sequence 232, Application US/10923068
 ; Publication No. US20050042664A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wu, Herren
 ; APPLICANT: Dail, Acqua, William
 ; APPLICANT: Damschroder, Melissa
 ; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
 ; FILE REFERENCE: A6600US
 ; CURRENT APPLICATION NUMBER: US/10/923,068
 ; CURRENT FILING DATE: 2004-08-20
 ; NUMBER OF SEQ ID NOS: 518
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 232
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-923-068-232

Query Match 100.0%; Score 81; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 WVRQAPGKLEWVA 14
 |||||
 DB 1 WVRQAPGKLEWVA 14

Search completed: November 21, 2005, 12:33:36
 Job time : 17.3333 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 21, 2005, 12:04:27 ; Search time 0.25641 Seconds
(without alignments)
61.686 Million cell updates/sec

Title: US-10-632-706-156
Perfect score: 81
Sequence: 1 WVRQAPGKLEWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA_New:*

- 1: /cgn2_6/ptodata/2/pubpa/US10_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpa/PCT_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	120	7	US-11-077-978-7
2	81	100.0	121	7	US-11-077-978-2
3	81	100.0	121	7	US-11-077-978-3
4	81	100.0	138	1	US-10-789-273-8
5	81	100.0	138	1	US-10-789-273-12
6	81	100.0	250	1	US-10-512-184-27
7	81	100.0	261	1	US-10-512-184-35
8	81	100.0	313	1	US-10-512-184-72
9	79	97.5	252	1	US-10-512-184-28
10	78	96.3	98	1	US-10-789-273-10
11	78	96.3	98	1	US-11-144-248-32
12	78	96.3	121	1	US-10-789-273-9
13	78	96.3	122	7	US-11-144-248-24
14	78	96.3	124	7	US-11-144-248-8
15	78	96.3	125	7	US-11-144-248-16
16	78	96.3	139	1	US-10-721-763-33
17	78	96.3	444	7	US-11-172-320-6
18	78	96.3	470	7	US-11-144-248-45
19	78	96.3	470	7	US-11-144-248-46
20	77	95.1	98	7	US-11-144-248-30
21	77	95.1	102	1	US-10-997-201A-6
22	77	95.1	118	1	US-10-648-816-9
23	77	95.1	118	1	US-10-648-816-10
24	77	95.1	118	1	US-10-648-816-11
25	77	95.1	118	1	US-10-648-816-12

26	77	95.1	118	1	US-10-648-816-13	Sequence 13, Appl
27	77	95.1	118	1	US-10-648-816-14	Sequence 14, Appl
28	77	95.1	121	1	US-10-648-816-15	Sequence 15, Appl
29	77	95.1	121	1	US-10-648-816-16	Sequence 16, Appl
30	77	95.1	174	7	US-11-144-248-4	Sequence 4, Appl
31	77	95.1	470	7	US-11-144-248-49	Sequence 49, Appl
32	77	95.1	473	7	US-11-144-248-50	Sequence 50, Appl
33	77	95.1	116	7	US-11-174-186-17	Sequence 17, Appl
34	77	95.1	116	7	US-11-144-248-34	Sequence 34, Appl
35	77	95.1	98	7	US-10-726-554-8	Sequence 8, Appl
36	77	95.1	114	1	US-10-502-145-25	Sequence 25, Appl
37	77	95.1	119	1	US-10-502-145-25	Sequence 25, Appl
38	77	95.1	154	1	US-10-721-763-25	Sequence 25, Appl
39	77	95.1	258	1	US-10-512-184-26	Sequence 26, Appl
40	77	95.1	327	1	US-10-512-184-62	Sequence 62, Appl
41	77	95.1	327	1	US-10-512-184-64	Sequence 64, Appl
42	77	95.1	328	1	US-10-512-184-63	Sequence 63, Appl
43	77	95.1	576	1	US-10-512-184-65	Sequence 65, Appl
44	77	95.1	625	1	US-10-512-184-47	Sequence 47, Appl
45	77	95.1	14	1	US-10-839-799-127	Sequence 127, App
					US-10-839-799-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-11-077-978-7
Sequence 7, Application US/11077978
Publication No. US20050244333A1
GENERAL INFORMATION:
APPLICANT: Yazaki, Paul J.
APPLICANT: Sherman, Mark A.
APPLICANT: Shively, John E.
APPLICANT: Raubitschek, Andrew A.
APPLICANT: Wu, Anna M.
TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
FILE REFERENCE: 54435.8012.US01
CURRENT APPLICATION NUMBER: US/11/077,978
CURRENT FILING DATE: 2005-03-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 120
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Variable heavy chain of humanized anti-p185HER2 antibody 4D5,
US-11-077-978-7
Query Match 100.0%; Score 81; DB 7; Length 120;
Best Local Similarity 100.0%; Pred. NO. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVRQAPGKLEWVA 14
DB 36 WVRQAPGKLEWVA 49
RESULT 2
US-11-077-978-2
Sequence 2, Application US/11077978
Publication No. US20050244333A1
GENERAL INFORMATION:
APPLICANT: Yazaki, Paul J.
APPLICANT: Sherman, Mark A.
APPLICANT: Shively, John E.
APPLICANT: Raubitschek, Andrew A.
APPLICANT: Wu, Anna M.
TITLE OF INVENTION: A Humanized Anti-CEA T84.66 Antibody and Uses Thereof
FILE REFERENCE: 54435.8012.US01
CURRENT APPLICATION NUMBER: US/11/077,978
CURRENT FILING DATE: 2005-03-11


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; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: prt
; ORGANISM: Artificial Sequence
FEATURES
; OTHER INFORMATION: Description of Artificial Sequence: scFv SG3 with
; OTHER INFORMATION: specificity against Fusarium spp.; originates from
; OTHER INFORMATION: Gallus gallus.
; US-10-512-184-27

```

Query Match	100.0%	Score 81	DB 1	Length 250
Best Local Similarity	100.0%	Pred. No.	2.2e-06	
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	1	WVRQAPGKLEWVA	14
Db	38	WVRQAPGKLEWVA	51

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RESULT 7
US-10-512-184--35
; Sequence 35, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; PIR REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 261
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: gcfv p1p9 with
; OTHER INFORMATION: specifically against Phoma lingam, originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184--35

```

Query Match	100.0%	Score 81;	DB 1;	Length 261;
Best Local Similarity	100.0%	Pred. No. 2,3	-05;	
Matches	14;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	WVROAPGKGLEWVA	14	
		6		
Db	38	WVROAPGKGLEWVA	51	

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RESULT 9
US-10-512-184-72
; Sequence 72, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;
; LENGTH: 313
; TYPE: PRT
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```

; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: precursor
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; OTHER INFORMATION: fusion protein comprising MBP - linker -
;
; OTHER INFORMATION: scFv P4p9.
;
; OS-10-512-184-72

```

Query Match	100.0%	Score 81	DB 1	Length 313
Best Local Similarity	100.0%	Pred. No.	2.7e-06	
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 WVRQAPGKGLEWVA 14
|||
Db 90 WVRQAPGKGLEWVA 103

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RESULT 9
US-10-512-184-28
; Sequence: 28, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; PILE REFERENCE: 3581_01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 252
; TYPE: prt
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: bcfv FPCWPA5
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-28

```

Query Match	97.5%	Score 79;	DB 1;	Length 253;
Best Local Similarity	92.9%	Pred. No. 4.4e-06;		
Matches 13; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	WVROAPGKGLEWVA	14	
DB	38	WVROAPGKGMWVA	51	

```

/ RESULT 10
/ US-10-789-273-10
/ Sequence 10, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurig
/ APPLICANT: Saldama, Jose
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
/ FILE REFERENCE: ELN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789, 273
/ CURRENT FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 98
/ TYPE: prt
/

```

! ORGANISM: Homo sapiens
US-10-789-273-10

Query Match	96.3%	Score 78	DB 1	Length 98
Best Local Similarity	92.9%	Pred. No. 2.8e-06		
Matches 13	Conservative	1	Mismatches 0	Indels 0
			Gaps	0

```
QY      1  WVRQAPGKGLEWVA  14
          |||||
Db      36  WVRQAPGKGLEWVS  49
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RESULT 11
11-144

```

US-11-144-248-32
Sequence 32, Application US/11/144248
Publication No. US20050244400A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvatan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: AIX-PP2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-32

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Query Match	96.3%	Score 78;	DB 7;	Length 98;
Best Local Similarity	92.9%	Pred. No. 2.8e-06;		
Matches 13; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 WVRQAPGKGLEWVA 14
         |||||:
Db      36 WVRQAPGKGLEWVS 49

```

RESULT 12
US-10-789

```

1 Sequence 9, Application US/107899273
2 Publication No. US20050249725A1
3 GENERAL INFORMATION:
4 APPLICANT: Basi, Gurjit
5 APPLICANT: Saldanha, Jose
6 APPLICANT: Vednock, Ted
7 TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
8 TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
9 FILE REFERENCE: ELN-002CP
10 CURRENT APPLICATION NUMBER: US/10/789,273
11 CURRENT FILING DATE: 2004-02-27
12 PRIOR APPLICATION NUMBER: US/10/388,389
13 PRIOR FILING DATE: 2003-03-12
14 PRIOR APPLICATION NUMBER: US 10/010,942
15 PRIOR FILING DATE: 2001-12-06
16 PRIOR APPLICATION NUMBER: US 60/251,892
17 PRIOR FILING DATE: 2000-12-06
18 NUMBER OF SEQ ID NOS: 63
19 SOFTWARE: FastSeq for Windows Version 4.0
20 SEQ ID NO 9
21 LENGTH: 121
22 TYPE: PRT
23 ORGANISM: Homo sapiens

```

US-10-789-273-9

Query Match	96.3%	Score 78	DB 1	Length 121
Best Local Similarity	92.9%	Pred. No.	3,4e-06	
Matches 13	Conservative 1	Mismatches	0	Indels 0
		Gaps	0	

QY 1 WVRQAPGKGLEWVA 14
|||:|
Db 36 WVRQAPGKGLEWVS 49

RESULT 13

```

US-11-144-248-24
Sequence 24, Application US/11/144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 122
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-24

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Query Match	96.3%	Score 78	DB 7	Length 122
Best Local Similarity	92.9%	Pred. No.	3.4e-06	
Matches 13	Conservative	1	Mismatches 0	Indels 0
				Gaps 0

```
QY      1  WVRQAPGKGLEWVA  14
          |||||:
Db      36  WVRQAPGKGLEWVS  49
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RESULT 14

```

US-11-144-248-8
; Sequence 8, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PE2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-8

```

Query Match 96.3%; Score 78; DB 7; Length 124;
Best Local Similarity 92.9%; Pred. No. 3.4e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
|||||
Db 35 WVRQAPGKGLWVS 48

RESULT 15

US-11-144-248-16
; Sequence 16, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope B.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-144-248-16

Query Match 96.3%; Score 78; DB 7; Length 125;
Best Local Similarity 92.9%; Pred. No. 3.5e-06;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVRQAPGKGLWVA 14
|||||
Db 36 WVRQAPGKGLWVS 49

Search completed: November 21, 2005, 12:33:51
Job time : 0.35641 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:32 / Search time 22.7601 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-157

Perfect score: 93

Sequence: 1 TISDGSSTYPPDSVKG 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: Genesep19808:*
2: Genesep19908:*
3: Genesep20008:*
4: Genesep20018:*
5: Genesep20028:*
6: Genesep20038:*
7: Genesep20038:*
8: Genesep20048:*
9: Genesep20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	17	8	ADR38751 Mouse hea
2	93	100.0	17	8	ADR38743 Mouse hea
3	93	100.0	17	8	ADR38739 Mouse hea
4	93	100.0	17	8	ADR38747 Mouse hea
5	93	100.0	17	8	ADR38755 Mouse hea
6	93	100.0	17	8	ADR38755 Mouse hea
7	93	100.0	17	8	ADR38755 Mouse hea
8	93	100.0	17	8	ADR38755 Mouse hea
9	93	100.0	17	8	ADR38755 Mouse hea
10	93	100.0	17	8	ADR38755 Mouse hea
11	93	100.0	17	8	ADR38755 Mouse hea
12	93	100.0	17	8	ADR38755 Mouse hea
13	93	100.0	17	8	ADR38755 Mouse hea
14	93	100.0	17	8	ADR38755 Mouse hea
15	93	100.0	17	8	ADR38755 Mouse hea
16	93	100.0	17	8	ADR38755 Mouse hea
17	93	100.0	17	8	ADR38755 Mouse hea
18	93	100.0	17	8	ADR38755 Mouse hea
19	93	100.0	17	8	ADR38755 Mouse hea
20	93	100.0	17	8	ADR38755 Mouse hea
21	93	100.0	17	8	ADR38755 Mouse hea
22	93	100.0	17	8	ADR38755 Mouse hea
23	93	100.0	17	8	ADR38755 Mouse hea
24	93	100.0	17	8	ADR38755 Mouse hea

25	93	100.0	301	4	AAB61959
26	93	100.0	301	4	AAB61959
27	93	100.0	352	2	AA062272
28	93	100.0	449	5	AA018400
29	93	100.0	449	9	AA036337
30	93	100.0	468	8	AD007413
31	93	100.0	468	8	AD012196
32	93	100.0	553	2	AA011508
33	93	100.0	553	2	AA011508
34	93	100.0	553	4	AAB61960
35	93	100.0	553	4	AAB61960
36	93	100.0	697	8	AD007403
37	93	100.0	697	8	AD012180
38	93	100.0	701	8	AD012186
39	93	100.0	702	9	AA054975
40	93	100.0	731	8	AD007407
41	93	100.0	731	8	AD012184
42	93	100.0	735	8	AD007411
43	93	100.0	735	8	AD012188
44	93	100.0	984	9	AA054976
45	93	100.0	984	9	AA054976

ALIGNMENTS

RESULT 1
ADR38751 standard; peptide; 17 AA.
ID ADR38751 standard; peptide; 17 AA.
AC ADR38751;
DT 02-DEC-2004 (first entry)
DE Mouse heavy chain anti-BONT-antibody CD2 seqid 153.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW CD2; complementarily determining region 2.
XX
OS Mus sp.
XX
FN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PP 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
PI Marks JD, Amerdoffer P;
XX WPI: 2004-652009/63.
DR
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 153; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (II) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C35, C39, I6, 3D12, B4, I63, huc25, Ar1, Ar2, WRI (V), WRI (T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is

CC	specifically bound by an antibody expressed by clones as mentioned in (I)
CC	; producing (I); and a composition (III) comprising several anti-
CC	botulinum neurotoxin antibodies, where each antibody is specific for a
CC	different epitope of a botulinum neurotoxin and the combination of
CC	antibodies shows greater toxin neutralisation than the single antibodies
CC	in supple. The following are disclosed: a pharmaceutical composition
CC	comprising (I); and a kit comprising a botulinum neurotoxin which
CC	BONT/A antibody and for neutralising (I) in supple., where each of (I) is
CC	specific for a different epitope of the botulinum neurotoxin and the
CC	combination of antibodies shows greater toxin neutralisation than the
CC	single antibodies in supple. (I) is useful for diagnosing the botulism
CC	or for treating pathologies associated with botulinum neurotoxin
CC	poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC	enables rapid detection or diagnosis of botulism. This is the amino acid
CC	sequence of mouse heavy chain anti-BONT-antibody CDR2.
XX	
SQ	Sequence 17 AA;
Query Match	100.0%; Score 93; DB 8; Length 17;
Best Local S'milarity	100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Gy	1 TISDGSSTYYPDSSVKG 17 1 TISDGSSTYYPDSSVKG 17
Dd	
RESULT 2	
ADR38743	
ID	ADR38743 standard; peptide; 17 AA.
XX	
AC	ADR38743;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Mouse heavy chain anti-BONT-antibody CD2 seqid 145.
XX	
KW	antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KM	BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KV	toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW	CDR; complementarity determining region 2.
XX	
OS	Mus sp.
CS	
PN	US2004175385-A1.
XX	
PD	09-SEP-2004.
XX	
PF	01-AUG-2003; 2003US-00632706.
XX	
PR	31-AUG-1998; 98US-00144886.
PR	01-AUG-2002; 2002US-0040721P.
XX	
PA	(RBGC) UNIV CALIFORNIA.
XX	
PI	Marks JD, Amersdorfer P;
XX	
DR	WPI; 2004-652009/63.
XX	
PT	New isolated antibody that neutralizes botulinum neurotoxin type A,
PT	useful for diagnosing botulism or for treating pathologies associated
XX	with botulinum neurotoxin poisoning.
XX	
PS	Example 4; SEQ ID NO 145; 110pp; English.
XX	
CC	The invention describes an isolated antibody (I) that specifically binds
CC	to an epitope specifically bound by an antibody expressed by a specific
CC	clone where (I) binds to and neutralises botulinum neurotoxin type A
CC	(BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC	specifically bound by an antibody expressed by a clone chosen from clone
CC	825, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC	3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum

CC	neurotoxin type A (BoNT/A). Also described are a polypeptide (II)
CC	comprising BoNT/A neutralising epitope having an epitope that is
CC	specifically bound by an antibody expressed by clones as mentioned in (I)
CC	; producing (I); and a composition (III) comprising several anti-
CC	botulinum neurotoxin antibodies, where each antibody is specific for a
CC	different epitope of a botulinum neurotoxin and the combination of
CC	antibodies shows greater toxin neutralisation than the single antibodies
CC	in surplus. The following are disclosed: a pharmaceutical composition
CC	comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC	BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC	involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC	specific for a different epitope of the botulinum neurotoxin and the
CC	combination of antibodies shows greater toxin neutralisation than the
CC	single antibodies in surplus. (I) is useful for diagnosing the botulism
CC	or for treating pathologies associated with botulinum neurotoxin
CC	poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC	enables rapid detection or diagnosis of botulism. This is the amino acid
CC	sequence of mouse heavy chain anti-BoNT-antibody CDR2.
SQ	Sequence 17 AA:
Query Match	100.0%; Score 93; DB 8; Length 17;
Best Local Similarity	100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 TISDGGSTTYTPDSVKG 17
D6	1 TISDGGSTTYTPDSVKG 17
RESULT 3	
ADNR38739	
ID	ADR38739 standard; peptide; 17 AA.
AC	ADR38739;
DT	02-DEC-2004 (first entry)
XX	
DE	Mouse heavy chain anti-BoNT-antibody CD2 segid 141.
XX	
KW	antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KM	BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW	toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
CDR2; complementarity determining region 2.	
XX	
OS	Mus sp.
XX	
PN	US2004175365-A1.
PD	09-SEP-2004.
PJ	
PF	01-AUG-2003; 2003US-00632706.
XX	
PR	31-AUG-1998; 98US-00144886.
PPR	01-AUG-2002; 2002US-0400721P.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Marks JD, Amerdorter P;
XX	
DR	WPI, 2004-652009/63.
PT	
XX	New isolated antibody that neutralizes botulinum neurotoxin type A,
XX	useful for diagnosing botulism or for treating pathologies associated
XX	with botulinum neurotoxin poisoning.
PS	Example 4, SEQ ID NO 141; 110pp; English.
CC	The invention describes an isolated antibody (I) that specifically binds
CC	to an epitope specifically bound by an antibody expressed by a specific
CC	clone where (I) binds to and neutralises botulinum neurotoxin type A
CC	(BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC	specifically bound by an antibody expressed by a clone chosen from clone

CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and INGI1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising a botulinum neurotoxin which
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody CDR2.

XX Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TISDGSSTYYPDSVKG 17
 |||||
 Db 1 TISDGSSTYYPDSVKG 17

RESULT 4

ADR38747 standard; peptide; 17 AA.

ADR38747;

02-DEC-2004 (first entry)

Mouse heavy chain anti-BoNT-antibody CD2 seqid 149.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A.
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW CDR2; complementarity determining region 2.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amerdorter P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 149; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A.

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and INGI1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising a botulinum neurotoxin which
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody CDR2.

XX Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 17, Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TISDGSSTYYPDSVKG 17
 |||||
 Db 1 TISDGSSTYYPDSVKG 17

RESULT 5

ADR38755 standard; peptide; 17 AA.

ADR38755;

02-DEC-2004 (first entry)

Mouse heavy chain anti-BoNT-antibody CD2 seqid 157.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A.
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW CDR2; complementarity determining region 2.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amerdorter P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 157; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralizes botulinum neurotoxin type A
CC (Bont/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (Bont/A). Also described are: a polypeptide (II)
CC comprising Bont/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC, producing (I), and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC Bont/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin (I)
CC poisoning. (I) exhibits specificity and affinity towards Bont/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-Bont-antibody CDR2.

XX Sequence 17 AA;

Query Match 100.0%; Score 93; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17
|||
Db 1 TISDGSYTYPPDSVKG 17

RESULT 6
ABUS6860
ID ABUS6860 standard; protein; 66 AA.

XX ABUS6860;

XX 04-APR-2003 (first entry)

XX Bont/A Hc binding antibody scTv VH region from C39 #1.

DE Botulinum neurotoxin type A; Bont/A; mouse; heavy chain variable region;
KW scFv; antibody; botulism; antibacterial; single chain antibody; VH;
KM immunoglobulin.

XX Mus sp.

XX US2002155114-A1.

XX 24-OCT-2002.

XX 31-AUG-1998; 98US-00144886.

XX 31-AUG-1998; 98US-00144886.

XX (MARK/) MARKS J D.
XX (AMER/) AMERSDORFER P.

XX Marks JD, Amersdorfer P;

XX WPI; 2003-182618/18.

XX Novel antibody that specifically binds and neutralizes botulinum
PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
PT treating botulism.

XX Claim 6; Page 22; 31pp; English.

XX

CC The invention relates to an isolated antibody that specifically binds to
CC an epitope specifically bound by an antibody expressed by a clone such as
CC clone S25, C25, C39, 1C6 and clone 1F3, where the antibody binds to and
CC neutralises botulinum neurotoxin type A (Bont/A). Also included are a
CC polypeptide comprising Bont/A neutralising epitope comprising an epitope
CC which is specifically bound by the antibody, where the polypeptide is not
CC a full-length botulinum neurotoxin Hc fragment and making an anti-Bont/A
CC antibody that neutralises Bont/A (by contacting several antibodies with
CC an epitope specifically bound by an antibody expressed by any of the
CC novel clones and isolating an antibody that specifically binds to the
CC epitope). The antibody is useful for neutralising a Bont/A, by contacting
CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
CC chain variable region complementarily determining region) and with a
CC second anti-Bont/A antibody which comprises a VH CDR, where the second
CC antibody binds to a different epitope than the first anti-Bont/A
CC antibody. The antibody is useful in the treatment of pathologies
CC associated with botulinum neurotoxin poisoning, for rapid
CC detection/diagnosis of botulism and in the detection and/or
CC quantification of Bont/A in a biological sample obtained from an organism
CC which is indicative of a Clostridium botulinum infection of the organism.
CC The present sequence is a heavy chain variable region (VH) of a single
CC chain antibody (scTv) of the invention

XX Sequence 66 AA;

Query Match 100.0%; Score 93; DB 6; Length 66;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17
|||
Db 50 TISDGSYTYPPDSVKG 66

RESULT 7
ABUS6861
ID ABUS6861 standard; protein; 66 AA.

XX ABUS6861;

XX 04-APR-2003 (first entry)

XX Bont/A Hc binding antibody scTv VH region from C25 #1.

DE Botulinum neurotoxin type A; Bont/A; mouse; heavy chain variable region;
KW scFv; antibody; botulism; antibacterial; single chain antibody; VH;
KM immunoglobulin.

XX Mus sp.

XX US2002155114-A1.

XX 24-OCT-2002.

XX 31-AUG-1998; 98US-00144886.

XX 31-AUG-1998; 98US-00144886.

XX (MARK/) MARKS J D.
XX (AMER/) AMERSDORFER P.

XX Marks JD, Amersdorfer P;

XX WPI; 2003-182618/18.

XX Novel antibody that specifically binds and neutralizes botulinum
PT neurotoxin type A useful for neutralizing botulinum neurotoxin and
PT treating botulism.

XX Claim 6; Page 22; 31pp; English.

XX The invention relates to an isolated antibody that specifically binds to
CC an epitope specifically bound by an antibody expressed by a clone such as

CC clone S25, C35, C39, 106 and clone 1F3, where the antibody binds to and
 CC neutralizes botulinum neurotoxin type A (BoNT/A). Also included are a
 CC polypeptide comprising BoNT/A neutralising epitope comprising an epitope
 CC which is specifically bound by the antibody, where the polypeptide is not
 CC a full-length botulinum neurotoxin H c fragment and making an anti-BoNT/A
 CC antibody that neutralises BoNT/A (by contacting several antibodies with
 CC an epitope specifically bound by an antibody expressed by any of the
 CC novel clones and isolating an antibody that specifically binds to the
 CC epitope). The antibody is useful for neutralising a BoNT/A, by contacting
 CC botulinum neurotoxin type A with the antibody comprising VH CDR (heavy
 CC chain variable region complementarily determining region) and with a
 CC second anti-BoNT/A antibody which comprises a VH CDR, where the second
 CC antibody binds to a different epitope than the first anti-BoNT/A
 CC antibody. The antibody is useful in the treatment of pathologies
 CC associated with botulinum neurotoxin poisoning, for rapid
 CC detection/diagnosis of botulinum in the detection and/or
 CC quantification of BoNT/A in a biological sample obtained from an organism.
 CC which is indicative of a Clostridium botulinum infection of the organism.
 CC The present sequence is a heavy chain variable region (VH) of a single
 CC chain antibody (scFv) of the invention

CC Sequence 66 AA;

Query Match 100.0%; Score 93; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred. No. 5.7e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYKVG 17
 |||||
 DB 50 TISDGSYYTPDSYKVG 66

RESULT 8

ADR38657 standard; peptide; 118 AA.

AC ADR38657;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region scFv seqid 59.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KW heavy chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX MPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 59; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C35, 106, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
 CC scFv.

CC Sequence 118 AA;

Query Match 100.0%; Score 93; DB 8; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYKVG 17
 |||||
 DB 50 TISDGSYYTPDSYKVG 66

RESULT 9

ADR38658 standard; peptide; 118 AA.

AC ADR38658;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region scFv seqid 60.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 KW heavy chain variable region; single chain antibody; scFv.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX MPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 1; SEQ ID NO 60; 110pp; English.

PS

CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC 825, C25, C39, 1C6, 3D12, B4, 1F3, huC25, A1, A2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralises botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of a mouse heavy chain variable fragment anti-botulinum toxin
 CC scfv.

XX Sequence 118 AA:

Query Match 100.0%; Score 93; DB 8; Length 118;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSSTYTPDSVKG 17

|||||

50 TISDGSSTYTPDSVKG 66

RESULT 10

AARS4930

ID AARS4930 standard; peptide: 120 AA.

XX AARS4930;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 19-OCT-1994 (first entry)

XX Fc receptor humanized VH chain 022 KLVH.

XX Fc receptor; FcR; humanized antibody; hab; IgG; cancer; allergy;

KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;

KW CDR; complementarity determining region; VH; heavy chain variable region;

KW VK; kappa chain variable region; mononuclear phagocyte; PCR;

KW polymerase chain reaction; primer; site-directed mutagenesis; KLVH;

XX monoclonal antibody; Mab.

XX Homo sapiens.

XX Mus sp.

XX WO9410332-A1.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-US010384.

XX 04-NOV-1992; 92GB-00023377.

XX (MEDA-) MEDAREX INC.

XX Tempest PR, Harris WJ, Carr FJ;

XX WPI; 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or for
 PT treatment of e.g. cancer, allergies and infectious and auto-immune
 PT diseases.

XX Disclosure; Page 14-15; 36pp; English.

XX Humanized antibodies (habs) for IgG Fc receptors on human phagocytes

CC comprising the CDR of mouse monoclonal antibody 22 (from hybridoma 022WCL-

CC 1), VH chains from human IgE NEMN or KOL, and VK chains from Ig REI.

CC Sequences are provided for mouse 022 VH (AARS4931), humanized NEMN-based

CC VH (022 NMVH, AARS4929), humanized KOL-based VH (022 KLVH, AARS4930),

CC mouse 022 VK (AARS4933), and humanized REI-based VK (022 huVK, AARS4932).

CC During hab production, VH and VK cDNAs were PCR amplified using primers

CC given in A065378-87. Mutagenesis of clone M13VPCR2 KOL VH (L71R) was

CC performed using oligos A065388-89. The habs can be used in

CC heteroantibody, bifunctional antibody and immunotoxin production.

CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to

CC correct OS field.)

XX Sequence 120 AA:

Query Match 100.0%; Score 93; DB 2; Length 120;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSSTYTPDSVKG 17

|||||

50 TISDGSSTYTPDSVKG 66

RESULT 11

AARS4929

ID AARS4929 standard; peptide: 120 AA.

XX AARS4929;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 19-OCT-1994 (first entry)

XX Fc receptor humanized VH chain 022 NMVH.

XX Fc receptor; FcR; humanized antibody; hab; IgG; cancer; allergy;

KW autoimmune disease; heteroantibody; bifunctional antibody; immunotoxin;

KW CDR; complementarity determining region; VH; heavy chain variable region;

KW VK; kappa chain variable region; mononuclear phagocyte; PCR;

KW polymerase chain reaction; primer; site-directed mutagenesis; NMVH;

XX monoclonal antibody; Mab.

XX Homo sapiens.

XX Mus sp.

XX WO9410332-A1.

XX 11-MAY-1994.

XX 04-NOV-1993; 93WO-US010384.

XX 04-NOV-1992; 92GB-00023377.

XX (MEDA-) MEDAREX INC.

XX Tempest PR, Harris WJ, Carr FJ;

XX WPI; 1994-167486/20.

XX New humanised antibodies to Fc receptors - used for diagnosis or for
 PT treatment of e.g. cancer, allergies and infectious and auto-immune
 PT diseases.

XX Disclosure; Page 14; 36pp; English.

XX 11-OCT-2002 (first entry)
 DT Humanised murine CBE11 heavy chain variable domain #3.
 XX
 DE Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;
 XX neoplasia; LT-beta-R; light chain; heavy chain; variable region.
 KM
 OS Mus sp.
 OS Synthetic.
 XX
 PN WO200230986-A2.
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US032140.
 XX
 PR 13-OCT-2000; 2000US-0240285P.
 PR 13-MAR-2001; 2001US-0275289P.
 PR 21-JUN-2001; 2001US-029987P.
 XX
 PA (BIOI) BIOGEN INC.
 XX
 PI Garber E, Lyne P, Saldanha JW;
 PI WPI; 2002-58337/62.
 DR N-PSDB; AAL48454.
 XX
 PT New humanized anti-lymphotoxin-beta receptor antibody, useful for
 PT treating or reducing the advancement, severity or effects of neoplasia,
 PT particularly solid tumors (i.e. carcinomas) including colorectal cancer
 PT and breast cancer.
 XX
 PS Disclosure; Page 15; 41pp; English.
 XX
 CC The present invention relates to humanised anti-lymphotoxin beta receptor
 CC (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
 CC binding antibody CBE11 and can be used to treat neoplasia in humans. The
 CC present sequence is a humanised murine CBE11 heavy chain variable region
 XX
 SQ Sequence 120 AA;

Query Match 100.0%; Score 93; DB 5; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
 |||||
 DB 50 TISDGSYTYPPDSVKG 66

RESULT 15
 AAO18395
 ID AAO18395 standard; protein; 120 AA.
 XX
 AC AAO18395;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Humanised murine CBE11 heavy chain variable domain #1.
 XX
 KM Mouse; humanised antibody; lymphotoxin beta receptor; antibody; cancer;
 KM neoplasia; LT-beta-R; light chain; heavy chain; variable region.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 PN WO200230986-A2.
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US032140.
 XX

PR 13-OCT-2000; 2000US-0240285P.
 PR 13-MAR-2001; 2001US-0275289P.
 PR 21-JUN-2001; 2001US-029987P.
 XX
 PA (BIOI) BIOGEN INC.
 XX
 PI Garber E, Lyne P, Saldanha JW;
 PI WPI; 2002-58337/62.
 DR N-PSDB; AAL48452.
 XX
 PT New humanized anti-lymphotoxin-beta receptor antibody, useful for
 PT treating or reducing the advancement, severity or effects of neoplasia,
 PT particularly solid tumors (i.e. carcinomas) including colorectal cancer
 PT and breast cancer.
 XX
 PS Disclosure; Page 14; 41pp; English.
 XX
 CC The present invention relates to humanised anti-lymphotoxin beta receptor
 CC (LT-beta-R) antibodies. These are derived from the murine LT-beta-R
 CC binding antibody CBE11 and can be used to treat neoplasia in humans. The
 CC present sequence is a humanised murine CBE11 heavy chain variable region
 XX
 SQ Sequence 120 AA;

Query Match 100.0%; Score 93; DB 5; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
 |||||
 DB 50 TISDGSYTYPPDSVKG 66

Search completed: November 21, 2005, 12:20:02
 Job time : 23.7601 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 4.14103 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-157

Perfect score: 93
Sequence: 1 TISDGSSTYTPDSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	93	100.0	98 1	HVMS96
2	93	100.0	101 2	C27889
3	93	100.0	119 2	B27889
4	93	100.0	152 2	B26471
5	87	93.5	83 2	C25913
6	87	93.5	94 2	S14580
7	87	93.5	102 2	S14581
8	87	93.5	108 2	PH1010
9	87	93.5	119 2	F27888
10	87	93.5	120 2	S55537
11	87	93.5	120 2	S55536
12	87	93.5	122 2	E27888
13	84	90.3	121 2	I27887
14	84	90.3	123 2	S63597
15	84	90.3	124 2	C27888
16	84	90.3	254 2	B31790
17	84	90.3	548 2	S38864
18	83	89.2	121 2	A27888
19	81	87.1	117 1	HVMS57
20	81	87.1	118 2	PH0096
21	81	87.1	120 2	S55539
22	78	83.9	119 2	D27889
23	78	83.9	120 2	S55538
24	78	83.9	121 2	B27888
25	77	82.8	121 2	H27887
26	77	82.8	121 2	D27888
27	77	82.8	136 2	S31615
28	75	80.6	119 2	B34353
29	74	79.6	108 2	PL0248

30	74	79.6	118 2	PH0097	Ig heavy chain V r
31	74	79.6	138 2	S09258	Ig heavy chain V r
32	73	78.5	114 1	PH1009	Ig heavy chain V r
33	73	78.5	117 1	HVMS39	Ig heavy chain pre
34	73	78.5	121 2	H27888	Ig heavy chain V r
35	72	77.4	112 2	A27889	Ig heavy chain V r
36	70	75.3	108 2	PH1006	Ig heavy chain V r
37	70	75.3	123 2	C27888	Ig heavy chain V r
38	69	74.2	111 2	PH1007	Ig heavy chain V r
39	69	74.2	118 2	S20641	Ig heavy chain V r
40	69	74.2	124 2	I27888	Ig heavy chain V r
41	67	72.0	117 1	HVMS84	Ig heavy chain pre
42	67	72.0	118 2	S00700	Ig heavy chain V r
43	67	72.0	119 2	A43413	Ig heavy chain V r
44	66	71.0	113 2	S26468	Ig heavy chain V r
45	66	71.0	117 1	HVMS34	Ig heavy chain pre

ALIGNMENTS

RESULT 1

HVMS96
Ig heavy chain V region (6.96) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C/Accession: J070501
R/Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A/Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary in
A/Reference number: J070501, MUID:89279149; PMID:249654
A/Accession: J070501
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-98 <LENA>
A/Cross-references: UNIPROT:P18528; UNIPARC:UPI0000278DB
A/Experimental source: STRAIN BALB/cJ
A/Note: This sequence belongs to the VH7183 subfamily
C/Superfamily: Immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>
P:122-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 93; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSSTYTPDSVKG 17
DB 50 TISDGSSTYTPDSVKG 66

RESULT 2

C27889
Ig heavy chain V region (H220-25) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: C27889
R/Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a de
A/Reference number: A91043; MUID:86300658; PMID:2427335
A/Accession: C27889
A/Molecule type: DNA
A/Residues: 1-101 <CAT>
A/Cross-references: UNIPARC:UPI0000176A0C
A/Experimental source: strain Balb/c
A/Note: This sequence was determined from the germ-line gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 93; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17
Db 32 TISDGSYTYPPDSVKG 48

RESULT 3

B27889
Ig heavy chain V region (H146-24B3) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: B27889
R/Cotton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a
A/Reference number: A91043; MUID:86300658; PMID:2427335
A/Accession: B27889
A/Molecule type: DNA
A/Residues: 1-119 <CAT>
A/Cross-references: UNIPARC:UPI0000176B67
A/Experimental source: strain Balb/c
A/Note: this sequence was determined from the germ-line gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17
Db 50 TISDGSYTYPPDSVKG 66

RESULT 4

B26471
Ig heavy chain precursor V region (MAK33) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C/Accession: B26471; S70410
R/Buckel, P.; Hubner-Parjusz, C.; Matres, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A/Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A/Reference number: A91572; MUID:87248058; PMID:3110009
A/Accession: B26471
A/Molecule type: mRNA
A/Residues: 1-152 <BUC>
A/Cross-references: UNIPARC:UPI000011677B; GB:M16163; NID:G195405; PIDN:AAA38292.1; PID:
R/LeDeque, S.G.; Gearhart, P.U.
J. Exp. Med. 172, 1717-1727, 1990
A/Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary
A/Reference number: S70410; MUID:91079775; PMID:2258702
A/Accession: S70410
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-19 <LEB>
A/Cross-references: UNIPARC:UPI0000115B81; EMBL:X53776; NID:G52475; PIDN:CAA37792.1; PIT
C/Genetics: 16/1
A/Intons: 16/1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-15/Product: Ig heavy chain V region MAK33 #status predicted <MAT>
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 93; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17
Db 69 TISDGSYTYPPDSVKG 85

RESULT 5

C25913
Ig heavy chain V region (BFL14) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 31-Dec-2004
C/Accession: C25913
R/Lewler, A.M.; Lin, P.S.; Gearhart, P.U.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A/Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A/Reference number: A94148; MUID:87175692; PMID:3104915
A/Accession: C25913
A/Molecule type: DNA
A/Residues: 1-83 <LAW>
A/Cross-references: UNIPROT:Q920E7; UNIPARC:UPI00001769E3
C/Superfamily: immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 93.5%; Score 87; DB 2; Length 83;
Best Local Similarity 94.1%; Pred. No. 2.6e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17
Db 35 TISDGSYTYPPDSVKG 51

RESULT 6

S14580
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S14580
R/Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A/Description: Natural polyclonal reactive antibodies differ from Ag-induced antibodies in VH CI
A/Reference number: S14484
A/Accession: S14580
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-94 <CHE>
A/Cross-references: UNIPARC:UPI0000115F39; EMBL:X58652; NID:G51293; PIDN:CAA41509.1; PID:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.5%; Score 87; DB 2; Length 94;
Best Local Similarity 94.1%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TISDGSYTYPPDSVKG 17
Db 42 TISDGSYTYPPDSVKG 58

RESULT 7

S14581
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S14581
R/Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A/Description: Natural polyclonal reactive antibodies differ from Ag-induced antibodies in VH CI
A/Reference number: S14484
A/Accession: S14581
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-102 <CHE>

Query Match 93.5%; Score 87; DB 2; Length 94;
Best Local Similarity 94.1%; Pred. No. 3e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A:Cross-references: UNIPARC:UPI0000115F3A; EMBL:X58653; NID:G51295; PIDN:CAA41510.1; PII
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:7-90/Domain: Immunoglobulin homology <IMM>

Query Match 93.5%; Score 87; DB 2; Length 102;
Best Local Similarity 94.1%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
||| |||||
DB 42 TISGSGSYTYPPDSVKG 58

RESULT 8

PH1010
Ig heavy chain V region (clone 17a.93) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PH1010
R:Titelman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1010

A:Status: nucleic acid sequence not shown

A:Residues: 1-108 <TIL>

A:Cross-references: UNIPARC:UPI0000176D1A

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin
F:15-97/Domain: Immunoglobulin homology <IMM>

RESULT 9

F27888
Ig heavy chain V region (H158-89H4) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: F27888
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a

A:Reference number: A91043; MUID:86300658; PMID:2427335

A:Accession: F27888

A:Status: preliminary

A:Residues: 1-119 <CAT>

A:Cross-references: UNIPARC:UPI0000176B68

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin
F:15-98/Domain: Immunoglobulin homology <IMM>

Query Match 93.5%; Score 87; DB 2; Length 119;

Best Local Similarity 94.1%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
||| |||||
DB 50 TISGSGSYTYPPDSVKG 66

RESULT 10
S55537
Ig heavy chain V region pe21 - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C:Accession: S55537
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

utations in the variable region genes

A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55537

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOE>

A:Cross-references: UNIPARC:UPI0000116201; EMBL:X82590; NID:G854306; PIDN:CAA57926.1; PII

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin
F:14-97/Domain: Immunoglobulin homology <IMM>

RESULT 11

S55536
Ig heavy chain V region pe20 - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C:Accession: S55536
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

utations in the variable region genes

A:Reference number: S55528; MUID:95239763; PMID:7536850

A:Accession: S55536

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <BOE>

A:Cross-references: UNIPARC:UPI0000116200; EMBL:X82589; NID:G854304; PIDN:CAA57925.1; PII

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotrimer; Immunoglobulin
F:14-97/Domain: Immunoglobulin homology <IMM>

RESULT 12

E27888
Ig heavy chain V region (H35-C6) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: E27888
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a

A:Reference number: A91043; MUID:86300658; PMID:2427335

Query Match 93.5%; Score 87; DB 2; Length 120;

Best Local Similarity 94.1%; Pred. No. 3.8e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
||| |||||
DB 49 TISGSGSYTYPPDSVKG 65

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 25.1575 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-157

Perfect score: 93
Sequence: 1 TISDGSSTYTPDSVKG 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	93	100.0	98	1	HV57_MOUSE	P18528 mus musculu
2	90	96.8	487	2	Q99KA4_MOUSE	Q99KA4 mus musculu
3	87	93.5	119	2	Q920E7_MOUSE	Q920E7 mus musculu
4	87	93.5	196	2	Q65ZL8_MOUSE	Q65ZL8 mus musculu
5	84	90.3	255	2	Q6RB05_MOUSE	Q6RB05 mus musculu
6	81	87.1	117	1	HV58_MOUSE	P18529 mus musculu
7	73	78.5	117	1	HV59_MOUSE	P18530 mus musculu
8	67	72.0	117	1	HV54_MOUSE	P18525 mus musculu
9	67	72.0	589	2	Q5XHD5_XENILA	Q5XHD5 xenopus lae
10	66	71.0	117	1	HV55_MOUSE	P18526 mus musculu
11	65.5	70.4	97	1	HV56_MOUSE	P18527 mus musculu
12	65	69.9	98	2	Q4TU56_TETNG	Q4TU56 tetradon n
13	64	68.8	479	2	Q5BK12_RAT	Q5BK12 rattus norv
14	63.5	66.3	467	2	Q4VBH1_RAT	Q4VBH1 rattus norv
15	62	66.7	464	2	Q6MZU6_HUMAN	Q6MZU6 homo sapien
16	60	64.5	99	2	Q4TSM5_TETNG	Q4TSM5 tetradon n
17	60	64.5	479	2	Q5POK3_RAT	Q5POK3 rattus norv
18	59	63.4	96	2	Q4TSS4_TETNG	Q4TSS4 tetradon n
19	59	63.4	480	2	Q91XEL_MOUSE	Q91XEL mus musculu
20	59	63.4	584	2	Q6INK3_XENILA	Q6INK3 xenopus lae
21	58.5	62.9	117	1	HV53_MOUSE	P18524 mus musculu
22	58.5	62.9	614	2	Q6DDQ7_XENILA	Q6DDQ7 xenopus lae
23	58	62.4	119	1	HV11_HUMAN	P01773 homo sapien
24	58	62.4	119	2	Q5F2I8_MOUSE	Q5F2I8 mus musculu
25	55.5	59.7	367	2	Q5W8X4_XENTR	Q5W8X4 xenopus tro
26	55.5	59.7	486	2	Q91Z07_MOUSE	Q91Z07 mus musculu
27	54.5	58.6	121	2	Q9UI71_HUMAN	Q9UI71 homo sapien
28	54.5	58.6	469	2	Q569F4_HUMAN	Q569F4 homo sapien
29	54.5	58.6	593	2	Q6INM5_XENILA	Q6INM5 xenopus lae
30	54	58.1	465	2	Q5IUJ0_RAT	Q5IUJ0 rattus norv
31	54	58.1	597	2	Q96BB9_HUMAN	Q96BB9 homo sapien

32	54	58.1	1021	2	Q7SAK8_NEUCR	Q7SAK8 neurospora
33	54	58.1	1037	2	Q6MPG6_NEUCR	Q6MPG6 neurospora
34	54	58.1	1090	2	Q4NDB8_PMITC	Q4NDB8 arthroacte
35	53	57.0	117	1	HV3C_HUMAN	P01764 homo sapien
36	53	57.0	461	2	Q5MTV3_RAT	Q5MTV3 rattus norv
37	53	57.0	465	2	Q6P6C4_HUMAN	Q6P6C4 homo sapien
38	53	57.0	475	2	Q6MZ06_HUMAN	Q6MZ06 homo sapien
39	53	57.0	605	2	Q6GMY2_HUMAN	Q6GMY2 homo sapien
40	52.5	56.5	96	2	Q4SX82_TETNG	Q4SX82 tetradon n
41	52	55.9	236	2	Q6ZP85_HUMAN	Q6ZP85 homo sapien
42	52	55.9	281	2	Q7SAG0_ASHGO	Q7SAG0 ashbya gos
43	50.5	54.3	116	1	HV05_CARAU	P19181 carassius a
44	50	53.8	121	1	HV3J_HUMAN	P01771 homo sapien
45	50	53.8	494	2	Q96K68_HUMAN	Q96K68 homo sapien

ALIGNMENTS

```
RESULT 1
HV57_MOUSE          STANDARD,          PRT,          98 AA.
ID HV57_MOUSE
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 6..96.
DS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
RA "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
CC -I- SIMILARITY: Contains 1 Ig-1 like (immunoglobulin-like) domain.
-----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC PIR: J0501; HWS96.
DR HSSP; P01783; IIGC.
DR SMR; P18528; 1-98.
DR InterPro; IPR007110; Ig-1-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV, 1.
KW PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region.
FT DOMAIN 1 >98
FT NON_TER 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F9JFBP95B CRC64;
-----
Query Match          100.0%; Score 93; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TISDGSSTYTPDSVKG 17
Db 50 TISDGSSTYTPDSVKG 66
-----
RESULT 2
Q99KA4_MOUSE
ID Q99KA4_MOUSE PRELIMINARY; PRT; 487 AA.
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AC 099K4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE 1gh-VJ558 protein.
GN Name=1gh-VJ558;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=42386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helel F.,
RA Datschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomshyukl S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Director MGC Project;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AA04786.1; -; mRNA.
DR HSP; P01810; 2FBJ.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR MGI; MGI:96486; 1gh-VJ558.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; 1g-1ike.
DR InterPro; IPR003597; 1g_c1.
DR InterPro; IPR003006; 1g_MHC.
DR InterPro; IPR003596; 1g_v.
DR Pfam; Pf07654; C1-bet; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; 1g_LIKE; 4.
DR PROSITE; PS00290; 1g_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 487 AA; 52555 MW; 7DC8B96DB33077B CRC64;

Query Match 96.8%; Score 90; DB 2; Length 487;
Best Local Similarity 94.1%; Pred. No. 2.3e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TISDGSYTYPPDSVK 17
Db 69 TISDGSYTYPPDNVKG 85

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DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Prein-mimicking anti-idiotypic heavy chain variable region
DE (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Actin J.D., Iape A., Jennings I.G., Horatidis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87175692; PubMed=3104915;
RA Lawler A.M., Lin P.S., Gearhart P.J.;
RT "Adult B-cell repertoire is biased toward two heavy-chain variable-
RT region genes that rearrange frequently in fetal pre-B cells."
RL Proc. Natl. Acad. Sci. U.S.A. 84:2454-2458(1987).
DR EMBL; AF307937; AA109421.1; -; Genomic_DNA.
DR PIR; C25913; C25913.
DR HSP; P01783; 1IGC.
DR SMK; Q920E7; 1-119.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; 1g-1ike.
DR InterPro; IPR003596; 1g_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; 1g_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13026 MW; F6B90404381CA7C CRC64;

Query Match 93.5%; Score 87; DB 2; Length 119;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TISDGSYTYPPDSVK 17
Db 50 TISDGSYTYPPDSVK 66

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```

RESULT 3
ID Q920E7_MOUSE PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

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RESULT 4
ID Q65ZL8_MOUSE PRELIMINARY; PRT; 196 AA.
AC Q65ZL8;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Vh7183-DSP2-JH3-CHI protein (Fragment).
GN Name=Vh7183-DSP2-JH3-CHI;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAIB/c;
RX MEDLINE=95362300; PubMed=7635518;
RA Komori T., Sugiyama H.;
RT "An aberrant splicing using a 3' cryptic splice site within the CHI
RT exon induces truncated mu-chain production."
RL Immunology 85:166-170(1995).
DR EMBL; S79401; AAB35023.2; -; mRNA.
DR SMK; Q65ZL8; 20-195.
DR InterPro; IPR003599; 1g.
DR InterPro; IPR007110; 1g-1ike.
DR InterPro; IPR003596; 1g_v.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; 1g_LIKE; 1.
FT NON_TER 196
SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

```


FT	CHAIN	1	19	Ig heavy chain V region 7-39.
FT	REGION	20	117	Framework-1.
FT	REGION	20	49	Framework-1.
FT	REGION	50	54	Complementarity-determining-1.
FT	REGION	55	68	Framework-2.
FT	REGION	69	85	Complementarity-determining-2.
FT	REGION	86	117	Framework-3.
FT	DISULFID	41	115	By similarity.
FT	NON TER	117	117	
SEQ	SEQUENCE	117 AA;	12972 MW;	DSCA4167D0F1774F CRC64;
Query Match	Similarity	78.5%;	Score 73;	DB 1;
Best Local	Similarity	82.4%;	Pred. No. 0.0023;	Length 117;
Matches	14; Conservative	1;	Mismatches	2; Indels
				0; Gaps
QY	1 TISDGSSTYTPDSSYKG	17		
DB	69 SISGGSSTYTPDSSYKG	85		

ID	NAME	STANDARD	PRT	117 AA
AC	PI8525			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Ig heavy chain V region 5-84 precursor.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontiformes; Glires; Rodentia; Sciurognathi;			
OC	Muridea; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=BAH/cj			
RX	MEDLINE=85279149; PubMed=24996554; DOI=10.1084/jem.169.6.2007;			
RA	Lewy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.C.;			
RT	"Early onset of somatic mutation in immunoglobulin VH genes during the			
RT	primary immune response.";			
RL	J. Exp. Med. 169:2007-2019(1989).			
CC	-I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
DR	PID; J70505; HVMS84.			
DR	PID; IAR1; X-ray; Da--			
DR	Ensembl; ENSMUSG00000062386; Mus musculus.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_V.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PSS0835; IG_LIKE; 1.			
KW	3D-structure; Immunoglobulin domain; Immunoglobulin V region; signal.			
FT	SIGNAL	1	19	
FT	CHAIN	20	117	
FT	REGION	20	49	
FT	REGION	50	54	
FT	REGION	55	68	
FT	REGION	69	85	
FT	REGION	86	117	
FT	DISULFID	41	115	
FT	NON TER	117	117	
FT	SEQUENCE	117 AA;	12872 MW;	234055CBA6469861 CRC64;
QY	Query Match	72.0%;	Score 67;	DB 1; Length 117;
QY	Best Local Similarity	75.0%;	Pred. NO. 0.02;	
QY	Matches	12; Conservative	2; Mismatches	2; Indels 0; Gaps 0;

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Db          70  ISNCGCGSTYPTDTRVKG  85
RESULT  9
ID      05XHD5_XENLA  PRELIMINARY;      PRT;      589  AA.
AC      05XHD5;
DT      25-OCT-2004 (TREMBlrel. 28, Created)
DT      25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT      25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE      Hypotheetical protein.
OS      Xenopus laevis (African clawed frog).
OC      Euryarchaea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC      Xenopodinae; Xenopus; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=whole;
RX      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA      Klein S.L., Strusberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA      Richardson P.;
RA      "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT      initiative.";
RL      Dev. Dyn. 225:384-391(2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=whole;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Datchenko L., Marzulla K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein W.J., Udell T.B., Tshihyuk S., Carninci P., Prange C.,
RA      Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
RA      Bosak S.A., McGwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywniak M.I., Skalka U., Smillius D.E.,
RA      Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=whole;
RA      Klein S., Gerhard D.S.; to the EMBL/GenBank/DBJ databases.
RL      Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC084123; AA848423.1; -, mRNA.
DR      GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR      GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR      GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig cl.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig V.
DR      Pfam; PF07654; CI-sec; 3.
DR      SMART; SM00409; Ig; 4.
DR      SMART; SM00407; IGC1; 4.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG_LIKE; 5.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN; 4.
DR      Hypothetical protein.
SQ      SEQUENCE 589 AA; 65361 MW; DIA212659D6E9FCE CRC64;

```

Query Match 72.0%; Score 67; DB 2; Length 589;
 Best Local Similarity 81.2%; Pred. No. 0.11;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISDGGSTYTPDSYK 17
 |||||
 DB 68 ISDGGSTYTPDSYK 83

RESULT 10

HV55_MOUSE STANDARD; PRT; 117 AA.

AC P18526;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DT Ig heavy chain V region 345 precursor.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

[1] NUCLEOTIDE SEQUENCE.

RA STRAIN=BALE/cj;
 RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1 MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

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 use as long as its content is in no way modified and this statement is not
 removed.

[1] PIR; J0502; HVMS34.

DR HSSP; P01783; IIGC.
 DR SMR; P18526; 20-117.
 DR Ensembl; ENSMUSG0000062386; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin domain; Immunoglobulin V region; Signal.

KW SIGNAL 1 19 Ig heavy chain V region 345.
 FT CHAIN 20 117 Framework-1.

FT REGION 20 49 Complementarity-determining-1.
 FT REGION 50 54 Complementarity-determining-1.

FT REGION 55 68 Framework-2.
 FT REGION 69 85 Complementarity-determining-2.

FT REGION 86 117 Framework-3.
 FT DISULFID 41 115 By similarity.

FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12902 MW; 4938084627ACA99A CRC64;

Query Match 71.0%; Score 66; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 0.028;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISDGGSTYTPDSYK 17
 |||||
 DB 70 ISDGGSTYTPDSYK 85

RESULT 11

HV56_MOUSE STANDARD; PRT; 97 AA.

AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V region 914.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

[1] NUCLEOTIDE SEQUENCE.

RA STRAIN=BALE/cj;
 RX MEDLINE=89279149; PubMed=2499654; DOI=10.1084/jem.169.6.2007;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the
 primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).

CC -1 MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
 CC -1 SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

[1] PIR; J0504; HVMS91.

DR HSSP; P01783; IIGC.
 DR SMR; P18527; 1-97.
 DR Ensembl; ENSMUSG0000062386; Mus musculus.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin domain; Immunoglobulin V region.

KW DOMAIN 1 >97 Ig-like.

FT NON TER 97 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33F55DA893 CRC64;

Query Match 70.4%; Score 65.5; DB 1; Length 97;
 Best Local Similarity 82.4%; Pred. No. 0.028;
 Matches 14; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 TISDGGSTYTPDSYK 17
 :|||
 DB 50 SISDGS-STYTPDSYK 65

RESULT 12

Q4TU56_TETNG PRELIMINARY; PRT; 98 AA.

DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Chromosome undetermined SCAF649, whole genome shotgun sequence.
 DE (Fragment).

GN ORFNames=GSTENG00004372001;

OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

NCBI_TaxID=99883;

[1] NUCLEOTIDE SEQUENCE.

RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Maucell E., Bouneau L., Flecher C., Ozouf-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Casarelli S.,
 RA Anthouard V., Ubin J., Casarelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Caticolico L., Poulain J., De Bernardis V.,
 RA Crenaud C., Duprat S., Brottier P., Coutanceau J.P., Gonzy J.,
 RA Parra G., Lardier G., Chaple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mestrov J.,

RA Lundblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lander V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach U., Roest Crolius H.,
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NCIBLOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CA60100649; CAF87076.1; -; Genomic_DNA.
FT NON_TERR 1
SQ SEQUENCE 98 AA; 10862 MW; 0EB7F34DB9C4648D CRC64;
QY
Query Match 69.9%; Score 65; DB 2; Length 98;
Best Local Similarity 70.6%; Pred. No. 0.033;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 47 TISDGSYYTYPDSVKG 63
ID Q5BK12_RAT PRELIMINARY; PRT; 479 AA.
AC Q5BK12;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Igna protein.
GN Name=Igha;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NCIBLOTIDE SEQUENCE.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomshyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NCIBLOTIDE SEQUENCE.
RG NIH MGC Project;
RC TISSUE=Splice;
CC Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC091247; AA91247.1; -; mRNA.
DR SMR, Q5BK12; 20-241.
DR GO:0003823; P:antigen binding; IRA.
PR InterPro: IPR003599; IG.

DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-sec; 2.
DR SMART, SM00409; IG; 3.
DR SMART, SM00407; IG; 3.
DR SMART, SM00406; IG; 1.
DR PROSITE, PS50835; IG-LIKE; 3.
DR PROSITE, PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 479 AA; 52329 MW; 8B16164A8437C5 CRC64;
QY
Query Match 68.8%; Score 64; DB 2; Length 479;
Best Local Similarity 70.6%; Pred. No. 0.25;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Db 69 TVTSGGSNTYLDPSVKG 85
ID Q4VBH1_RAT PRELIMINARY; PRT; 467 AA.
AC Q4VBH1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE LOC29354 protein.
GN Name=LOC29354;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NCIBLOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Tomshyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NCIBLOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
CC Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
DR EMBL: BC095846; AA95846.1; -; mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-cl.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-sec; 3.

DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 KW Immunoglobulin domain; Repeat.
 SQ SEQUENCE 467 AA; 51651 MW; 1PF0328F50160ED3 CRC64;

Query Match 66.3%; Score 63.5; DB 2; Length 467;
 Best Local Similarity 86.7%; Pred. No. 0.3;
 Matches 13; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 3 SDGGSYTYPPDSVKG 17
 :|||||
 DB 72 TDGGS-TYPPDSVKG 85

RESULT 15

Q6MZU6_HUMAN PRELIMINARY; PRT; 464 AA.
 AC Q6MZU6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686C15213.
 GN Name=DKFZp686C15213;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo
 CX NCB1_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Rectum tumor;
 RG The German cDNA Consortium;
 RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Pobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640874; CAB45931.1; -; mRNA.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; Cl-sec; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 464 AA; 51099 MW; 2PCA72C66E8A0ABC CRC64;

Query Match 66.7%; Score 62; DB 2; Length 464;
 Best Local Similarity 80.0%; Pred. No. 0.5;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 SDGGSYTYPPDSVKG 17
 :|||||
 DB 72 SRGGSYTYADSVKG 86

Search completed: November 21, 2005, 12:04:11
 Job time : 26.1575 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 / Search time 6.41392 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-157

Perfect score: 93

Sequence: 1 TISDGSITYYPDSVKG 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCOM-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	100.0	120	2	US-08-435-516-1
2	93	100.0	120	2	US-08-435-516-2
3	93	100.0	120	2	US-08-435-516-3
4	93	100.0	123	2	US-09-344-587-13
5	93	100.0	300	1	US-08-661-052-4
6	93	100.0	300	2	US-09-188-082-4
7	93	100.0	300	2	US-09-364-088-4
8	93	100.0	300	2	US-09-102-716-4
9	93	100.0	301	1	US-08-661-052-14
10	93	100.0	301	2	US-09-188-082-14
11	93	100.0	301	2	US-09-364-088-14
12	93	100.0	301	2	US-09-102-716-14
13	93	100.0	352	2	US-09-203-958A-2
14	93	100.0	553	1	US-08-661-052-16
15	93	100.0	553	2	US-09-188-082-16
16	93	100.0	553	2	US-09-364-088-16
17	93	100.0	553	2	US-09-102-716-16
18	87	93.5	89	2	US-09-840-459-49
19	87	93.5	89	2	US-09-497-625A-49
20	87	93.5	98	2	US-09-840-459-38
21	87	93.5	98	2	US-09-840-459-39
22	87	93.5	98	2	US-09-497-625A-38
23	87	93.5	98	2	US-09-497-625A-39
24	87	93.5	109	1	US-08-793-490-6
25	87	93.5	116	1	US-08-888-366-10
26	87	93.5	116	1	US-08-888-366-12
27	87	93.5	118	2	US-09-269-332-46

ALIGNMENTS

28	87	93.5	118	2	US-09-269-332-56	Sequence 56, Appl
29	87	93.5	118	2	US-09-269-332-88	Sequence 88, Appl
30	87	93.5	118	2	US-09-269-332-90	Sequence 90, Appl
31	87	93.5	137	2	US-09-269-332-76	Sequence 76, Appl
32	87	93.5	137	2	US-09-269-332-77	Sequence 77, Appl
33	87	93.5	142	2	US-09-069-628-24	Sequence 24, Appl
34	87	93.5	143	2	US-09-069-628-23	Sequence 23, Appl
35	87	93.5	145	2	US-09-069-628-26	Sequence 26, Appl
36	86	92.5	98	2	US-09-840-459-45	Sequence 45, Appl
37	86	92.5	98	2	US-09-497-625A-45	Sequence 45, Appl
38	84	90.3	120	2	US-09-232-290-42	Sequence 42, Appl
39	84	90.3	456	2	US-09-495-880A-11	Sequence 11, Appl
40	83	89.2	123	1	US-08-356-272-3	Sequence 3, Appl
41	83	89.2	124	2	US-09-518-737-2	Sequence 25, Appl
42	82	88.2	141	2	US-09-069-628-25	Sequence 25, Appl
43	82	88.2	141	2	US-08-875-674A-1	Sequence 1, Appl
44	81	87.1	119	2	US-08-875-674A-3	Sequence 3, Appl
45	81	87.1	159	1	US-08-653-402B-2	Sequence 2, Appl

RESULT 1
US-08-435-516-1
Sequence 1, Application US/08435516
Patent No. 650931
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
TITLE OF INVENTION: IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
FILING DATE: 04-NOV-1992; -02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Bech E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-435-516-1
Query Match 100.0%; Score 93; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TISDGSITYYPDSVKG 17
Db 50 TISDGSITYYPDSVKG 66
RESULT 2
US-08-435-516-2
Sequence 2, Application US/08435516

Patent No. 6500931
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION NUMBER: US/08/435,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
FILING DATE: 04-NOV-1992; -02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-435-516-2

Query Match 100.0%; Score 93; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPPSVKG 17
|||
Db 50 TISDGSYYTPPSVKG 66

RESULT 3
US-08-435-516-3
Sequence 3, Application US/08435516
Patent No. 6500931
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO Fc RECEPTORS FOR
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 92 23377.4; PCT/US93/10384
FILING DATE: 04-NOV-1992; -02-NOV-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-435-516-3

Query Match 100.0%; Score 93; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPPSVKG 17
|||
Db 50 TISDGSYYTPPSVKG 66

RESULT 4
US-09-344-587-13
Sequence 13, Application US/09344587
Patent No. 6331402
GENERAL INFORMATION:
APPLICANT: Praest, Gerald
APPLICANT: Nussbaum, Sabine
APPLICANT: Moesner, Ellen
APPLICANT: Lenz, Helmut
TITLE OF INVENTION: REDUCTION OF INTERFERENCE OF IMMUNOASSAYS BY SUBSTANCES
FILE REFERENCE: BMID 9928 4897/00/US-1m
CURRENT APPLICATION NUMBER: US/09/344,587
EARLIER FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: DE 19828466.7
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 123
TYPE: PRT
ORGANISM: Mus musculus
US-09-344-587-13

Query Match 100.0%; Score 93; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPPSVKG 17
|||
Db 50 TISDGSYYTPPSVKG 66

RESULT 5
US-08-661-052-4
Sequence 4, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yaehwan M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-661-052-4

Query Match 100.0%; Score 93; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYYTPDSYVG 17
Db 50 TISDGSYYTPDSYVG 66

RESULT 6
US-09-188-082-4
Sequence 4, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-188-082-4

Query Match 100.0%; Score 93; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYYTPDSYVG 17
Db 50 TISDGSYYTPDSYVG 66

RESULT 7
US-09-364-088-4
Sequence 4, Application US/09364088
Patent No. 6365161
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th Floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-364-088-4

Query Match 100.0%; Score 93; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TISDGSYYTPDSYVG 17
Db 50 TISDGSYYTPDSYVG 66

RESULT 8
US-09-102-716-4
Sequence 4, Application US/09102716

Patent No. 6395272
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
Joel Goldstein
Robert Graziano
Cheslan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-102-716-4
Query Match 100.0%; Score 93; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CQ 1 TISDGSYTYPPDSVKG 17
Db 50 TISDGSYTYPPDSVKG 66
RESULT 9
US-08-661-052-14
Sequence 14, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
Joel Goldstein
Robert Graziano
Cheslan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-14
Query Match 100.0%; Score 93; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CQ 1 TISDGSYTYPPDSVKG 17
Db 69 TISDGSYTYPPDSVKG 85
RESULT 10
US-09-188-082-14
Sequence 14, Application US/09188082
Patent No. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
Joel Goldstein
Robert Graziano
Cheslan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-14

Query Match 100.0%; Score 93; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 2,1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYVG 17
DB 69 TISDGSYYTPDSYVG 85

RESULT 11

US-09-364-088-14
Sequence 14, Application US/09364088
Patent No. 6365161
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo, et al.
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD
TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street, 24th floor
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,088
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/188,082
FILING DATE: 07-JUNE-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MXI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-14

Query Match 100.0%; Score 93; DB 2; Length 301;
Best Local Similarity 100.0%; Pred. No. 2,1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYVG 17
DB 69 TISDGSYYTPDSYVG 85

RESULT 12

US-09-102-716-14
Sequence 14, Application US/09102716
Patent No. 6395272

GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo

Joel Goldstein

Robert Graziano

Chezia Somsundaram

TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD

TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/102,716

FILING DATE: 22-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/661,052

FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-5941

TELEFAX: (617)227-7400

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 301 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-102-716-14

Query Match 100.0%; Score 93; DB 2; Length 301;

Best Local Similarity 100.0%; Pred. No. 2,1e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSYVG 17
DB 69 TISDGSYYTPDSYVG 85

RESULT 13

US-09-203-958A-2
Sequence 2, Application US/09203958A
Patent No. 6682928
GENERAL INFORMATION:
APPLICANT: Keler, Tibor
APPLICANT: GOLDSTEIN, Joel
APPLICANT: GRAZIANO, Robert
APPLICANT: DEO, Yashwant M.
TITLE OF INVENTION: CELLS EXPRESSING ANTI-PC RECEPTOR
TITLE OF INVENTION: BINDING COMPONENTS
FILE REFERENCE: MXI-099CPA
CURRENT APPLICATION NUMBER: US/09/203,958A
PRIOR FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 60/067232
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: faecseq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 352
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-203-958A-2

Query Match 100.0%; Score 93; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17
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Db 216 TISDGSYYTPDSVKG 232

RESULT 14
US-08-661-052-16
Sequence 16, Application US/08661052

PATENT NO. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chetan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
ZIP: 02109-1875
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-16

Query Match 100.0%; Score 93; DB 1; Length 553;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 69 TISDGSYYTPDSVKG 85

RESULT 15
US-09-188-082-16
Sequence 16, Application US/09188082
PATENT NO. 6270765
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo

APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chetan Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
ZIP: 02109-1875
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-188-082-16

Query Match 100.0%; Score 93; DB 2; Length 553;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 69 TISDGSYYTPDSVKG 85

Search completed: November 21, 2005, 12:07:39
Job time : 7.41392 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:50:51 ; Search time 21.0476 Seconds
(without alignments)
337.478 Million cell updates/sec

Title: US-10-632-706-157

Perfect score: 93

Sequence: 1 TISDGSSTYPPDSVKG 17

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA-Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	93	100.0	17	4	US-10-632-706-141
2	93	100.0	17	4	US-10-632-706-145
3	93	100.0	17	4	US-10-632-706-149
4	93	100.0	17	4	US-10-632-706-153
5	93	100.0	17	4	US-10-632-706-157
6	93	100.0	118	3	US-09-144-886-62
7	93	100.0	118	3	US-09-144-886-63
8	93	100.0	118	4	US-10-632-706-59
9	93	100.0	118	4	US-10-632-706-60
10	93	100.0	120	4	US-10-229-335-1
11	93	100.0	120	4	US-10-229-335-2
12	93	100.0	120	4	US-10-229-335-3
13	93	100.0	120	4	US-10-412-406-2
14	93	100.0	120	4	US-10-412-406-10
15	93	100.0	120	4	US-10-412-406-12
16	93	100.0	120	4	US-10-412-406-14
17	93	100.0	120	4	US-10-412-406-16
18	93	100.0	352	3	US-09-203-958A-2
19	93	100.0	352	5	US-10-764-131-2
20	93	100.0	663	4	US-10-412-406-32
21	93	100.0	4852	4	US-10-412-406-33
22	90	96.8	123	3	US-09-144-886-60
23	90	96.8	123	3	US-10-632-706-57
24	87	93.5	17	4	US-10-281-479A-26
25	87	93.5	17	4	US-10-275-180A-26
26	87	93.5	17	4	US-10-286-132A-26
27	87	93.5	17	4	US-10-477-377-9

28	87	93.5	89	3	US-09-840-439-49	Sequence 49, Appl
29	87	93.5	89	4	US-10-766-773-49	Sequence 49, Appl
30	87	93.5	89	4	US-10-766-610-49	Sequence 49, Appl
31	87	93.5	89	4	US-10-733-563-49	Sequence 49, Appl
32	87	93.5	98	3	US-09-840-439-38	Sequence 38, Appl
33	87	93.5	98	3	US-09-840-439-39	Sequence 38, Appl
34	87	93.5	98	4	US-10-766-773-38	Sequence 38, Appl
35	87	93.5	98	4	US-10-766-773-39	Sequence 38, Appl
36	87	93.5	98	4	US-10-766-610-38	Sequence 38, Appl
37	87	93.5	98	4	US-10-766-610-39	Sequence 38, Appl
38	87	93.5	98	4	US-10-733-563-38	Sequence 39, Appl
39	87	93.5	98	4	US-10-733-563-39	Sequence 39, Appl
40	87	93.5	118	3	US-09-423-800-46	Sequence 46, Appl
41	87	93.5	118	3	US-09-423-800-56	Sequence 46, Appl
42	87	93.5	118	4	US-10-182-018-46	Sequence 46, Appl
43	87	93.5	118	4	US-10-182-018-56	Sequence 46, Appl
44	87	93.5	118	4	US-10-169-003-46	Sequence 46, Appl
45	87	93.5	118	4	US-10-169-003-56	Sequence 56, Appl

ALIGNMENTS

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RESULT 1
US-10-632-706-141
; Sequence 141, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOERPER, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURES:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-141
Query Match 100.0%; Score 93; DB 4; Length 17;
Best local similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 TISDGSSTYPPDSVKG 17
Db 1 TISDGSSTYPPDSVKG 17
RESULT 2
US-10-632-706-145
; Sequence 145, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 145
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-145

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 3
US-10-632-706-149
/ Sequence 149, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 149
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-149

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 4
US-10-632-706-153
/ Sequence 153, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 153
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-153

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 5
US-10-632-706-157
/ Sequence 157, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 157
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-157

Query Match      100.0%; Score 93; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TISDGSYYTPDSVKG 17
       |||
Db      1 TISDGSYYTPDSVKG 17

RESULT 6
US-09-144-886-62
/ Sequence 62, Application US/09144886
/ Patent No. US20020155114A1
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Amerdortier, Peter
/ TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
/ FILE REFERENCE: 2500.117USO
/ CURRENT APPLICATION NUMBER: US/09/144,886
/ CURRENT FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 98
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 62
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
/ OTHER INFORMATION: C39 region VH epitope 2
```


US-09-144-886-62

Query Match 100.0%; Score 93; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
|||||
DB 50 TISDGSYTYPPDSVKG 66

RESULT 7

US-09-144-886-63
Sequence 63, Application US/09144886
Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-63

Query Match 100.0%; Score 93; DB 3; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
|||||
DB 50 TISDGSYTYPPDSVKG 66

RESULT 8

US-10-632-706-59
Sequence 59, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
PRIOR FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 59
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-10-632-706-59

Query Match 100.0%; Score 93; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
|||||
DB 50 TISDGSYTYPPDSVKG 66

RESULT 9

US-10-632-706-60
Sequence 60, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
TITLE OF INVENTION: NEUROTOXINS
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
PRIOR FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 60
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody
US-10-632-706-60

Query Match 100.0%; Score 93; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
|||||
DB 50 TISDGSYTYPPDSVKG 66

RESULT 10

US-10-229-335-1
Sequence 1, Application US/10229335
Publication No. US2003014483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
IMMUNOBLOBULIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P.O. Box 953, 1545 Route 22 East
CITY: Annandale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-229-335-1

Query Match 100.0%; Score 93; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
|||
Db 50 TISDGSYTYPPDSVKG 66

RESULT 11
US-10-229-335-2
Sequence 2, Application US/10229335
Publication No. US2003014483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P.O. Box 953, 1545 Route 22 East
CITY: Annandale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-229-335-2

Query Match 100.0%; Score 93; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
|||
Db 50 TISDGSYTYPPDSVKG 66

RESULT 12
US-10-229-335-3

Sequence 3, Application US/10229335
Publication No. US2003014483A1
GENERAL INFORMATION:
APPLICANT: MEDAREX, INC.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO FC RECEPTORS FOR
IMMUNOBLOBLIN G ON HUMAN MONONUCLEAR PHAGOCYTES
NUMBER OF SEQUENCES: 28
STREET: P.O. Box 953, 1545 Route 22 East
CITY: Annandale
STATE: New Jersey
COUNTRY: USA
ZIP: 08801
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,335
FILING DATE: 26-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/435,516
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-229-335-3

Query Match 100.0%; Score 93; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYTYPPDSVKG 17
|||
Db 50 TISDGSYTYPPDSVKG 66

RESULT 13
US-10-412-406-2
Sequence 2, Application US/10412406
Publication No. US2004005839A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: GARBER, Ellen
APPLICANT: LYNS, Paul
APPLICANT: SALDHANA, Jose W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINA100CN
CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: PCT/US01/32140
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: murine
US-10-412-406-2

Query Match 100.0%; Score 93; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17
|||||
DB 50 TISDGSYYTPDSVKG 66

RESULT 14
US-10-412-406-10

Sequence 10, Application US/10412406
Publication No. US20040058394A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: GARBER, Ellen
APPLICANT: LYNE, Paul
APPLICANT: SALDHANA, Jose W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINA100CN
CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: PCT/US01/32140
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 120
TYPE: PRT
ORGANISM: Homo Sapien
US-10-412-406-10

Query Match 100.0%; Score 93; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17
|||||
DB 50 TISDGSYYTPDSVKG 66

RESULT 15
US-10-412-406-12

Sequence 12, Application US/10412406
Publication No. US20040058394A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: GARBER, Ellen
APPLICANT: LYNE, Paul
APPLICANT: SALDHANA, Jose W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES
FILE REFERENCE: BINA100CN
CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: PCT/US01/32140

PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 120
TYPE: PRT
ORGANISM: Homo Sapien
US-10-412-406-12

Query Match 100.0%; Score 93; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TISDGSYYTPDSVKG 17
|||||
DB 50 TISDGSYYTPDSVKG 66

Search completed: November 21, 2005, 12:33:37
Job time : 22.0476 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:04:27 ; Search time 0.31355 Seconds
(without alignments)
61.666 Million cell updates/sec

Title: US-10-632-706-157
Perfect score: 93
Sequence: 1 TISDGSYYTPDSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	81.7	444	7	US-11-172-320-6
2	55	59.1	125	7	US-11-144-248-16
3	54	58.1	98	1	US-10-789-273-10
4	54	58.1	98	7	US-11-144-248-32
5	54	58.1	121	1	US-10-789-273-9
6	54	58.1	138	1	US-10-789-273-4
7	54	58.1	138	1	US-10-789-273-8
8	54	58.1	138	1	US-10-789-273-12
9	54	58.1	470	7	US-11-144-248-46
10	53	57.0	98	7	US-11-144-248-30
11	53	57.0	473	7	US-11-144-248-50
12	51	54.8	122	7	US-11-144-248-24
13	50	53.8	124	7	US-11-144-248-8
14	50	53.8	250	1	US-10-512-184-27
15	50	53.8	470	7	US-11-144-248-45
16	48	51.6	139	1	US-10-721-763-33
17	43	46.2	174	7	US-11-144-248-4
18	43	46.2	470	7	US-11-144-248-49
19	42	45.2	802	1	US-10-510-386-2
20	41	44.1	120	7	US-11-077-978-7
21	40	43.0	102	1	US-10-997-201A-6
22	39	41.9	605	1	US-10-689-742-140
23	39	39.8	1841	7	US-11-057-058-63
24	37	39.8	258	1	US-10-512-184-26
25	37	39.8	327	1	US-10-512-184-62

26	37	39.8	327	1	US-10-512-184-64	Sequence 64, Appl
27	37	39.8	328	1	US-10-512-184-63	Sequence 63, Appl
28	37	39.8	429	7	US-11-074-176-248	Sequence 248, Appl
29	37	39.8	576	1	US-10-512-184-65	Sequence 65, Appl
30	37	39.8	625	1	US-10-512-184-47	Sequence 47, Appl
31	36	38.7	119	7	US-11-010-954-5	Sequence 5, Appl
32	36	38.7	600	1	US-10-131-826A-462	Sequence 462, Appl
33	36	38.7	1142	7	US-11-109-156-22	Sequence 22, Appl
34	35	37.6	203	1	US-10-510-386-122	Sequence 122, Appl
35	35	37.6	218	7	US-11-180-997-2	Sequence 2, Appl
36	35	37.6	394	1	US-10-131-826A-520	Sequence 520, Appl
37	35	37.6	716	1	US-10-131-826A-512	Sequence 512, Appl
38	35	37.6	1316	7	US-11-091-643-4	Sequence 4, Appl
39	35	37.1	133	7	US-11-010-748A-2	Sequence 2, Appl
40	34.5	37.1	133	7	US-11-010-748A-3	Sequence 3, Appl
41	34.5	37.1	133	7	US-11-010-748A-4	Sequence 4, Appl
42	34.5	37.1	626	1	US-11-010-748A-1	Sequence 1, Appl
43	34	36.6	261	1	US-10-512-184-35	Sequence 35, Appl
44	34	36.6	313	1	US-10-512-184-72	Sequence 72, Appl
45	34	36.6	314	1	US-10-982-545-11	Sequence 11, Appl

ALIGNMENTS

```

RESULT 1
US-11-172-320-6
Sequence 6, Application US/11172320
Publication No. US20050244413A1
GENERAL INFORMATION:
APPLICANT: Adolf, Guenther
APPLICANT: Baum, Anke
APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cytotoxic CD4 Antibody Immunconjugates and
TITLE OF INVENTION: Chemotherapeutic Agents
FILE REFERENCE: 1/1363
CURRENT APPLICATION NUMBER: US/11/172,320
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: US/10/645,215
PRIOR FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: EP 02 018 686.2
PRIOR FILING DATE: August 21, 2002
PRIOR APPLICATION NUMBER: US 60/405,956
PRIOR FILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-11-172-320-6
Query Match 81.7%; Score 76; DB 7; Length 444;
Best Local Similarity 82.4%; Pred. No. 8.5e-06;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 TISDGSYYTPDSVKG 17
DB 50 TISDGSYYTPDSVKG 66
RESULT 2
US-11-144-248-16
Sequence 16, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.

```

```
/ APPLICANT: Corvalan, Jose R.
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-16
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Query Match      59.1%; Score 54; DB 7; Length 125;
Best Local Similarity 68.8%; Pred. No. 0.0047;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY      2 ISDGGSTYYPDSSVKG 17
         ||| ||| ||| |||
Db       51 ISGGGGSTYYADSVKG 66
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```
RESULT 3
US-10-789-273-10
```

```
/ Sequence 10, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ FILE REFERENCE: BLN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ PRIOR FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-10
```

```
Query Match      58.1%; Score 54; DB 1; Length 98;
Best Local Similarity 68.8%; Pred. No. 0.0052;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGGSTYYPDSSVKG 17
         ||| ||| ||| |||
Db       51 ISGGGGSTYYADSVKG 66
```

```
RESULT 4
US-11-144-248-32
```

```
/ Sequence 32, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
```

```
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 32
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-32
```

```
Query Match      58.1%; Score 54; DB 7; Length 98;
Best Local Similarity 68.8%; Pred. No. 0.0052;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGGSTYYPDSSVKG 17
         ||| ||| ||| |||
Db       51 ISGGGGSTYYADSVKG 66
```

```
RESULT 5
US-10-789-273-9
```

```
/ Sequence 9, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ FILE REFERENCE: BLN-002CP
/ CURRENT APPLICATION NUMBER: US/10/789,273
/ PRIOR FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: US/10/388,389
/ PRIOR FILING DATE: 2003-03-12
/ PRIOR APPLICATION NUMBER: US 10/010,942
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-9
```

```
Query Match      58.1%; Score 54; DB 1; Length 121;
Best Local Similarity 68.8%; Pred. No. 0.0065;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGGSTYYPDSSVKG 17
         ||| ||| ||| |||
Db       51 ISGGGGSTYYADSVKG 66
```

```
RESULT 6
US-10-789-273-4
```

```
/ Sequence 4, Application US/10789273
/ Publication No. US20050249725A1
/ GENERAL INFORMATION:
/ APPLICANT: Basl, Gurliq
/ APPLICANT: Saldanha, Jose
/ APPLICANT: Vednock, Ted
/ TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
/ FILE REFERENCE: BLN-002CP
```

```
;; CURRENT APPLICATION NUMBER: US/10/789,273
;; CURRENT FILING DATE: 2004-02-27
;; PRIOR APPLICATION NUMBER: US/10/388,389
;; PRIOR FILING DATE: 2003-03-12
;; PRIOR APPLICATION NUMBER: US 10/010,942
;; PRIOR FILING DATE: 2001-12-06
;; PRIOR APPLICATION NUMBER: US 60/251,892
;; PRIOR FILING DATE: 2000-12-06
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 138
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: (1)...(19)
US-10-789-273-4
```

```
Query Match          58.1%; Score 54; DB 1; Length 138;
Best Local Similarity 58.8%; Pred. No. 0.0075;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 TISDGSYYTPDSYVG 17
      :|||:|||:|
Db      69 SIRSGGRTYYSDNVKG 85
```

```
RESULT 7
US-10-789-273-8
; Sequence 8, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: Basl, Gurig
;; APPLICANT: Saldanha, Jose
;; APPLICANT: Yednock, Ted
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
;; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
;; FILE REFERENCE: ELN-002CP
;; CURRENT APPLICATION NUMBER: US/10/789,273
;; CURRENT FILING DATE: 2004-02-27
;; PRIOR APPLICATION NUMBER: US/10/388,389
;; PRIOR FILING DATE: 2003-03-12
;; PRIOR APPLICATION NUMBER: US 10/010,942
;; PRIOR FILING DATE: 2001-12-06
;; PRIOR APPLICATION NUMBER: US 60/251,892
;; PRIOR FILING DATE: 2000-12-06
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 138
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Humanized 3D6 heavy chain variable region
;; NAME/KEY: SIGNAL
;; LOCATION: (1)...(19)
US-10-789-273-8
```

```
Query Match          58.1%; Score 54; DB 1; Length 138;
Best Local Similarity 58.8%; Pred. No. 0.0075;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 TISDGSYYTPDSYVG 17
      :|||:|||:|
Db      69 SIRSGGRTYYSDNVKG 85
```

```
RESULT 8
US-10-789-273-12
; Sequence 12, Application US/10789273
; Publication No. US20050249725A1
```

```
;; GENERAL INFORMATION:
;; APPLICANT: Basl, Gurig
;; APPLICANT: Saldanha, Jose
;; APPLICANT: Yednock, Ted
;; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
;; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
;; FILE REFERENCE: ELN-002CP
;; CURRENT APPLICATION NUMBER: US/10/789,273
;; CURRENT FILING DATE: 2004-02-27
;; PRIOR APPLICATION NUMBER: US/10/388,389
;; PRIOR FILING DATE: 2003-03-12
;; PRIOR APPLICATION NUMBER: US 10/010,942
;; PRIOR FILING DATE: 2001-12-06
;; PRIOR APPLICATION NUMBER: US 60/251,892
;; PRIOR FILING DATE: 2000-12-06
;; NUMBER OF SEQ ID NOS: 63
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12
;; LENGTH: 138
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Humanized 3D6 light chain variable region
;; NAME/KEY: SIGNAL
;; LOCATION: (1)...(19)
US-10-789-273-12
```

```
Query Match          58.1%; Score 54; DB 1; Length 138;
Best Local Similarity 58.8%; Pred. No. 0.0075;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 TISDGSYYTPDSYVG 17
      :|||:|||:|
Db      69 SIRSGGRTYYSDNVKG 85
```

```
RESULT 9
US-11-144-248-46
; Sequence 46, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
```

```
;; APPLICANT: Cohen, Bruce D.
;; APPLICANT: Beebe, Jean
;; APPLICANT: Miller, Penelope E.
;; APPLICANT: Moyer, James D.
;; APPLICANT: Corvalan, Jose R.
;; APPLICANT: Gallo, Michael
;; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
;; FILE REFERENCE: ABX-PF2
;; CURRENT APPLICATION NUMBER: US/11/144,248
;; CURRENT FILING DATE: 2005-06-02
;; PRIOR APPLICATION NUMBER: US/10/038,591
;; PRIOR FILING DATE: 2002-01-04
;; PRIOR APPLICATION NUMBER: 60/259,927
;; PRIOR FILING DATE: 2001-01-05
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 46
;; LENGTH: 470
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-248-46
```

```
Query Match          58.1%; Score 54; DB 7; Length 470;
Best Local Similarity 68.8%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      2 ISDGSYYTPDSYVG 17
      :|||:|||:|
Db      70 ISGSGSTYYADSVKG 85
```

RESULT 10

```
US-11-144-248-30
/ Sequence 30, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyet, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 30
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-30
```

```
Query Match      57.0%; Score 53; DB 7; Length 98;
Best Local Similarity 68.8%; Pred. No. 0.0075;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGSYTYYPDSVKG 17
DB      51 ISSGSGTYYADSVKG 66
```

RESULT 11

```
US-11-144-248-50
/ Sequence 50, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyet, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 50
/ LENGTH: 473
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-50
```

```
Query Match      57.0%; Score 53; DB 7; Length 473;
Best Local Similarity 68.8%; Pred. No. 0.004;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGSYTYYPDSVKG 17
DB      70 ISSGSGTYYADSVKG 85
```

RESULT 12

US-11-144-248-24

```
/ Sequence 24, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyet, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-24
```

```
Query Match      54.8%; Score 51; DB 7; Length 122;
Best Local Similarity 62.5%; Pred. No. 0.02;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGSYTYYPDSVKG 17
DB      51 ITGSGGTYYADSVKG 66
```

RESULT 13

```
US-11-144-248-8
/ Sequence 8, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyet, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-8
```

```
Query Match      53.8%; Score 50; DB 7; Length 124;
Best Local Similarity 62.5%; Pred. No. 0.029;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 ISDGSYTYYPDSVKG 17
DB      50 ISGSGGTYYADSVKG 65
```

RESULT 14

```
US-10-512-184-27
```



```

; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with
; OTHER INFORMATION: specificity against Fusarium spp.; originates from
; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

```

```

Query Match          53.8%; Score 50; DB 1; Length 250;
Best Local Similarity 62.5%; Pred. No. 0.061;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      2 ISDGSSTYYPDSVKG 17
Db      53 ISDGSSTYYPDSVKG 68

```

```

RESULT 15
US-11-144-248-45
; Sequence 45, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-45

```

```

Query Match          53.8%; Score 50; DB 7; Length 470;
Best Local Similarity 62.5%; Pred. No. 0.12;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      2 ISDGSSTYYPDSVKG 17
Db      70 ISGSGGTFYADSVKG 85

```

Search completed: November 21, 2005, 12:33:52
Job time : 1.41136 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 / Search time 40.1648 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-158

Perfect score: 154
Sequence: 1 QVQLVQSGGVMHPRSLKLSKCSGSGPTFS 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003s:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	100.0	30	ADR38764	Adx38764 Mouse hea
2	154	100.0	30	ADR38756	Adx38756 Mouse hea
3	154	100.0	30	ADR38768	Adx38768 Mouse hea
4	154	100.0	30	ADR38760	Adx38760 Mouse hea
5	138	89.6	97	ADY38091	Anti-H1L1
6	138	89.6	97	ADY38091	Anti-SARS
7	138	89.6	114	ABE11024	Human ant
8	138	89.6	115	ABE11024	Anti-IL-4
9	138	89.6	115	ABE11028	Human ant
10	138	89.6	115	ABE11023	Human ant
11	138	89.6	115	ABE11027	Human ant
12	138	89.6	115	ABE11025	Human ant
13	138	89.6	115	ABE11031	Human ant
14	138	89.6	115	ABE11022	Human ant
15	138	89.6	115	ABE11020	Human ant
16	138	89.6	115	ABE11029	Human ant
17	138	89.6	115	ABE11030	Human ant
18	138	89.6	115	ABE11019	Human ant
19	138	89.6	115	ABE11026	Human ant
20	138	89.6	115	ABE11021	Human ant
21	138	89.6	115	ABE11021	Human ant
22	138	89.6	115	ABE11021	Human ant
23	138	89.6	115	ABE11021	Human ant
24	138	89.6	115	ABE11021	Human ant

25	138	89.6	115	9	AEA08905	AEA08905 Heavy cha
26	138	89.6	115	9	AEA08988	AEA08988 Heavy cha
27	138	89.6	115	9	AEA08911	AEA08911 Heavy cha
28	138	89.6	115	9	AEA08913	AEA08913 Heavy cha
29	138	89.6	115	9	AEA08983	AEA08983 Heavy cha
30	138	89.6	115	9	AEA08994	AEA08994 Heavy cha
31	138	89.6	115	9	AEA08989	AEA08989 Heavy cha
32	138	89.6	115	9	AEA08903	AEA08903 Heavy cha
33	138	89.6	115	9	AEA08995	AEA08995 Heavy cha
34	138	89.6	115	9	AEA08985	AEA08985 Heavy cha
35	138	89.6	115	9	AEA08987	AEA08987 Heavy cha
36	138	89.6	115	9	AEA08915	AEA08915 Heavy cha
37	138	89.6	115	9	AEA08990	AEA08990 Heavy cha
38	138	89.6	115	9	AEA08981	AEA08981 Heavy cha
39	138	89.6	115	9	AEA08985	AEA08985 Heavy cha
40	138	89.6	115	9	AEA08989	AEA08989 Heavy cha
41	138	89.6	115	9	AEA08901	AEA08901 Heavy cha
42	138	89.6	115	9	AEA08982	AEA08982 Heavy cha
43	138	89.6	115	9	AEA08984	AEA08984 Heavy cha
44	138	89.6	115	9	AEA08986	AEA08986 Heavy cha
45	138	89.6	115	9	AEA08986	AEA08986 Heavy cha

ALIGNMENTS

RESULT 1
ID ADR38764 standard; peptide; 30 AA.
XX
AC ADR38764;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BONT-antibody framework 1 seqid 166.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 1.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
XX
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amerdorfer P;
XX
XX WPI; 2004-652009/63.
XX
DR New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 166; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, At1, Ar2, WRI(V), WRI(T), 3-1,
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) ; and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BONT-antibody framework region 1.
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 154; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.5e-13;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLVDSGGGVHPRGRLKLSKCSAGSGFTFS 30
 1 QVQLVDSGGGVHPRGRLKLSKCSAGSGFTFS 30
 Db 1 QVQLVDSGGGVHPRGRLKLSKCSAGSGFTFS 30
 RESULT 2
 ADR38756
 ID ADR38756 standard; peptide; 30 AA.
 AC ADR38756;
 DT 02-DEC-2004 (first entry)
 XX
 XX Mouse heavy chain anti-BONT-antibody framework 1 segid 158.
 DE
 XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW framework 1.
 KM
 XX
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA
 PI Marks JD, Amerdorfer P;
 PI
 DR WPI; 2004-652009/63.
 DR
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 PT
 XX Example 4; SEQ ID NO 158; 110pp; English.
 XX
 XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S23, C25, C33, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) ; and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BONT-antibody framework region 1.
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 154; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.5e-13;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QVQLVDSGGGVHPRGRLKLSKCSAGSGFTFS 30
 1 QVQLVDSGGGVHPRGRLKLSKCSAGSGFTFS 30
 Db 1 QVQLVDSGGGVHPRGRLKLSKCSAGSGFTFS 30
 RESULT 3
 ADR38768
 ID ADR38768 standard; peptide; 30 AA.
 AC ADR38768;
 DT 02-DEC-2004 (first entry)
 XX
 XX Mouse heavy chain anti-BONT-antibody framework 1 segid 170.
 DE
 XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW framework 1.
 KM
 XX
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA
 PI Marks JD, Amerdorfer P;
 PI
 DR WPI; 2004-652009/63.
 DR
 XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 PT
 XX Example 4; SEQ ID NO 170; 110pp; English.
 XX
 XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone

CC S25, C25 C39, 1C6, 3D12, B4, 1P3, hnc25, Ar1, Ar2, WR1 (V), WR1(T), 3-1,
CC 3-8, 3-10 and 1mN1, where (1) refers to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves connecting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulinism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 1.
XX
SQ Sequence 30 AA;

Query Match	100.0%	Score 154	DB 8	length 30
Best Local Similarity	100.0%	Pred. No.	2.5e-13	
Matches 30, Conservative	0	Mismatches	0	Indels 0; Gaps 0

QY

1 QVQLVSGGGVNHPRSLKLSGAGSFTTS 30

Db

1 QVQLVSGGGVNHPRSLKLSGAGSFTTS 30

RESULT 4
ADR38760
ID ADR38760 standard; peptide; 30 AA

Mouse heavy chain anti-BONT-antibody framework 1 segid 162.

KM antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KM BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KM framework 1.

SO **Mus sp.**

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marks JD, Amersdorfer P;

DR WPI; 2004-652009/63.

PT New Isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.

PS Example 4; SEQ ID NO 162; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A

BoNT/A1m isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone 855, C25, G39, 1C6, 3D12, B5, 1F3, hMc25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising a botulinum neurotoxin which BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinum or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulinum. This is the amino acid sequence of mouse heavy chain anti-BoNT-antibody framework region 1.

```

SQ Sequence 30 AA;
Query March 100.0%; Score 154; DB 8; Length 30;
Best Local Similarity 100.0%; Prod. No. 2.5e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY

1 QVQLVSGGGVHPRGSLKLSGAGSGFTPS 30

Db

1 QVQLVSGGGVHPRGSLKLSGAGSGFTPS 30

RESULT 5
AAB40091
ID AAB40091 standard; protein; 97 AA.

AA	Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 617
DE	

KM Human; neutralising antibody; interleukin-12; IL-12; antiinflammatoxy;
KM complementarity determining region; CDR; antirheumatic; antiarthritis;
KM antisclerotic; neuroprotective; antipsoriatic; antischamatic; cardiant
KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KM multiple sclerosis; rheumatoid arthritis.

OS Homo sapiens.

PN WO200056772-A1.

PD 28-SEP-2000

PF 24-MAR-2000; 2000WO-US007946.

PR 25-MAR-1999; 99US-0126603P.

PA (BADI) BASF AG.
PA (GEMY) GENETICS INST INC.

PA (GEMY) GENETICS INST INC.

PI Salfeld JG, Roguska M, Paekind M, Banerjee S, Tracey DB, White M,
PI Kamakacalan Z, Labkovsky B, Sakorafas P, Friedrich S, Wyles A,
PI Veldman GM, Venturini A, Barnes NW, Widom A, Elynn JG, Duncan AR,
PI Dedyswite EJ, Carmen S, Smith S, Holcet TL, Du Fou SL;

DR WPI; 2000-638250/61.

PT. New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohn's disease and multiple sclerosis.

XX PS Claim 75; Page 121; 377pp; English.

XX CC This invention relates to a new human antibody specific for human

CC interleukin-12 (IL-12). The invention also includes antigen binding

CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human

CC anti-IL-12 antibody heavy and light chain complementarity determining

CC region (CDR) amino acid sequences, and also includes variable region

CC amino acid sequences. Other variable region amino acid sequences are

CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771

CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063

CC represent other CDR sequences. Light chain CDR3 consensus sequences are

CC given in AAB40064-B40067. Primers used in the identification and

CC construction of the antibodies of the invention are given in AAC61062-

CC C61071. The antibody of the invention is a neutralizing antibody and has

CC antineoplastic, antitachytic, antisclerotic, antiinflammatory,

CC antiprotective, antidiarrhetic, antiasthmatic, cardiant, antiparasitic,

CC antibacterial and immunosuppressive activity. The antibodies or antigen-

CC binding fragments are useful in the treatment of disorders associated

CC with detrimental release of human IL-12, especially Crohn's disease,

CC multiple sclerosis and rheumatoid arthritis. They can also be used in the

CC manufacture of a pharmaceutical composition to treat human IL-12

CC disorders

XX CC

XX Sequence 97 AA;

Query Match 89.6%; Score 138; DB 3; Length 97;

Best Local Similarity 86.7%; Pred. No. 1.1e-10; Mismatches 1; Indels 0; Gaps 0;

Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVDSGGGVVHPGRSLKLSGAGSGFTFS 30

1 EVQLVDSGGGVVHPGRSLKLSGAGSGFTFS 30

DB 1 EVQLVDSGGGVVHPGRSLKLSGAGSGFTFS 30

RESULT 6

ADY93868

ID ADY93868 standard; protein; 97 AA.

XX AC ADY93868;

XX DT 16-JUN-2005 (first entry)

XX DB Anti-SARS DP44 germ-line antibody VH region BQ ID NO.18.

XX KW glycoprotein; respiratory-gen.; virucide; sars coronavirus infection;

XX KM antibody; heavy chain variable region.

XX OS SARS coronavirus.

XX PN US2005069869-A1.

XX PD 31-MAR-2005.

XX PF 04-AUG-2004; 2004US-00911838.

XX PR 04-AUG-2003; 2003US-0492529P.

XX PR 09-OCT-2003; 2003US-0510251P.

XX PR 18-FEB-2004; 2004US-0585670P.

XX PR 26-APR-2004; 2004US-0565595P.

XX PA (AMBR/) AMBROSINO D.

XX PA (HERRN/) HERNANDEZ H.

XX PA (GREE/) GREENOUGH T.

XX PA (LUZU/) LUZURIAGA K.

XX PA (SOMA/) SOMASUNDARAN M.

XX PA (BABC/) BABCOCK G J.

XX PA (THOM/) THOMAS W D.

XX PA (SULL/) SULLIVAN J.

XX PI Ambrosino D, Hernandez H, Greenough T, Luzuriaga K,

XX PI Somasundaran M, Babcock GJ, Thomas WD, Sullivan J;

DR WPI; 2005-252952/26.

XX PT New isolated nucleic acid encoding a SARS-CoV spike glycoprotein

XX PT polypeptide, and optimized for expression in a human host, useful for

XX PT diagnosing, preventing and/or treating SARS-CoV infection.

XX PS Example 17; SEQ ID NO 18; 138pp; English.

XX CC The invention relates to an isolated nucleic acid comprising a sequence

CC encoding a SARS coronavirus (SARS-CoV) spike glycoprotein (S protein), or

CC its fragment, where the sequence has been optimized for expression in a

CC human host. Also described: (1) a nucleic acid expression vector

CC comprising the above nucleic acid; (2) an isolated cell comprising the

CC expression vector of (1); (3) a polypeptide encoded by the above nucleic

CC acid; (4) an isolated polypeptide comprising an extracellular portion of

CC the SARS-CoV S polypeptide located between amino acids 15-119 of

CC ADY93852; or its fragment; (5) an isolated antibody, or its antigen

CC binding fragment, that specifically binds to the polypeptide of (3); (6)

CC an isolated antibody, or its antigen binding fragment, that specifically

CC binds to an antigen binding fragment of an anti-S protein antibody; (7) a

CC composition comprising a polypeptide of (4) or an antibody, or its

CC antigen binding fragment, and a pharmaceutical carrier; (8) making an S

CC protein, or its fragment, of SARS-CoV; (9) making an antibody, or its

CC antigen binding fragment, that specifically binds to an S protein of SARS

CC -CoV; (10) evaluating a biological sample for the presence of SARS-CoV;

CC (11) evaluating an antibody, or its antigen binding fragment, for

CC inhibition of infection by SARS-CoV; (12) treating a subject at risk for,

CC or exposed to SARS-CoV; (13) an immunocombustible comprising the antibody

CC of (5) linked to a therapeutic agent; (14) an isolated nucleic acid

CC molecule encoding the antibody, its antigen-binding portion, variable

CC heavy chain or variable light chain of (5); (15) an expression vector

CC comprising the nucleic acid molecule of (14); (16) a host cell comprising

CC the expression vector of (15); (17) a transgenic mammal comprising human

CC immunoglobulin heavy and light chain transgenes, where the mouse

CC expresses the antibody of (5); (18) a hybridoma prepared from the mammal

CC of (17), where the hybridoma produces the antibody; and (19) preparing an

CC anti-S protein antibody. The methods and compositions of the present

CC invention are useful for the diagnosis, prevention and/or treatment of

CC SARS-CoV infection. The present sequence represents an anti-SARS antibody

XX heavy chain variable region from the present invention.

XX S0 Sequence 97 AA;

Query Match 89.6%; Score 138; DB 9; Length 97;

Best Local Similarity 86.7%; Pred. No. 1.1e-10; Mismatches 1; Indels 0; Gaps 0;

Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVDSGGGVVHPGRSLKLSGAGSGFTFS 30

1 EVQLVDSGGGVVHPGRSLKLSGAGSGFTFS 30

DB 1 EVQLVDSGGGVVHPGRSLKLSGAGSGFTFS 30

RESULT 7

AEAL1024

ID AEAL1024 standard; protein; 114 AA.

XX AC AEAL1024;

XX DT 28-JUL-2005 (first entry)

XX DE Human anti-IL-4R heavy chain variable region, SEQ ID NO:66.

XX KW HIV infection; anti-hiv; infection; inflammation; antiinflammatory;

XX KW cancer; cytostatic; antibody; chimeric antibody;

XX KW heavy chain variable region; antibody engineering; anti-IL-4R.

XX OS Homo sapiens.

XX PN WO2005047325-A2.

XX PD 26-MAY-2005.

XX PF 04-NOV-2004; 2004WO-US037241.

```
XX 07-NOV-2003; 2003US-0517970P.
XX (AMGE-) AMGEN INC.
XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;
XX WPI; 2005-372347/38.
XX N-PSDB; ABA11010.
XX Polypeptide having cynomolgus monkey antibody heavy chain variable region
XX or light chain variable region, useful in diagnosing antigen in
XX biological samples, and for treating disease e.g., inflammation and
XX cancer.
XX Example 3; SEQ ID NO 66; 138bp; English.
XX The invention relates to an isolated polypeptide (I) comprising (a) one
XX of 4 sequences: ABA10964, ABA10966, ABA10968 and ABA10970; or ABA10970 or
XX ABA10972, and antibody heavy chain variable region, or (b) ABA10988, and
XX antibody light chain variable region. In (I), the antibody heavy chain or
XX light chain variable region is a cynomolgus monkey antibody heavy chain
XX variable region or cynomolgus monkey antibody light chain variable
XX region. The antibody heavy chain variable region or light chain variable
XX region is a human or mouse antibody heavy chain variable region or light
XX chain variable region. Also included are: an isolated polynucleotide (II)
XX comprising a sequence encoding (I); an isolated antibody (A1) comprising
XX a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a
XX second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the
XX effects of an antibody, comprising introducing into a cynomolgus monkey a
XX chimeric antibody comprising light chain and heavy chain variable regions
XX from an antibody and light chain and heavy chain constant regions from a
XX cynomolgus monkey, and evaluating the effects of the chimeric antibody in
XX the cynomolgus monkey; an expression vector (VI) comprising (II); a cell
XX (III) comprising VI; and a method of producing (I). (A1) further
XX comprises a human antibody heavy chain variable region and a human
XX antibody light chain variable region or a mouse antibody heavy chain
XX variable region and a mouse antibody light chain variable region. (III)
XX is useful for producing a chimeric antibody, which involves incubating
XX (III) under conditions suitable for expression of the chimeric antibody,
XX and isolating the chimeric antibody. (I) or (A1) is useful for diagnosing
XX antigen in biological samples, and for treating diseases such as HIV,
XX inflammation and cancer. The present sequence represents an anti-IL-4R
XX heavy chain variable region used to make the chimeric antibodies of the
XX invention.
XX Sequence 114 AA;
XX
XX Query Match 89.6%; Score 138; DB 9; Length 114;
XX Best Local Similarity 86.7%; Pred. No. 1.3e-10;
XX Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 QVQLVQSGGGLVHPGSLRLSCAAGSFTFS 30
XX :|||:|||||:|||||:|||||:|||||:
XX 1 EVQLVQSGGGLVHPGSLRLSCAAGSFTFS 30
XX
XX RESULT 8
XX ABB07232
XX ID ABB07232 standard; protein; 115 AA.
XX
XX AC ABB07232;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Anti-IL-4 receptor Mab 12B5 heavy chain variable region.
XX
XX KW Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
XX antitumor; dermatological; antitumor; antiinflammatory; cytotoxic;
XX antitumor; immunosuppressive; tuberculostatic; ophthalmological;
XX antitumor; antitumor.
XX
XX OS Homo sapiens.
```

```
XX Key Location/Qualifiers
XX Region 31..35 complementarity determining region (CDR) 1"
XX Region 50..65 complementarity determining region (CDR) 2"
XX Region 98..104 complementarity determining region (CDR) 3"
XX
XX WO200192340-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US017094.
XX
XX 26-MAY-2000; 2000US-00579808.
XX 19-SEP-2000; 2000US-0065343.
XX 15-FEB-2001; 2001US-00785934.
XX 01-MAY-2001; 2001US-00847816.
XX
XX (IMMUNEX CORP.
XX
XX Plueneke JD;
XX
XX WPI; 2002-114332/15.
XX N-PSDB; ABA94332.
XX
XX Novel human antibody which binds human interleukin (IL)-4 receptor and is
XX capable of inhibiting IL-4 induced biological activity, functions as IL-4
XX antagonist and is useful for treating septic arthritis, scleroderma.
XX Claim 4; Page 75-76; 85bp; English.
XX
XX The invention relates to a human antibody (an interleukin (IL)-4
XX antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of
XX inhibiting an IL-4-induced biological activity. (I) is also useful for
XX inhibiting both IL-4-induced biological activity and IL-13-induced
XX biological activity in vivo in a human, and for treating septic arthritis
XX in a human afflicted with septic arthritis, dermatitis herpetiformis,
XX conditions such as septic/reactive arthritis, dermatitis herpetiformis,
XX urticaria (especially chronic idiopathic urticaria), ulcers, gastric
XX inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
XX inflammation, bowel disease, other disorders of the digestive system in
XX which IL-4 plays a role (e.g., IL-4-induced inflammation of part of the
XX gastrointestinal tract), conditions in which IL-4-induced barrier
XX disruption plays a role (e.g., conditions characterized by decreased
XX epithelial barrier function in the lung or gastrointestinal tract),
XX scleroderma, hypertrophic scarring, Whipple's disease, benign prostate
XX hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
XX medication, Kawasaki disease, sickle cell disease or crisis, Churg-
XX Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
XX autoimmune lymphoproliferative syndrome, autoimmune hemolytic anemia,
XX Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
XX pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
XX diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
XX antagonists also find use as adjuvants to allergy immunotherapy and as
XX vaccine adjuvants, especially when directed to the immune response toward a
XX TH1 response would be beneficial in treating or preventing the disease.
XX The present sequence represents an anti-IL-4 receptor monoclonal antibody
XX (Mab) 12B5 heavy chain variable region
XX
XX Sequence 115 AA;
XX
XX Query Match 89.6%; Score 138; DB 5; Length 115;
XX Best Local Similarity 86.7%; Pred. No. 1.4e-10;
XX Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 QVQLVQSGGGLVHPGSLRLSCAAGSFTFS 30
XX :|||:|||||:|||||:|||||:|||||:
XX 1 EVQLVQSGGGLVHPGSLRLSCAAGSFTFS 30
XX
XX RESULT 9
```

ID AEA1028
 AC AEA1028;
 DT 28-JUL-2005 (first entry)
 XX
 DE Human anti-IL-4R heavy chain variable region, SEQ ID NO:70.
 XX
 XX HIV infection; anti-hiv; infection; inflammation; antiinflammatory;
 KW cancer; cytostatic; antibody; chimeric antibody;
 XX heavy chain variable region; antibody engineering; anti-IL-4R.
 OS Homo sapiens.
 XX
 XX MO2005047325-A2.
 PN
 XX 26-MAY-2005.
 PD
 XX
 XX 04-NOV-2004; 2004MO-US037241.
 PF
 XX 07-NOV-2003; 2003US-0517970P.
 PR
 XX
 XX (AMGE-) AMGEN INC.
 PA
 PI Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;
 XX WPI: 2005-372347/38.
 DR N-PSDB; AEA1014.
 DR
 XX
 XX Polypeptide having cynomolgus monkey antibody heavy chain variable region
 PT or light chain variable region, useful in diagnosing antigen in
 PT biological samples, and for treating disease e.g., inflammation and
 XX cancer.
 XX
 XX Example 3; SEQ ID NO 70; 138pp; English.
 PS
 XX
 XX The invention relates to an isolated polypeptide (I) comprising (a) one
 CC of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or
 CC AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and
 CC antibody light chain variable region. In (I), the antibody heavy chain or
 CC light chain variable region is a cynomolgus monkey antibody heavy chain
 CC variable region or cynomolgus monkey antibody light chain variable
 CC region. The antibody heavy chain variable region or light chain variable
 CC region is a human or mouse antibody heavy chain variable region or light
 CC chain variable region. Also included are: an isolated polynucleotide (II)
 CC comprising a sequence encoding (I); an isolated antibody (AI) comprising
 CC a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a
 CC second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the
 CC effects of an antibody, comprising introducing into a cynomolgus monkey a
 CC chimeric antibody comprising light chain and heavy chain variable regions
 CC from an antibody and light chain and heavy chain constant regions from a
 CC cynomolgus monkey, and evaluating the effects of the chimeric antibody in
 CC the cynomolgus monkey; an expression vector (VI) comprising (II); a cell
 CC (III) comprising VI; and a method of producing (I). (AI) further
 CC comprises a human antibody heavy chain variable region and a human
 CC antibody light chain variable region or a mouse antibody heavy chain
 CC variable region and a mouse antibody light chain variable region. (III)
 CC is useful for producing a chimeric antibody, which involves incubating
 CC (III) under conditions suitable for expression of the chimeric antibody,
 CC and isolating the chimeric antibody. (I) or (AI) is useful for diagnosing
 CC antigen in biological samples, and for treating diseases such as HIV,
 CC inflammation and cancer. The present sequence represents an anti-IL-4R
 CC heavy chain variable region used to make the chimeric antibodies of the
 CC invention.
 CC
 CC Sequence 115 AA;
 SQ
 Query March 89.6%; Score 138; DB 9; Length 115;
 Best Local Similarity 86.7%; Pred.No. 1,4e-10;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0

Db 1 EVOLVQSGGGLVHPGSLRLSCAGSGFRFS 30

RESULT 10
ID AEA11023
AEA11023 standard; protein; 115 AA.
AC AEA11023;
DT 28-JUL-2005 (first entry)
DE Human anti-IL-4R heavy chain variable region, SEQ ID NO:65.
XX
XX HIV infection; anti-hiv; infection; inflammation; antiinflammatory;
XX cancer; cytotoxic; antibody; chimeric antibody;
XX heavy chain variable region; antibody engineering; anti-IL-4R.
XX
XX Homo sapiens.
XX
XX MO2005047325-A2.
XX
XX 26-MAY-2005.
XX
XX 04-NOV-2004; 2004MO-US037241.
XX
XX 07-NOV-2003; 2003US-0517970P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;
XX
XX WPI: 2005-372347/38.
XX
XX DR N-PSDB; AEA11009.
XX
XX Polypeptide having cynomolgus monkey antibody heavy chain variable region
XX or light chain variable region, useful in diagnosing antigen in
XX biological samples, and for treating disease e.g., inflammation and
XX cancer.
XX
XX Example 3; SEQ ID NO 65; 138pp; English.
XX
XX The invention relates to an isolated polypeptide (I) comprising (a) one
XX of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or
XX AEA10972; and antibody heavy chain variable region, or (b)AEA10988, and
XX antibody light chain variable region. In (I), the antibody heavy chain or
XX light chain variable region is a cynomolgus monkey antibody heavy chain
XX variable region or cynomolgus monkey antibody light chain variable
XX region. The antibody heavy chain variable region or light chain variable
XX region is a human or mouse antibody heavy chain variable region or light
XX chain variable region. Also included are: an isolated polynucleotide (II)
XX comprising a sequence encoding (I); an isolated antibody (AI) comprising
XX a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a
XX second polypeptide having SEQ ID No. 30; a method of evaluating (MI) the
XX effects of an antibody, comprising introducing into a cynomolgus monkey a
XX chimeric antibody comprising light chain and heavy chain variable regions
XX from an antibody and light chain and heavy chain constant regions from a
XX cynomolgus monkey; and evaluating the effects of the chimeric antibody in
XX the cynomolgus monkey; an expression vector (VI) comprising (II); a cell
XX comprising VI; and a method of producing (I). (AI) further
XX comprises a human antibody heavy chain variable region and a human
XX antibody light chain variable region or a mouse antibody heavy chain
XX variable region and a mouse antibody light chain variable region. (II)
XX is useful for producing a chimeric antibody, which involves incubating
XX (III) under conditions suitable for expression of the chimeric antibody,
XX and isolating the chimeric antibody. (I) or (AI) is useful for diagnosing
XX antigen in biological samples, and for treating diseases such as HIV,
XX inflammation and cancer. The present sequence represents an anti-IL-4R
XX heavy chain variable region used to make the chimeric antibodies of the
XX invention.
XX
XX Sequence 115 AA;

is useful for producing a chimeric antibody, which involves incubating (iii) under conditions suitable for expression of the chimeric antibody, and isolating the chimeric antibody (i) or (ai) is useful for diagnosing antigen in biological samples, and for treating diseases such as HIV, inflammation and cancer. The present sequence represents an anti-IL-4R heavy chain variable region used to make the chimeric antibodies of the invention.

Sequence 115 AA:

Query Match 89.6%; Score 138; DB 9; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.4e-10;

Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGGVDVHPGRLKLSGCSGFTFS 30
:|||||:|||||:|||||:|||||:|||||
D 1 EVQLVQSGGVDVHPGSLRLSCGSGFTFS 30

RESULT 13

AEAI1031
ID AEA11031 standard; protein; 115 AA.

AC AEA11031;

XX 28-JUL-2005 (first entry)

XX Human anti-IL-4R heavy chain variable region, SEQ ID NO:73.

XX HIV infection; anti-hiv; infection; inflammation; antinflammatory;

XX cancer; cytostatic; antibody; chimeric antibody;

XX heavy chain variable region; antibody engineering; anti-IL-4R.

XX Homo sapiens.

XX WO2005047325-A2.

XX 26-MAY-2005.

XX 04-NOV-2004; 2004MO-US037241.

XX 07-NOV-2003; 2003US-0517970P.

XX (AMGB-) AMGEN INC.

XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;

XX WPI; 2005-372347/38.

XX N-PSDB; AEA11017.

XX Polypeptide having cynomolgus monkey antibody heavy chain variable region or light chain variable region, useful in diagnosing antigen in biological samples, and for treating disease e.g., inflammation and cancer.

XX Example 3; SEQ ID NO 73; 138pp; English.

XX The invention relates to an isolated polypeptide (i) comprising (a) one of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and antibody light chain variable region. In (i), the antibody heavy chain or light chain variable region is a cynomolgus monkey antibody heavy chain variable region or cynomolgus monkey antibody light chain variable region. The antibody heavy chain variable region or light chain variable region is a human or mouse antibody heavy chain variable region or light chain variable region. In (i), the antibody heavy chain or light chain variable region is a cynomolgus monkey antibody heavy chain variable region or cynomolgus monkey antibody light chain variable region. Also included are: an isolated polynucleotide (ii) comprising a sequence encoding (i); an isolated antibody (ai) comprising a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a second polypeptide having SEQ ID No. 30; a method of evaluating (wi) the effects of an antibody, comprising introducing into a cynomolgus monkey a chimeric antibody comprising light chain and heavy chain variable regions from an antibody and light chain and heavy chain constant regions from a cynomolgus monkey, and evaluating the effects of the chimeric antibody in

the cynomolgus monkey; an expression vector (vi) comprising (ii); a cell (iii) comprising vi; and a method of producing (i). (ai) further comprises a human antibody heavy chain variable region and a human antibody light chain variable region or a mouse antibody heavy chain variable region and a mouse antibody light chain variable region. (iii) is useful for producing a chimeric antibody, which involves incubating (iii) under conditions suitable for expression of the chimeric antibody, and isolating the chimeric antibody. (i) or (ai) is useful for diagnosing antigen in biological samples, and for treating diseases such as HIV, inflammation and cancer. The present sequence represents an anti-IL-4R heavy chain variable region used to make the chimeric antibodies of the invention.

Sequence 115 AA:

Query Match 89.6%; Score 138; DB 9; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.4e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGGVDVHPGRLKLSGCSGFTFS 30
:|||||:|||||:|||||:|||||:|||||
D 1 EVQLVQSGGVDVHPGSLRLSCGSGFTFS 30

RESULT 14

AEAI1022
ID AEA11022 standard; protein; 115 AA.

AC AEA11022;

XX 28-JUL-2005 (first entry)

XX Human anti-IL-4R heavy chain variable region, SEQ ID NO:64.

XX HIV infection; anti-hiv; infection; inflammation; antinflammatory;

XX cancer; cytostatic; antibody; chimeric antibody;

XX heavy chain variable region; antibody engineering; anti-IL-4R.

XX Homo sapiens.

XX WO2005047325-A2.

XX 26-MAY-2005.

XX 04-NOV-2004; 2004MO-US037241.

XX 07-NOV-2003; 2003US-0517970P.

XX (AMGB-) AMGEN INC.

XX Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;

XX WPI; 2005-372347/38.

XX N-PSDB; AEA11008.

XX Polypeptide having cynomolgus monkey antibody heavy chain variable region or light chain variable region, useful in diagnosing antigen in biological samples, and for treating disease e.g., inflammation and cancer.

XX Example 3; SEQ ID NO 64; 138pp; English.

XX The invention relates to an isolated polypeptide (i) comprising (a) one of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10978; or AEA10970 or AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and antibody light chain variable region. In (i), the antibody heavy chain or light chain variable region is a cynomolgus monkey antibody heavy chain variable region or cynomolgus monkey antibody light chain variable region. The antibody heavy chain variable region or light chain variable region is a human or mouse antibody heavy chain variable region or light chain variable region. In (i), the antibody heavy chain or light chain variable region is a cynomolgus monkey antibody heavy chain variable region or cynomolgus monkey antibody light chain variable region. Also included are: an isolated polynucleotide (ii) comprising a sequence encoding (i); an isolated antibody (ai) comprising a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a

CC second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the
 CC effects of an antibody, comprising introducing into a cynomolgus monkey a
 CC chimeric antibody comprising light chain and heavy chain variable regions
 CC from an antibody and light chain and heavy chain constant regions from a
 CC cynomolgus monkey, and evaluating the effects of the chimeric antibody in
 CC the cynomolgus monkey; an expression vector (VI) comprising (II); a cell
 CC comprising a human antibody heavy chain variable region and a human
 CC antibody light chain variable region or a mouse antibody heavy chain
 CC variable region and a mouse antibody light chain variable region. (III)
 CC is useful for producing a chimeric antibody, which involves incubating
 CC (III) under conditions suitable for expression of the chimeric antibody,
 CC and isolating the chimeric antibody. (I) or (A1) is useful for diagnosing
 CC antigen in biological samples, and for treating diseases such as HIV,
 CC inflammation and cancer. The present sequence represents an anti-IL-4R
 CC heavy chain variable region used to make the chimeric antibodies of the
 CC invention.

XX Sequence 115 AA;

Query Match 89.6%; Score 138; DB 9; Length 115;
 Best Local Similarity 86.7%; Pred. No. 1.4e-10;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPPGRLSKLSCAGSGFTFS 30
 :|||||:|||||:|||||:|||||:|||||
 Db 1 EVQLVQSGGGLVHPGSLRLSCAGSGFTFS 30

RESULT 15
 AEA11020
 ID AEA11020 standard; protein; 115 AA.

AC AEA11020;

DT 28-JUL-2005 (first entry)

XX Human anti-IL-4R heavy chain variable region, SEQ ID NO:62.

DE HIV infection; anti-HIV; infection; inflammation; anti-inflammatory;

KW cancer; cytoskeletal; antibody; chimeric antibody;

KW heavy chain variable region; antibody engineering; anti-IL-4R.

XX Homo sapiens.

OS WO2005047325-A2.

PN 26-MAY-2005.

XX 04-NOV-2004; 2004WO-US037241.

XX 07-NOV-2003; 2003US-0517970P.

XX (AMGE-) AMGEN INC.

PI Aldrich T, Shen W, Jacobsen FW, Morris AE, Allen MJ;

XX WPI: 2005-372347/38.

DR N-PSDB; AEA11006.

XX Polypeptide having cynomolgus monkey antibody heavy chain variable region
 PT or light chain variable region, useful in diagnosing antigen in
 PT biological samples, and for treating disease e.g., inflammation and
 PT cancer.

XX Example 3, SEQ ID NO 62; 138pp, English.

XX The invention relates to an isolated polypeptide (I) comprising (a) one
 CC of 4 sequences: AEA10964, AEA10966, AEA10968 and AEA10970 or
 CC AEA10972, and antibody heavy chain variable region, or (b) AEA10988, and
 CC antibody light chain variable region. In (I), the antibody heavy chain or
 CC light chain variable region is a cynomolgus monkey antibody heavy chain
 CC variable region or cynomolgus monkey antibody light chain variable

CC region. The antibody heavy chain variable region or light chain variable
 CC region is a human or mouse antibody heavy chain variable region or light
 CC chain variable region. Also included are: an isolated polynucleotide (II)
 CC comprising a sequence encoding (I); an isolated antibody (A1) comprising
 CC a first polypeptide having SEQ ID No. 6, 8, 10, 12, 14 or 20, and a
 CC second polypeptide having SEQ ID No. 30; a method of evaluating (M1) the
 CC effects of an antibody, comprising introducing into a cynomolgus monkey a
 CC chimeric antibody comprising light chain and heavy chain variable regions
 CC from an antibody and light chain and heavy chain constant regions from a
 CC cynomolgus monkey, and evaluating the effects of the chimeric antibody in
 CC the cynomolgus monkey; an expression vector (VI) comprising (II); a cell
 CC comprising (III) and a method of producing (I). (A1) further
 CC comprises a human antibody heavy chain variable region and a human
 CC antibody light chain variable region or a mouse antibody heavy chain
 CC variable region and a mouse antibody light chain variable region. (III)
 CC is useful for producing a chimeric antibody, which involves incubating
 CC (III) under conditions suitable for expression of the chimeric antibody,
 CC and isolating the chimeric antibody. (I) or (A1) is useful for diagnosing
 CC antigen in biological samples, and for treating diseases such as HIV,
 CC inflammation and cancer. The present sequence represents an anti-IL-4R
 CC heavy chain variable region used to make the chimeric antibodies of the
 CC invention.

XX Sequence 115 AA;

Query Match 89.6%; Score 138; DB 9; Length 115;
 Best Local Similarity 86.7%; Pred. No. 1.4e-10;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPPGRLSKLSCAGSGFTFS 30
 :|||||:|||||:|||||:|||||:|||||
 Db 1 EVQLVQSGGGLVHPGSLRLSCAGSGFTFS 30

Search completed: November 21, 2005, 12:20:03
 Job time : 41.1648 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 7.30769 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-158

Sequence: 1 QVQLVQSGGIVHPGSRILKLSGAGSGFTFS 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	89.6	116	2	S12557 Ig heavy chain - h
2	137	89.0	119	1	GIHUNI Ig heavy chain V-I
3	137	89.0	121	2	S19666 Ig heavy chain V r
4	134	87.0	94	2	PL0120 Ig heavy chain V-I
5	134	87.0	98	2	PL0116 Ig heavy chain V-I
6	134	87.0	98	2	S29546 Ig heavy chain V r
7	134	87.0	113	2	S57410 Ig heavy chain V-J
8	134	87.0	113	2	S38490 Ig heavy chain - h
9	134	87.0	118	2	S31116 Ig heavy chain - h
10	134	87.0	119	2	S31111 Ig heavy chain - h
11	134	87.0	119	2	F36005 Ig heavy chain V r
12	134	87.0	120	2	S31112 Ig heavy chain - h
13	134	87.0	121	2	S31605 Ig heavy chain V r
14	134	87.0	122	2	S31117 Ig heavy chain - h
15	134	87.0	122	2	E36005 Ig heavy chain V r
16	134	87.0	122	2	S31119 Ig heavy chain - h
17	134	87.0	128	2	S48797 Ig heavy chain V r
18	134	87.0	130	2	S31601 Ig heavy chain V r
19	134	87.0	130	2	PL0098 Ig heavy chain pre
20	134	87.0	132	2	S31603 Ig heavy chain V r
21	134	87.0	133	2	S31590 Ig heavy chain V r
22	134	87.0	133	2	A49028 Ig heavy chain V-I
23	134	87.0	133	2	S31679 Ig heavy chain V r
24	134	87.0	137	2	S31701 Ig heavy chain V r
25	134	87.0	139	2	S31674 Ig heavy chain V r
26	131	85.1	97	2	S44115 Ig heavy chain V r
27	131	85.1	114	2	S46390 Ig heavy chain V-I
28	131	85.1	122	1	M3HUM Ig heavy chain V-I
29	130	84.4	97	2	S26886 Ig heavy chain V r

30	130	84.4	120	2	S36273 Ig heavy chain V r
31	130	84.4	127	2	S38489 Ig heavy chain - h
32	129	83.8	96	2	PH0873 Ig heavy chain V r
33	128	83.1	115	2	S57445 Ig heavy chain V-J
34	128	83.1	151	2	A60943 Ig heavy chain pre
35	127	82.5	98	2	S29543 Ig heavy chain V r
36	127	82.5	134	2	S31688 Ig heavy chain V r
37	127	82.5	135	2	S31598 Ig heavy chain V r
38	127	82.5	140	2	S70442 Ig heavy chain pre
39	126	81.8	123	2	S38493 Ig heavy chain - h
40	126	81.8	134	2	S31699 Ig heavy chain V r
41	125	81.2	97	2	S26885 Ig heavy chain V r
42	125	81.2	121	1	GIHUNI Ig heavy chain V-I
43	125	81.2	122	1	M3HUM Ig heavy chain V-I
44	125	81.2	126	1	GIHUNI Ig heavy chain V-I
45	125	81.2	127	2	S19878 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S12557 Ig heavy chain - human (fragment)

C/Species: Homo sapiens (man) ; C/Date: 21-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S12557 R/Macnada, F.; Shih, E.K.; Hirabayashi, Y.; Nagaoka, H.; Yoshida, M.C.; Zong, S.Q.; Honji

EMBO J. 9, 2501-2506, 1990

A/Title: Organization of variable region segments of the human immunoglobulin heavy chain

ns. A/Reference number: S12557; MUID:90316107; PMID:2114977

A/Accession: S12557 A/Status: preliminary

A/Molecule type: DNA A/Residues: 1-116 <MAT>

A/Cross-references: UNIPARC:UPI000013DE0E A/Superfamily: Immunoglobulin V region; immunoglobulin homology

F/34-116/Domain: Immunoglobulin homology <IMM>

Query Match 89.6%; Score 138; DB 2; Length 116; Best Local Similarity 86.7%; Pred. No. 1.9e-11; Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPGSRILKLSGAGSGFTFS 30
DB 20 EVQLVQSGGIVHPGSRILKLSGAGSGFTFS 49

RESULT 2

GIHUNI Ig heavy chain V-III region (Nie) - human

C/Species: Homo sapiens (man) C/Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C/Accession: A91668; A02053 R/Ponstingl, H.; Hilschmann, N.

Hoppe-Sejler's Z. Physiol. Chem. 357, 1571-1604, 1976 A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

igen Primärstruktur. A/Reference number: A91668; MUID:77070269; PMID:826475

A/Accession: A91668 A/Molecule type: protein

A/Residues: 1-119 <PON> A/Cross-references: UNIPROT:P01770; UNIPARC:UPI000012CEFA

R/Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N. A/Title: The sequence of the gamma-1 C region of this chain is also given

Hoppe-Sejler's Z. Physiol. Chem. 357, 1515-1940, 1976 A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglobulin

embroider cleavage products, and the disulfide bridges. A/Reference number: A91667; MUID:77070267; PMID:1002129

A/Content: annotation; disulfide bond C/Comment: This chain was isolated from an IgG1 myeloma protein.

A:Gene: GDB:IGHV
 A:Cross-references: GDB:128528; OMIM:147070
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
 F/15-98/Domain: immunoglobulin homology <IMM>
 F/1/Modified site: pyroglutamic acid (Gln) #status experimental
 F/22-96/Disulfide bonds: #status experimental

Query Match 89.0%; Score 137; DB 1; Length 119;
 Best Local Similarity 90.0%; Pred. No. 2.6e-11;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVQLVSGGCVVHPGRSLKLSGAGSPTFS 30
 DB 1 QVQLVSGGCVVHPGRSLKLSGAGSPTFS 30

RESULT 3

S19666
 Ig heavy chain V region (VH3DJH4) - human
 C:Species: Homo sapiens (man)
 C>Date: 22-Jan-1993 #sequence_rev1sion 22-Jan-1993 #text_change 20-Jun-2000
 C:Accession: S19666

R:Marker, J.D.; Hoozenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 227, 581-597, 1991

A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19666

A:Residues: 1-121 <MM>

A:Cross-references: UNIPARC:UPI0000115F5; EMBL:X61646; NID:937688; PIDN:CAA43827.1; PIR

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 89.0%; Score 137; DB 2; Length 121;
 Best Local Similarity 90.0%; Pred. No. 2.7e-11;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVQLVSGGCVVHPGRSLKLSGAGSPTFS 30
 DB 1 QVQLVSGGCVVHPGRSLKLSGAGSPTFS 30

RESULT 4
 PL0120
 Ig heavy chain V-III region (TD-Vo) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1990 #sequence_rev1sion 07-Jun-1990 #text_change 31-Dec-2004

C:Accession: PL0120

R:Bird, J.; Gallil, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A:Reference number: PL0116; MUID:88286083; PMID:2840480

A:Accession: PL0120

A:Residues: 1-94

A:Cross-references: UNIPROT:Q8WTK1; UNIPROT:Q9UJ93; UNIPARC:UPI0000176X2C

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL

A:Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement

C:Superfamily: immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F/31-35/Region: complementarity-determining 1

F/49-65/Region: complementarity-determining 2

RESULT 5
 PL0116
 Ig heavy chain V-III region (AW-Vx) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jun-1990 #sequence_rev1sion 07-Jun-1990 #text_change 23-Jul-1999

C:Accession: PL0116; S26892

R:Bird, J.; Gallil, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A:Reference number: PL0116; MUID:88286083; PMID:2840480

A:Accession: PL0116

A:Residues: 1-98

A:Cross-references: UNIPARC:UPI0000031F3A

A:Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL

A:Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26892

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <MM>

A:Cross-references: UNIPARC:UPI0000031F3A; EMBL:Z12349; NID:932918; PIDN:CAA78219.1; PID:

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F/31-35/Region: complementarity-determining 1

F/49-65/Region: complementarity-determining 2

Query Match 87.0%; Score 134; DB 2; Length 98;
 Best Local Similarity 86.7%; Pred. No. 5.5e-11;
 Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVQLVSGGCVVHPGRSLKLSGAGSPTFS 30
 DB 1 QVQLVSGGCVVHPGRSLKLSGAGSPTFS 30

RESULT 6
 S29546
 Ig heavy chain V region (COS-8 / DP-46) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 07-Jan-1994 #sequence_rev1sion 17-Nov-1995 #text_change 23-Jul-1999

C:Accession: S29546; S26888

R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.

submitted to the EMBL Data Library, October 1992

A:Reference number: S29543

A:Accession: S29546

A:Molecule type: DNA

A:Residues: 1-98 <MM>

A:Cross-references: UNIPARC:UPI00002DD16; EMBL:Z17394; NID:932843; PIDN:CAA78997.1; PID:

A:Note: designated COS-8

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <MM>

A:Cross-references: UNIPARC:UPI00002DD16; EMBL:Z12346; NID:932912; PIDN:CAA78216.1; PID:

A:Note: designated DP-46

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Qy 1 QVQLVQSGGVSHPGSRSLKSCAGSGFTFS 30
|||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFS 30

RESULT 7
S57410
Ig heavy chain V-J region - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S57410
R:Paterson, G.; Kennedy, P.G.B.; Willison, H.J.
Submitted to the EMBL Data Library, June 1995
A:Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neurog
A:Reference number: S57408
A:Accession: S57410
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <PAT>
A:Cross-references: UNIPARC:UPI00001137A9; EMBL:X87893; NID:9871363; PIDN:CAA61144.1; PI
C:Keywords: immunoglobulin V region; immunoglobulin homology
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 113;
Best Local Similarity 86.7%; Pred. No. 6.4e-11;
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGSRSLKSCAGSGFTFS 30
|||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFS 30

RESULT 8
S38490
Ig heavy chain - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38490
R:Markes, J.D.; Overhand, W.H.; Bye, J.M.; Finnern, R.; Gorlick, B.D.; Voak, D.; Thorpe, S
Submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a B
A:Reference number: S38488
A:Accession: S38490
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-113 <MAR>
A:Cross-references: UNIPARC:UPI0000116549; EMBL:Z23030; NID:9414027; PIDN:CAA80565.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 113;
Best Local Similarity 86.7%; Pred. No. 6.4e-11;
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGSRSLKSCAGSGFTFS 30
|||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFS 30

RESULT 9

S31116
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C:Accession: S31116
R:Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Bur, J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252

A:Accession: S31116
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-118 <RAA>
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 118;
Best Local Similarity 86.7%; Pred. No. 6.6e-11;
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGSRSLKSCAGSGFTFS 30
|||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFS 30

RESULT 10

S31111
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31111
R:Raaphorst, F.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Bur, J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31111
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: UNIPARC:UPI0000176DC2; EMBL:X62959
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 119;
Best Local Similarity 86.7%; Pred. No. 6.7e-11;
Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGVSHPGSRSLKSCAGSGFTFS 30
|||:|||||:|||||:|||||:|||||
Db 1 QVQLVESGGGVQPGSRSLRLSCAASGFTFS 30

RESULT 11

F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C:Accession: F36005
R:Schroeder, U.; H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: F36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026
C:Genetics:
A:Gene: IGH@; IGHV1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 119;
Best Local Similarity 86.7%; Pred. No. 6.7e-11;

Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSKASGFTFS 30
 |||||:|||||:|||||:|||||:|||||
 Db 1 QVQLVESGGGVVQPGRSRLRLSCAASGFTFS 30

RESULT 12

S31112

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31112

R/Rapporteur, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, B.J.; Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement

A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31112

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-120 <RAA>

A/Cross-references: UNIPARC:UPI0000176C8C; EMBL:X62961

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 120;
 Best Local Similarity 86.7%; Pred. No. 6,7e-11;
 Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSKASGFTFS 30
 |||||:|||||:|||||:|||||:|||||
 Db 1 QVQLVESGGGVVQPGRSRLRLSCAASGFTFS 30

RESULT 13

G36005

Ig heavy chain V region (M74) - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004

C/Accession: G36005

R/Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: G36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-121 <SCH>

A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C2C; GB:M34031

C/Genetics: GDB:IGH@; IGHDI1

A/Status: preliminary

A/Cross-references: GDB:118731; OMIM:146910

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 121;
 Best Local Similarity 86.7%; Pred. No. 6,8e-11;
 Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSKASGFTFS 30
 |||||:|||||:|||||:|||||:|||||
 Db 1 QVQLVESGGGVVQPGRSRLRLSCAASGFTFS 30

RESULT 14

S31117

Ig heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31117

R/Rapporteur, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, B.J.; Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement

A/Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31117

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-122 <RAA>

A/Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 122;
 Best Local Similarity 86.7%; Pred. No. 6,8e-11;
 Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSKASGFTFS 30
 |||||:|||||:|||||:|||||:|||||
 Db 1 QVQLVESGGGVVQPGRSRLRLSCAASGFTFS 30

RESULT 15

E36005

Ig heavy chain V region (M72) - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

C/Accession: E36005

R/Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene

A/Reference number: A36005; MUID:90349571; PMID:2117273

A/Accession: E36005

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-122 <SCH>

A/Cross-references: UNIPARC:UPI0000176C30; GB:M34030

C/Genetics: GDB:IGH@; IGHDI1

A/Status: preliminary

A/Cross-references: GDB:118731; OMIM:146910

A/Map position: 14q32.33-14q32.33

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.0%; Score 134; DB 2; Length 122;
 Best Local Similarity 86.7%; Pred. No. 6,8e-11;
 Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVSGGCVVHPGRSLKLSKASGFTFS 30
 |||||:|||||:|||||:|||||:|||||
 Db 1 QVQLVESGGGVVQPGRSRLRLSCAASGFTFS 30

Search completed: November 21, 2005, 12:22:15
 Job time : 7.30769 sec

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:45:55 ; Search time 44.3956 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-158
Perfect score: 154
Sequence: 1 QVQLVDSGSGGVHPGRSLKLSGASGPTFS 30

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	137	89.0	119	1	HV31_HUMAN
2	134	87.0	613	2	Q8WUK1_HUMAN
3	131	85.1	122	1	HV32_HUMAN
4	131	85.1	461	2	Q5WV3_RAT
5	129	83.8	116	2	Q9UL93_HUMAN
6	129	83.8	465	2	Q510J0_RAT
7	127	82.5	240	2	Q552C9_HUMAN
8	127	82.5	479	2	Q5BK12_RAT
9	126	81.8	475	2	Q5RFE5_HUMAN
10	125	81.2	121	1	HV31_HUMAN
11	125	81.2	122	1	HV3H_HUMAN
12	125	81.2	126	1	HV3K_HUMAN
13	125	81.2	483	2	Q566J7_MOUSE
14	124	80.5	113	2	Q9UL90_HUMAN
15	124	80.5	467	2	Q4VBH1_RAT
16	124	80.5	472	2	Q6N089_HUMAN
17	124	80.5	573	2	Q8W038_HUMAN
18	123	79.9	98	1	HV57_MOUSE
19	123	79.9	122	2	Q9UL84_HUMAN
20	123	79.9	487	2	Q99KA4_MOUSE
21	123	79.9	606	2	Q6GMV2_HUMAN
22	122	79.2	470	2	Q6GCN4_HUMAN
23	121	78.6	118	2	Q9UL91_HUMAN
24	121	78.6	119	1	HV3P_HUMAN
25	121	78.6	120	1	HV3E_HUMAN
26	121	78.6	147	2	Q9Y509_HUMAN
27	121	78.6	478	2	Q6P181_HUMAN
28	120	77.9	117	1	HV54_MOUSE
29	120	77.9	131	2	Q9UL68_HUMAN
30	120	77.9	464	2	Q6WZU6_HUMAN
31	120	77.9	473	2	Q6WZV7_HUMAN

ALIGNMENTS

32	120	77.9	479	2	Q5POK9_RAT	Q5POK9_rattus norv
33	119	77.3	97	1	HV56_MOUSE	P18527_mus musculu
34	119	77.3	114	1	HV3B_HUMAN	P01763_homo sapien
35	119	77.3	519	2	Q6N092_HUMAN	Q6N092_homo sapien
36	118	76.6	112	2	Q9HCC1_HUMAN	Q9HCC1_homo sapien
37	118	76.6	115	1	HV3D_HUMAN	P01780_homo sapien
38	118	76.6	115	1	HV3S_HUMAN	P01779_homo sapien
39	118	76.6	116	1	HV3R_HUMAN	P01764_homo sapien
40	118	76.6	117	1	HV3C_HUMAN	P18526_mus musculu
41	118	76.6	117	1	HV3M_HUMAN	P01774_homo sapien
42	118	76.6	119	1	HV3W_MOUSE	Q65Z18_mus musculu
43	118	76.6	499	2	Q6NSK4_HUMAN	Q6NSK4_homo sapien
44	118	76.6	544	2	Q6P395_HUMAN	Q6P395_homo sapien
45	118	76.6				

RESULT 1
HV31_HUMAN STANDARD; PRT; 119 AA.
ID HV31_HUMAN
AC P01770;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region N1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=77070267; PubMed=826475;
RX MEDLINE=77070269; PubMed=826475;
RA Ponsenigl H, Hilschmann N;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein N1B). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RT Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [2]
RP DISRUPTED BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L, Schwarz J, Reichel W, Hilschmann N;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein N1B). I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR; A91668; G1HUNI.
CC HSP; P01772; 2P94.
CC SMR; P01770; 1-119.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin V region; Pyrolysine carboxylic acid.
CC DOMAIN 1 112 Ig-like.

FT MOD RES 1 1 Pyrrolidone carboxylic acid.
 FT DISUPID 22 96
 FT NON TER 119
 SQ SEQUENCE 119 AA, 13243 MW, C96935A6E55E165B CRC64;
 Query Match 89.0%; Score 137; DB 1; Length 119;
 Best Local Similarity 90.0%; Pred. No. 9e-11;
 Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVQLVSGGCVGVPGRSLKSLKSCAGSGFTFS 30
 DB 1 QVQLVSGGCVGVPGRSLKSLKSCAGSGFTFS 30

RESULT 2
 Q8WUK1_HUMAN
 ID Q8WUK1_HUMAN PRELIMINARY; PRT; 613 AA.
 AC Q8WUK1;
 DT 01-MAR-2002 (TRENBLUREL. 20; Created)
 DT 01-MAR-2002 (TRENBLUREL. 20; Last sequence update)
 DT 01-MAR-2004 (TRENBLUREL. 26; Last annotation update)
 DE IGHM protein.
 GN Name=IGHM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NOCLOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshikiyaki S., Carninci P., Prange C.,
 RA Raha S.S., Loguolino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skaleka U., Smallus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NOCLOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (BRC-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NOCLOTIDE SEQUENCE.
 RX PubMed=2117273;
 RA Schroeder H.W., Jr., Wang J.Y.;
 RT "Preferential utilization of conserved immunoglobulin heavy chain
 RT variable gene segments during human fetal life";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
 RN [4]
 RP NOCLOTIDE SEQUENCE.
 RX PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;
 RA Cuisinier A.M., Fumoux F., Fougereau M., Tomalle C.;
 RT "IGM kappa/lambda BBV human B cell clone: an early step of
 RT differentiation of fetal B cells or a distinct B lineage?";
 RL Mol. Immunol. 29:1363-1373(1992).
 RN [5]
 RP NOCLOTIDE SEQUENCE.

RX PubMed=1730252;
 RA Raapport F.M., Timmers B., Kenter M.J., Van Tol M.J., Vossen J.M.,
 RA Schuurman R.K.;
 RT "Restricted utilization of germ-line VH3 genes and short diverse third
 RT complementarily-determining regions (CDR3) in human fetal B lymphocyte
 RT immunoglobulin heavy chain rearrangements";
 RL Eur. J. Immunol. 22:247-251(1992).
 RN [6]
 RP NOCLOTIDE SEQUENCE.
 RX PubMed=1904154;
 RA Neale G.A., Kitchingman G.R.;
 RT "mRNA transcripts initiating within the human immunoglobulin mu heavy
 RT chain enhancer region contain a non-translatable exon and are
 RT extremely heterogeneous at the 5' end";
 RL Nucleic Acids Res. 19:2427-2433(1991).
 RN [7]
 RP NOCLOTIDE SEQUENCE.
 RX PubMed=2840480; DOI=10.1084/jem.168.1.229;
 RA Bird J., Gallil N., Link M., Stiles D., Sklar J.;
 RT "Continuing rearrangement but absence of somatic hypermutation in
 RT immunoglobulin genes of human B cell precursor leukemia";
 RL J. Exp. Med. 168:229-245(1988).
 RN [8]
 RP NOCLOTIDE SEQUENCE.
 RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;
 RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
 RT "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal
 RT B cell lines. Preferential utilization of the most 5H-proximal D
 RT segment (DQ52) and two unusual VH-related rearrangements";
 RL J. Exp. Med. 169:1391-1403(1989).
 RN [9]
 RP NOCLOTIDE SEQUENCE.
 RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
 RA Hillson U.L., Karr N.S., Opplinger I.R., Mannik M., Sasse E.H.;
 RT "The structural basis of germline-encoded VH3 immunoglobulin binding
 RT to staphylococcal protein A";
 RL J. Exp. Med. 178:331-336(1993).
 DR EMBL/BC020240; AAH20240.1; -; mRNA.
 DR PIR; F36005; F36005.
 DR PIR; G36005; G36005.
 DR PIR; PH1642; PH1642.
 DR PIR; PH1643; PH1643.
 DR PIR; PH1645; PH1645.
 DR PIR; PH1646; PH1646.
 DR PIR; PL0098; PL0098.
 DR PIR; PL0120; PL0120.
 DR PIR; S15590; S15590.
 DR PIR; S31116; S31116.
 DR PIR; S31119; S31119.
 DR PIR; S70442; S70442.
 DR HSSP; P01861; 1ADO.
 DR SMR; Q8WUK1.20-242.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM0406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 5.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 613 AA; 67296 MW; 60CF9590871E315 CRC64;

Query Match 87.0%; Score 134; DB 2; Length 613;
 Best Local Similarity 86.7%; Pred. No. 1.1e-09;
 Matches 26; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QVQLVSGGCVGVPGRSLKSLKSCAGSGFTFS 30
 DB 20 QVQLVSGGCVGVPGRSLKSLKSCAGSGFTFS 49

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RESULT 3
HV3G_HUMAN STANDARD; PRT; 122 AA.
ID P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
RT location of a possible JH segment."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).
CC -1- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC patient with macroglobulinemia. (immunoglobulin-like) domain.
CC -1- SIMILARITY: Contains 1 Ig-like.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02051; M3H0AM.
DR HSSP; P01772; 2FB4.
DR SMR; P01768; 2FB4.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-V.
DR InterPro; IPR003596; IG-V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0R17D52F1C2 CRC64;

Query Match 85.1%; Score 131; DB 1; Length 122;
Best Local Similarity 83.3%; Pred. No. 6.1e-10;
Matches 25; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPRGSLKSCAGSGFTFS 30
DB 1 QVQLVQSGGIVHPRGSLKSCAGSGFTFS 30

RESULT 4
Q5MTV3_RAT PRELIMINARY; PRT; 461 AA.
ID Q5MTV3;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DE LOC6367586 protein.
GN Name=LOC6367586.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT TISSUE=Lung;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
RA Schnerch A., Schein J.R., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL; BC088423; AACB8423.1; -, mRNA.
DR InterPro; IPR003599; IG-1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-sect; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGC1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 461 AA; 50949 MW; 25EA4BCE6E0F5A9 CRC64;

Query Match 85.1%; Score 131; DB 2; Length 461;
Best Local Similarity 83.3%; Pred. No. 2.2e-09;
Matches 25; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVQSGGIVHPRGSLKSCAGSGFTFS 30
DB 20 EVQLVQSGGIVQPKRSLKSCAGSGFTFS 49

RESULT 5
G0UL93_HUMAN PRELIMINARY; PRT; 116 AA.
ID G0UL93;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9644934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).

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RN [2]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hilleen J.L., Kair N.S., Oppliger I.R., Mannik M., Saseo E.H.,
RT "The structural basis of germ-line-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A."
RN J. Exp. Med. 178:331-336(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=2840480;
RA Bird U., Gallil N., Link M., Stiles D., Sklar J.,
RT "Continuing rearrangement but absence of somatic hypermutation in
RT immunoglobulin genes of human B cell precursor leukemia."
RN J. Exp. Med. 168:229-245(1988).
RL EMBL, AF035021; AAD56257.1; -, mRNA.
DR PIR, PH1644; PH1644.
DR PIR, P10120; P10120.
DR HSHP, P01772; 2PB4.
DR SMR, Q9U93; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IgV_1_LIKE; 1.
DR POSITE; PS50835; Ig-LIKE; 1.
FT NON_TER 1
FT TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 83.8%; Score 129; DB 2; Length 116;
Best Local Similarity 86.2%; Pred. No. 1.1e-09;
Matches 25; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 2 VOLVGGGVVHGRSLKSCAGSGFTFS 30
ID 051030_RAT PRELIMINARY; PRT; 465 AA.
AC 051030;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DR Hypothetical LOC299354.
GN Name=LOC299354;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Thymus;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datcenco L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltón E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Thymus;
RA NIH MGC Project;
RG Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL, BC088271; AAH88271.1; -, mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR07654; C1-set; 3.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; IgC1_2.
DR SMART; SM00406; IgV_1.
DR POSITE; PS50835; Ig-LIKE; 4.
DR Hypothetical protein; Immunoglobulin domain; Repeat.
KW SEQUENCE 465 AA; 51699 MW; 97CA533A213A424F CRC64;

Query Match 83.8%; Score 129; DB 2; Length 465;
Best Local Similarity 80.0%; Pred. No. 4.2e-09;
Matches 24; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Cy 1 QVOLVGGGVVHGRSLKSCAGSGFTFS 30
Db 20 EVLVSGGGGVVHGRSLKSCAGSGFTFS 49

RESULT 7
ID 055ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
AC 055ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DR Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C1q/7;
RA MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.B., Wang M.G., Winter G.,
RT "Complement recruitment using bispecific diabodies."
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL, Y13056; CAH73499.1; -, mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; Ig_2.
DR SMART; SM00406; IgV_1.
DR POSITE; PS50835; Ig-LIKE; 2.
FT NON_TER 1
FT TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F4B373 CRC64;

Query Match 82.5%; Score 127; DB 2; Length 240;
Best Local Similarity 83.3%; Pred. No. 4.2e-09;
Matches 25; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 1 QVOLVGGGVVHGRSLKSCAGSGFTFS 30
Db 1 QVOLVGGGVVHGRSLKSCAGSGFTFS 30

RESULT 8

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Q5BK12.RAT
ID Q5BK12.RAT PRELIMINARY; PRT; 479 AA.
AC Q5BK12
DT 10-MAY-2005 (TREMblrel. 30, Created)
DT 10-MAY-2005 (TREMblrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMblrel. 30, Last annotation update)
DE Igna protein.
OS Name=Igna;
GN Name=Igna;
OC Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
CC MURIDEA; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC
RE MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner U., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stjepieton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein W.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzyzanski M.I., Skalski U., Smallus D.B.,
RA Schnerch A., Schin J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC
RE NUCLEOTIDE SEQUENCE.
RC
RE NIH MGC Project;
RL EMBL; BC091247; AA91247.1; mRNA.
DR GO: GO:0003823; P: antigen binding; IRA.
DR InterPro; IPR003599; IG_1-like.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003596; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 479 AA; 52329 MW; 8B146164AE8437C5 CRC64;

Query Match 82.5%; Score 127; DB 2; Length 479;
Best Local Similarity 80.0%; Pred. No. 8.2e-09;
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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DT 10-MAY-2005 (TREMblrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gamma1 heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Bellard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
RT antibody T125."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AA062028.1; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003596; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT CHAIN 20 475 Potential.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;
chain.

Query Match 81.8%; Score 126; DB 2; Length 475;
Best Local Similarity 82.8%; Pred. No. 1.1e-08;
Matches 24; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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OY 1 QVQLVSGGAVHPGRSLKLSCTASGFTF 29
DB 20 QVQLVSGGAVHPGRSLKLSCTASGFTF 48

RESULT 10
HY3J HUMAN STANDARD; PRT; 121 AA.
ID HV3J HUMAN
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig heavy chain V-III region H1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RE MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RT cryoimmunoglobulin IgG H1L."
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -1- SIMILARITY: Contains 1 Ig-1-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR: A02054; G1HJHL.
DR HSPF; P01772; 2F84.

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DR SMR; P01771; 2-121.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FCS3610EF5DAB CRC64;

Query Match 81.2%; Score 125; DB 1; Length 121;
Best Local Similarity 80.0%; Pred. No. 4e-09; 3; Indels 0; Gaps 0;
Matches 24; Conservative 3; Mismatches 3;

Oy 1 QVQLVSGGAVHPGRSLKLSGAGSGFTFS 30
Db 1 QVQLVSGGAVHPGRSLKLSGAGSGFTFS 30

RESULT 11
ID HV3H HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G.; Lehman D.; Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02052; M3HUGA.
DR HSP; P01772; 2FB4.
DR SMR; P01769; 5-122.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13167 MW; 74E5B6959E84100A CRC64;

Query Match 81.2%; Score 125; DB 1; Length 122;
Best Local Similarity 76.7%; Pred. No. 4.1e-09; 3; Indels 0; Gaps 0;
Matches 23; Conservative 4; Mismatches 3;

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Oy 1 QVQLVSGGAVHPGRSLKLSGAGSGFTFS 30
Db 1 QVQLVSGGAVHPGRSLKLSGAGSGFTFS 30

RESULT 12
ID HV3H HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-II region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6864994;
RA Schmidt W.E.; Jung H.-D.; Palm W.; Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marguier M.; Dalsenhofer U.; Huber R.; Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02055; G1HUKU.
DR PDB; 2FB4; X-ray; H=2-126.
DR PDB; 2IG3; X-ray; H=2-126.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 96
FT DISULFID 105 110
FT NON TER 126 126
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT STRAND 62 64
FT HELIX 65 65
FT STRAND 66 67
FT TURN 67 73

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FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
SQ SEQUENCE 126 AA; 13718 MW; BAD71B52B16F8776 CRC64;

Query Match 81.2%; Score 125; DB 1; Length 126;
Best Local Similarity 80.0%; Pred. No. 4.2e-09;
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 OVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30
Db 1 OVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30

RESULT 13
OS66J7_MOUSE PRELIMINARY; PRT; 483 AA.
AC OS66J7_MOUSE PRELIMINARY; PRT; 483 AA.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LOC544903 protein.
GN Name=LOC544903;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dichtchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldi M.F., Cavaant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Bouffard G.G.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
EMBL: BC093501; AAH93501.1; -; mRNA.
DR SRR: Q566J7_20-240.
DR GO: GO:0003823; F:antigen binding; IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003597; IG-1.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF07654; Cl-set; 2.
DR SMART: SM00409; IG; 3.

DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 483 AA; 52371 MW; 20357D7F51A2886 CRC64;

Query Match 81.2%; Score 125; DB 2; Length 483;
Best Local Similarity 82.8%; Pred. No. 1.5e-08;
Matches 24; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VOLVQSGGVVHPGRSLKLSGAGSGFTFS 30
Db 21 VOLVQSGGVVHPGRSLKLSGAGSGFTFS 49

RESULT 14
OS9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
ID OS9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
AC OS9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
NCBI_TaxID=9606;
RX MEDLINE=96277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kall N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
[2]
NUCLEOTIDE SEQUENCE.
RC PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CD3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL: AF035024; AAD56260.1; -; mRNA.
DR PIR: S78486; S78486.
DR HSSP: F01772; 2FB4.
DR SRR: Q9UL90; 1-113.
DR InterPro: IPR007110; IG-1like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 80.5%; Score 124; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 5.2e-09;
Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 OVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30
Db 1 EVOLVQSGGVVHPGRSLKLSGAGSGFTFS 30

RESULT 15
Q4VBH1_RAT PRELIMINARY; PRT; 467 AA.
ID Q4VBH1_RAT PRELIMINARY; PRT; 467 AA.
AC Q4VBH1_RAT PRELIMINARY; PRT; 467 AA.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, last annotation update)
DE LOC29354 protein.
GN Name=LOC29354;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Tymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Tymus;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC EMBL, BC095846; AAH95846.1; -; mRNA.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR07110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; C1-beet; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGV; 1.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS50835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 467 AA; 51651 MW; 1FF0328F5016ED3 CRC64;
Query Match 80.5%; Score 124; DB 2; Length 467;
Best Local Similarity 76.7%; Pred. No. 2,1e-08;
Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 QVQVQSGGCVVHPRSLKSLKSCAGSGFTFS 30
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DB 20 EVQLVETGGGLVQPGKSLKSLKSCVAGSFTFS 49

Search completed: November 21, 2005, 12:04:12
Job time : 45.3956 secs

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: November 21, 2005, 11:49:31 ; Search time 11.3187 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-158

Perfect score: 154
Sequence: 1 QVQLVQSGGIVHPGRLKLSGAGSPTFS 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/6-COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCITUS-COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	138	89.6	97	2	US-09-534-717-617 Sequence 617, App
2	137	89.0	98	2	US-09-534-717-667 Sequence 667, App
3	137	89.0	115	2	US-09-726-219A-167 Sequence 167, App
4	137	89.0	115	2	US-09-534-717-23 Sequence 23, App
5	137	89.0	115	2	US-09-534-717-33 Sequence 33, App
6	137	89.0	115	2	US-09-534-717-37 Sequence 37, App
7	137	89.0	115	2	US-09-534-717-39 Sequence 39, App
8	137	89.0	115	2	US-09-534-717-41 Sequence 41, App
9	137	89.0	115	2	US-09-534-717-43 Sequence 43, App
10	137	89.0	115	2	US-09-534-717-45 Sequence 45, App
11	137	89.0	115	2	US-09-534-717-51 Sequence 51, App
12	137	89.0	115	2	US-09-534-717-55 Sequence 55, App
13	137	89.0	115	2	US-09-534-717-59 Sequence 59, App
14	137	89.0	115	2	US-09-534-717-61 Sequence 61, App
15	137	89.0	115	2	US-09-534-717-63 Sequence 63, App
16	137	89.0	115	2	US-09-534-717-65 Sequence 65, App
17	137	89.0	115	2	US-09-534-717-71 Sequence 71, App
18	137	89.0	115	2	US-09-534-717-73 Sequence 73, App
19	137	89.0	115	2	US-09-534-717-75 Sequence 75, App
20	137	89.0	115	2	US-09-534-717-77 Sequence 77, App
21	137	89.0	115	2	US-09-534-717-79 Sequence 79, App
22	137	89.0	115	2	US-09-534-717-81 Sequence 81, App
23	137	89.0	115	2	US-09-534-717-83 Sequence 83, App
24	137	89.0	115	2	US-09-534-717-85 Sequence 85, App
25	137	89.0	115	2	US-09-534-717-87 Sequence 87, App
26	137	89.0	115	2	US-09-534-717-89 Sequence 89, App
27	137	89.0	115	2	US-09-534-717-91 Sequence 91, App

28	137	89.0	225	2	US-09-456-090A-68 Sequence 68, App
29	137	89.0	225	2	US-09-456-090A-94 Sequence 94, App
30	137	89.0	225	2	US-09-456-090A-100 Sequence 100, App
31	137	89.0	225	2	US-09-456-090A-106 Sequence 106, App
32	137	89.0	225	2	US-09-453-234-62 Sequence 62, App
33	137	89.0	225	2	US-09-453-234-68 Sequence 68, App
34	137	89.0	225	2	US-09-453-234-94 Sequence 94, App
35	137	89.0	225	2	US-09-453-234-100 Sequence 100, App
36	137	89.0	225	2	US-09-453-234-106 Sequence 106, App
37	137	89.0	248	2	US-09-315-926A-80 Sequence 80, App
38	135	87.7	124	2	US-09-424-840B-16 Sequence 16, App
39	134	87.0	95	2	US-09-534-717-653 Sequence 653, App
40	134	87.0	98	1	US-08-211-202-118 Sequence 118, App
41	134	87.0	98	2	US-10-194-975-23 Sequence 23, App
42	134	87.0	98	2	US-10-194-975-24 Sequence 24, App
43	134	87.0	98	2	US-10-194-975-25 Sequence 25, App
44	134	87.0	98	2	US-10-194-975-26 Sequence 26, App
45	134	87.0	98	2	US-09-534-717-624 Sequence 624, App

ALIGNMENTS

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RESULT 1
US-09-534-717-617
; Sequence 617, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Saifeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 617
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-617

Query Match      89.6%; Score 138; DB 2; Length 97;
Best Local Similarity 86.7%; Pred. No. 1.8e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVQSGGIVHPGRLKLSGAGSPTFS 30
Db      1 EVQLVQSGGIVHPGRLKLSGAGSPTFS 30

RESULT 2
US-09-534-717-667
; Sequence 667, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Saifeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 667
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-667

Query Match      89.0%; Score 137; DB 2; Length 98;
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Best Local Similarity 90.0%; Pred. No. 2.5e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGVHPGRSLKLSGASGFTFS 30
|||:|||||
Db 1 QVQLVQSGGGVQPGRLRLSCASGFTFS 30

RESULT 3
US-09-726-219A-167
! Sequence 167, Application US/09726219A
! Patent No. 6806079
! GENERAL INFORMATION:
! Application: Cambridge Isotope Technology, Cambridge, MA

	Query Match	Similarity	Score	DB 2	Length
Best Local	89.0%	90.0%	137	115	
Matches	27	Conservative	1	Mismatches	2
				Indels	0
				Gaps	0

RESULT 4
US-09-534-717-23
; Sequence 23, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Seifeld et al.

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/ TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
/ FILE REFERENCE: BBI-093CD
/ CURRENT APPLICATION NUMBER: US/09/534,717
/ CURRENT FILING DATE: 2000-03-24
/ EARLIER APPLICATION NUMBER: 60/126,603
/ EARLIER FILING DATE: March 25, 1999
/ NUMBER OF SEQ ID NOS: 675
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 23
/ LENGTH: 115
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-534-717-23

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RESULT 5
US-09-534-717-33
; Sequence 33, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534, 717
; EARLIER FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126, 603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-33

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RESULT 6
US-09-534-717-37
: Sequence 37. Application US/09534717
: Patent No. 6914128
: GENERAL INFORMATION:
: APPLICANT: Jochen, Salfeld et al.
: TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
: FILE REFERENCE: BBI-093CP
: CURRENT APPLICATION NUMBER: US/09/534,717
: CURRENT FILING DATE: 2000-03-24
: EARLIER APPLICATION NUMBER: 60/126,603
: EARLIER FILING DATE: March 25, 1999
: NUMBER OF SEQ ID NOS: 675
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 37
: LENGTH: 115
: TYPE: PR1
: ORGANISM: Homo sapiens
: US-09-534-717-37

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Best Local Similarity 90.0%; Pred. No. 2.9e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30
Db 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30

RESULT 7

US-09-534-717-39
Sequence 39, Application US/09534717
Patent No. 6914128

GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-39

Query Match 89.0%; Score 137; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 2.9e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30
Db 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30

RESULT 8

US-09-534-717-41
Sequence 41, Application US/09534717
Patent No. 6914128

GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-41

Query Match 89.0%; Score 137; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 2.9e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30
Db 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30

RESULT 9

US-09-534-717-43
Sequence 43, Application US/09534717
Patent No. 6914128

GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

FILE REFERENCE: BBI-093CP
CURRENT APPLICATION NUMBER: US/09/534,717
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-43

Query Match 89.0%; Score 137; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 2.9e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30
Db 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30

RESULT 10

US-09-534-717-45
Sequence 45, Application US/09534717
Patent No. 6914128

GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-45

Query Match 89.0%; Score 137; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 2.9e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30
Db 1 QVOLVOSGGVHPGRSLKSCASGGFTFS 30

RESULT 11

US-09-534-717-47
Sequence 47, Application US/09534717
Patent No. 6914128

GENERAL INFORMATION:
APPLICANT: Jochen, Salfeld et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 47
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-47

Query Match 89.0%; Score 137; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 2.9e-11;

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 Search time 37.1429 Seconds
(without alignments)
337,478 Million cell updates/sec

Title: US-10-632-706-158

Perfect score: 1 QVQLVQSGGVSHPGSRSLKSLSCAGSGPTFS 30

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA Main.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	30	US-10-632-706-158	Sequence 158, App
2	154	100.0	30	US-10-632-706-162	Sequence 162, App
3	154	100.0	30	US-10-632-706-166	Sequence 166, App
4	154	100.0	30	US-10-632-706-170	Sequence 170, App
5	138	89.6	97	US-10-884-830-617	Sequence 617, App
6	138	89.6	97	US-10-911-838-18	Sequence 18, App
7	138	89.6	115	US-10-982-359-16	Sequence 16, App
8	138	89.6	115	US-10-982-359-18	Sequence 18, App
9	138	89.6	115	US-10-982-359-20	Sequence 20, App
10	138	89.6	115	US-10-982-359-22	Sequence 22, App
11	138	89.6	115	US-10-982-359-24	Sequence 24, App
12	138	89.6	115	US-10-982-359-26	Sequence 26, App
13	138	89.6	115	US-10-982-359-28	Sequence 28, App
14	138	89.6	115	US-10-982-359-30	Sequence 30, App
15	138	89.6	115	US-10-982-359-32	Sequence 32, App
16	138	89.6	115	US-10-982-359-34	Sequence 34, App
17	138	89.6	115	US-10-982-359-36	Sequence 36, App
18	138	89.6	115	US-10-982-359-38	Sequence 38, App
19	138	89.6	115	US-10-982-359-40	Sequence 40, App
20	138	89.6	116	US-10-408-901-14	Sequence 14, App
21	138	89.6	116	US-10-408-901-22	Sequence 22, App
22	138	89.6	116	US-10-687-799-54	Sequence 54, App
23	138	89.6	116	US-10-911-838-13	Sequence 13, App
24	138	89.6	119	US-10-815-449-5	Sequence 5, App
25	138	89.6	446	US-10-408-901-38	Sequence 38, App
26	138	89.6	446	US-10-408-901-46	Sequence 46, App
27	138	89.6	850	US-10-450-763-34993	Sequence 34993, A

28	137	89.0	98	5	US-10-884-830-667	Sequence 667, App
29	137	89.0	115	4	US-10-803-622-167	Sequence 167, App
30	137	89.0	115	4	US-10-803-623-167	Sequence 167, App
31	137	89.0	115	5	US-10-884-830-23	Sequence 23, App
32	137	89.0	115	5	US-10-884-830-33	Sequence 33, App
33	137	89.0	115	5	US-10-884-830-37	Sequence 37, App
34	137	89.0	115	5	US-10-884-830-39	Sequence 39, App
35	137	89.0	115	5	US-10-884-830-41	Sequence 41, App
36	137	89.0	115	5	US-10-884-830-43	Sequence 43, App
37	137	89.0	115	5	US-10-884-830-45	Sequence 45, App
38	137	89.0	115	5	US-10-884-830-47	Sequence 47, App
39	137	89.0	115	5	US-10-884-830-51	Sequence 51, App
40	137	89.0	115	5	US-10-884-830-53	Sequence 53, App
41	137	89.0	115	5	US-10-884-830-55	Sequence 55, App
42	137	89.0	115	5	US-10-884-830-57	Sequence 57, App
43	137	89.0	115	5	US-10-884-830-59	Sequence 59, App
44	137	89.0	115	5	US-10-884-830-61	Sequence 61, App
45	137	89.0	115	5	US-10-884-830-63	Sequence 63, App

ALIGNMENTS

RESULT 1
US-10-632-706-158
Sequence 158, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 158
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial
FEATURES:
FEATURE: OTHER INFORMATION: single chain antibody fragment
US-10-632-706-158
Query Match 100.0%; Score 154; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVQLVQSGGVSHPGSRSLKSLSCAGSGPTFS 30
Db 1 QVQLVQSGGVSHPGSRSLKSLSCAGSGPTFS 30
RESULT 2
US-10-632-706-162
Sequence 162, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806

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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-162

Query Match          100.0%; Score 154; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 QVQLVSGGCVVHPGRSLKLSKSCAGSGFTFS 30
Db      1 QVQLVSGGCVVHPGRSLKLSKSCAGSGFTFS 30

RESULT 3
US-10-632-706-166
; Sequence 166, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-166

Query Match          100.0%; Score 154; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 QVQLVSGGCVVHPGRSLKLSKSCAGSGFTFS 30
Db      1 QVQLVSGGCVVHPGRSLKLSKSCAGSGFTFS 30

RESULT 4
US-10-632-706-170
; Sequence 170, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 170
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-170

Query Match          100.0%; Score 154; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.8e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 QVQLVSGGCVVHPGRSLKLSKSCAGSGFTFS 30
Db      1 QVQLVSGGCVVHPGRSLKLSKSCAGSGFTFS 30

RESULT 5
US-10-884-830-617
; Sequence 617, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfield et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; PRIOR FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 617
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-617

Query Match          89.6%; Score 138; DB 5; Length 97;
Best Local Similarity 86.7%; Pred. No. 1.3e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Cy      1 QVQLVSGGCVVHPGRSLKLSKSCAGSGFTFS 30
Db      1 EVQLVSGGGLVHPGSLRLSKSCAGSGFTFS 20

RESULT 6
US-10-911-838-18
; Sequence 18, Application US/10911838
; Publication No. US20050069869A1
; GENERAL INFORMATION:
; APPLICANT: AMEROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: IIZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MJI-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
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PRIOR FILING DATE: 2003-08-04
NUMBER OF SEQ ID NOS: 148
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 97
TYPE: PRT
ORGANISM: SARS-Associated Coronavirus
US-10-911-838-18

Query Match 89.6%; Score 138; DB 5; Length 97;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30

RESULT 7
US-10-982-359-16
Sequence 16, Application US/10982359
Publication No. US20050112694A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
FILE REFERENCE: 3492-A
CURRENT APPLICATION NUMBER: US/10/982,359
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: 60/518,166
PRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 115
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-982-359-16

Query Match 89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30

RESULT 8
US-10-982-359-18
Sequence 18, Application US/10982359
Publication No. US20050112694A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
FILE REFERENCE: 3492-A
CURRENT APPLICATION NUMBER: US/10/982,359
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: 60/518,166
PRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 115
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-982-359-18

Query Match 89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30

RESULT 9
US-10-982-359-20
Sequence 20, Application US/10982359
Publication No. US20050112694A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
FILE REFERENCE: 3492-A
CURRENT APPLICATION NUMBER: US/10/982,359
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: 60/518,166
PRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 115
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-982-359-20

Query Match 89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30

RESULT 10
US-10-982-359-22
Sequence 22, Application US/10982359
Publication No. US20050112694A1
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
FILE REFERENCE: 3492-A
CURRENT APPLICATION NUMBER: US/10/982,359
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: 60/518,166
PRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 115
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-982-359-22

Query Match 89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30
:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVQSGGIVHPGSRSLKLSGAGSGFTFS 30

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RESULT 11
US-10-982-359-24
; Sequence 24, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-24

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPGRSLKLSGAGSGFTFS 30
Db      1 EVQLVSGGSGLVHPGSLRLSCAGSGFTFS 30

RESULT 12
US-10-982-359-26
; Sequence 26, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-26

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPGRSLKLSGAGSGFTFS 30
Db      1 EVQLVSGGSGLVHPGSLRLSCAGSGFTFS 30

RESULT 13
US-10-982-359-28
; Sequence 28, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
```

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; CURRENT APPLICATION NUMBER: US/10/982,359
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-28

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPGRSLKLSGAGSGFTFS 30
Db      1 EVQLVSGGSGLVHPGSLRLSCAGSGFTFS 30

RESULT 14
US-10-982-359-30
; Sequence 30, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-982-359-30

Query Match      89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 QVQLVSGGSGVHPGRSLKLSGAGSGFTFS 30
Db      1 EVQLVSGGSGLVHPGSLRLSCAGSGFTFS 30

RESULT 15
US-10-982-359-32
; Sequence 32, Application US/10982359
; Publication No. US20050112694A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES THAT BIND INTERLEUKIN-4 RECEPTOR
; FILE REFERENCE: 3492-A
; CURRENT APPLICATION NUMBER: US/10/982,359
; PRIOR FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/518,166
; PRIOR FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 115
; TYPE: PRT
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ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-982-359-32

Query Match 89.6%; Score 138; DB 5; Length 115;
Best Local Similarity 86.7%; Pred. No. 1.5e-10;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 QVQLVQSGGSGVHPGRSLKLSGAGSGFTFS 30
:|||||:|||||:|||||
Db 1 EVQLVQSGGSLVHPGSRSLKLSGAGSGFTFS 30

Search completed: November 21, 2005, 12:33:37
Job time : 37.1429 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 12:04:27 ; Search time 0.549451 Seconds
(without alignments)
61.686 Million cell updates/sec

Title: US-10-632-706-158
Perfect score: 154
Sequence: 1 OVQLVOSGGVHPGRSLKLSGASGPTFS 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New*
1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	81.2	139	1	US-10-721-763-33 Sequence 33, Appl
2	123	79.9	98	7	US-11-144-248-30 Sequence 30, Appl
3	123	79.9	473	7	US-11-144-248-50 Sequence 50, Appl
4	120	77.9	138	1	US-10-789-273-4 Sequence 4, Appl
5	120	77.9	263	1	US-10-512-184-29 Sequence 29, Appl
6	120	77.9	444	7	US-11-172-320-6 Sequence 6, Appl
7	119	77.3	470	7	US-11-144-248-49 Sequence 49, Appl
8	118	76.6	98	1	US-10-789-273-10 Sequence 10, Appl
9	118	76.6	98	7	US-11-144-248-32 Sequence 32, Appl
10	118	76.6	121	1	US-10-789-273-9 Sequence 9, Appl
11	118	76.6	122	7	US-11-144-248-24 Sequence 24, Appl
12	118	76.6	125	7	US-11-144-248-16 Sequence 16, Appl
13	118	76.6	138	1	US-10-789-273-8 Sequence 8, Appl
14	118	76.6	138	1	US-10-789-273-12 Sequence 12, Appl
15	118	76.6	470	7	US-11-144-248-46 Sequence 46, Appl
16	115	74.7	118	1	US-10-648-816-9 Sequence 9, Appl
17	115	74.7	118	1	US-10-648-816-11 Sequence 11, Appl
18	115	74.7	118	1	US-10-648-816-14 Sequence 14, Appl
19	115	74.7	121	1	US-10-648-816-15 Sequence 15, Appl
20	114	74.0	124	7	US-11-144-248-45 Sequence 45, Appl
21	112	72.7	124	7	US-11-144-248-8 Sequence 8, Appl
22	109	70.8	118	1	US-10-648-816-10 Sequence 10, Appl
23	109	70.8	118	1	US-10-648-816-12 Sequence 12, Appl
24	109	70.8	118	1	US-10-648-816-13 Sequence 13, Appl
25	109	70.8	121	1	US-10-648-816-16 Sequence 16, Appl

26	106.5	69.2	102	1	US-10-997-201A-6	Sequence 6, Appl
27	106	68.8	120	7	US-11-077-978-7	Sequence 7, Appl
28	106	68.8	121	7	US-11-077-978-2	Sequence 2, Appl
29	106	68.8	121	7	US-11-077-978-3	Sequence 3, Appl
30	105	68.2	123	1	US-10-932-334-88	Sequence 88, Appl
31	105	68.2	123	1	US-10-932-334-92	Sequence 92, Appl
32	105	68.2	124	1	US-10-932-334-13	Sequence 13, Appl
33	102	66.2	119	7	US-11-010-954-5	Sequence 5, Appl
34	98	63.6	116	7	US-11-174-186-17	Sequence 17, Appl
35	96	62.3	120	1	US-10-932-334-71	Sequence 71, Appl
36	96	62.3	123	1	US-10-932-334-87	Sequence 87, Appl
37	96	62.3	124	1	US-10-932-334-70	Sequence 70, Appl
38	96	62.3	143	1	US-10-932-334-52	Sequence 52, Appl
39	96	62.3	143	1	US-10-932-334-70	Sequence 18, Appl
40	94	61.0	116	7	US-11-174-186-18	Sequence 41, Appl
41	94	61.0	579	7	US-11-174-186-11	Sequence 113, Appl
42	93	60.4	76	1	US-10-839-799-113	Sequence 17, Appl
43	93	60.4	121	1	US-10-502-145-17	Sequence 76, Appl
44	92	59.7	117	1	US-10-932-334-76	Sequence 75, Appl
45	92	59.7	118	1	US-10-932-334-75	

ALIGNMENTS

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RESULT 1
US-10-721-763-33
; Sequence 33, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KAHUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTI BODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-33

Query Match      81.2%  Score 125, DB 1, Length 139;
Best Local Similarity 76.7%  Pred. No. 9e-09;
Matches 23; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

CY      1 OVQLVOSGGVHPGRSLKLSGASGPTFS 30
DB      20 EVQLVESGGGLVQPGKSLRLKLSGASGPTFS 49

RESULT 2
US-11-144-248-30
; Sequence 30, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope B.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvillan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
```

PRIOR APPLICATION NUMBER: US/10/038,591
 PRIOR FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 60/259,927
 PRIOR FILING DATE: 2001-01-05
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 30
 LENGTH: 98
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-144-248-30

Query Match 79.9%; Score 123; DB 7; Length 98;
 Best Local Similarity 80.0%; Pred. No. 1,1e-08;
 Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVSGGQGVHPGSRSLKSCAGSGFTFS 30
 DB 1 QVQLVSGGGLVYKPGSLRLSCAAGFTFS 30

RESULT 3
 US-11-144-248-50
 Sequence 50, Application US/11144248
 Publication No. US20050244408A1
 GENERAL INFORMATION:

APPLICANT: Cohen, Bruce D.
 APPLICANT: Beebe, Jean
 APPLICANT: Miller, Penelope E.
 APPLICANT: Moyer, James D.
 APPLICANT: Corvalan, Jose R.
 APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
 FILE REFERENCE: ARI-PF2
 CURRENT APPLICATION NUMBER: US/11/144,248
 CURRENT FILING DATE: 2005-06-02
 PRIOR APPLICATION NUMBER: US/10/038,591
 PRIOR FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 60/259,927
 PRIOR FILING DATE: 2001-01-05
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 50
 LENGTH: 473
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-144-248-50

Query Match 79.9%; Score 123; DB 7; Length 473;
 Best Local Similarity 80.0%; Pred. No. 4,2e-08;
 Matches 24; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVSGGQGVHPGSRSLKSCAGSGFTFS 30
 DB 20 QVQLVSGGGLVYKPGSLRLSCAAGFTFS 49

RESULT 4
 US-10-789-273-4
 Sequence 4, Application US/10789273
 Publication No. US20050249725A1
 GENERAL INFORMATION:
 APPLICANT: Basi, Gurid
 APPLICANT: Saidanna, Jose
 APPLICANT: Yednock, Ted
 TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
 TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
 FILE REFERENCE: ELM-002CP
 CURRENT APPLICATION NUMBER: US/10/789,273
 CURRENT FILING DATE: 2004-02-27
 PRIOR APPLICATION NUMBER: US/10/388,389
 PRIOR FILING DATE: 2003-03-12
 PRIOR APPLICATION NUMBER: US 10/010,942

PRIOR FILING DATE: 2001-12-06
 PRIOR APPLICATION NUMBER: US 60/251,892
 PRIOR FILING DATE: 2000-12-06
 NUMBER OF SEQ ID NOS: 63
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 138
 TYPE: PRT
 ORGANISM: Mus musculus
 NAME/KEY: SIGNAL
 LOCATION: (1)...(19)
 US-10-789-273-4

Query Match 77.9%; Score 120; DB 1; Length 138;
 Best Local Similarity 76.7%; Pred. No. 3,2e-08;
 Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVSGGQGVHPGSRSLKSCAGSGFTFS 30
 DB 20 EVQLVSGGGLVYKPGASLKSCAAGFTFS 49

RESULT 5
 US-10-512-184-29
 Sequence 29, Application US/10512184
 Publication No. US20050244901A1
 GENERAL INFORMATION:

APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
 TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
 TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
 TITLE OF INVENTION: resistance against fungi
 FILE REFERENCE: 3581.01US01
 CURRENT APPLICATION NUMBER: US/10/512,184
 CURRENT FILING DATE: 2004-10-22
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 29
 LENGTH: 263
 TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: scFv SPRI17
 OTHER INFORMATION: with specificity against Fusarium spp.; originates
 OTHER INFORMATION: from Mus musculus.
 US-10-512-184-29

Query Match 77.9%; Score 120; DB 1; Length 263;
 Best Local Similarity 76.7%; Pred. No. 5,5e-08;
 Matches 23; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QVQLVSGGQGVHPGSRSLKSCAGSGFTFS 30
 DB 3 EVQLVSGGGLVYKPGNSLKSCVTSFTFS 32

RESULT 6
 US-11-172-320-6
 Sequence 6, Application US/11172320
 Publication No. US2005024413A1
 GENERAL INFORMATION:
 APPLICANT: Adolf, Guenther
 APPLICANT: Baum, Anke
 APPLICANT: Heider, Karl-Heinz
 TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
 TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
 TITLE OF INVENTION: Chemotherapeutic Agents
 FILE REFERENCE: 1/1383
 CURRENT APPLICATION NUMBER: US/11/172,320
 CURRENT FILING DATE: 2005-06-30
 PRIOR APPLICATION NUMBER: US/10/645,215
 PRIOR FILING DATE: 2003-08-21
 PRIOR APPLICATION NUMBER: EP 02 018 686.2

PRIOR FILING DATE: August 21, 2002
PRIOR APPLICATION NUMBER: US 60/405,956
PRIOR FILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanised Murine Antibody B1W4 4 Heavy Chain
US-11-172-320-6

Query Match 77.9%; Score 120; DB 7; Length 444;
Best Local Similarity 76.7%; Pred. No. 8.5e-08;
Matches 23; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS 30

RESULT 7
US-11-144-248-49
Sequence 49, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvajan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-49

Query Match 77.3%; Score 119; DB 7; Length 470;
Best Local Similarity 76.7%; Pred. No. 1.1e-07;
Matches 23; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30
Db 20 QVQLVESGGGLVQPGGSLRLSCAASGFTFS 49

RESULT 8
US-10-789-273-10
Sequence 10, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Gurig
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-789-273-10

Query Match 76.6%; Score 118; DB 1; Length 98;
Best Local Similarity 73.3%; Pred. No. 4e-08;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS 30

RESULT 9
US-11-144-248-32
Sequence 32, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvajan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-32

Query Match 76.6%; Score 118; DB 7; Length 98;
Best Local Similarity 73.3%; Pred. No. 4e-08;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 QVQLVQSGGGLVHPGSRSLKSCASGFTFS 30
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS 30

RESULT 10
US-10-789-273-9
Sequence 9, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Gurig
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942

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/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US 60/251,892
/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 9
/ LENGTH: 121
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ OS-10-789-273-9

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Query Match	76.64;	Score 118;	DB 1;	Length 121;
Best Local Similarity	-73.34;	Pred. No. 4.8e-08;		
Matches 22;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0;

Oy

1 QVQLVQSGGGVHPRSLKLSGAGSFTFS 30
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1 EVQLTSGGGLVPGASLRSCAASGFTFS 30

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RESULT 11
US-11-144-248-24

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Sequence 24, Application US/11/144248
Publication No. US2005024408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PP2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 122
TYPE: PRN
ORGANISM: Homo sapiens
US-11-144-248-24

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Query Match	76.6%	Score 118;	DB 7;	Length 122;
Best Local Similarity	73.3%	Pred. No. 4.8e-08;		
Matches 22;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0

Oy 1 QVQLVQSGGCVHPGRSLKLSGASGFTFS 30
 :|||:|||:|||:|||:
Db 1 EVQLTSSGGGLVPGSRLRSLSCAAGFTFS 30

RESULT 12
US-11-144-248-16

Sequence 16, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvatan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,551
PRIOR FILING DATE: 2002-01-04

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Query Match	76.6%	Score 118	DB 7	Length 125
Best Local Similarity	73.3%	Pred. No. 4.9e+08		
Matches 22; Conservative		5; Mismatches 3; Indels 0; Gaps 0		

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QY      1 QVQLVSGGGVHPRSLKLSGASGFPTS 30
          :|||:|||:|||:|||:|||
Db      1 EVQLVESGGGLVPGGSLRLSCAAGFTFS 30
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RESULT 13
US-10-789-273-8

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1 Sequence 8, Application US/10789273
2 Publication No. US20050249725A1
3 GENERAL INFORMATION:
4 APPLICANT: Baei, Guirid
5 APPLICANT: Saidanba, Josee
6 APPLICANT: Yednock, Ted
7 TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
8 TITLE OF INVENTION: BETA-AMYLROID PEPTIDE
9 FILE REFERENCE: ELN-002CP
10 CURRENT APPLICATION NUMBER: US/10/789,273
11 CURRENT FILING DATE: 2004-02-27
12 PRIOR APPLICATION NUMBER: US/10/388,389
13 PRIOR FILING DATE: 2003-03-12
14 PRIOR APPLICATION NUMBER: US 10/010,942
15 PRIOR FILING DATE: 2001-12-06
16 PRIOR APPLICATION NUMBER: US 60/251,892
17 PRIOR FILING DATE: 2000-12-06
18 NUMBER OF SEQ ID NOS: 63
19 SOFTWARE: FastSeq for Windows Version 4.0
20 SEQ ID NO 8
21 LENGTH: 138
22 TYPE: PRT
23 ORGANISM: Artificial Sequence
24 FEATURE:
25 OTHER INFORMATION: Humanized 3D6 heavy chain variable region
26 FEATURE:
27 NAME/KEY: SIGNAL
28 LOCATION: (1)...(19)
29 US-10-789-273-8

```

Query Match	76.6%;	Score 118;	DB 1;	Length 138;
Best Local Similarity	-73.3%;	Pred. No. 5,3e-08;		
Matches	22;	Conservative	3;	Indels 0;
				Gaps 0;

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QY      1 QVQLVDSGGGVHPGRSLKLSGASGFTFS 20
        :|||:||||:|:|:|||||
DB      20 EVQLTSGGGGLVQPGSGRLRLSCAASGFTFS 45

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RESULT 14
US-10-789-273-12

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1 Sequence 12, Application US/10789273
2 Publication No. US20050249725A1
3
4 GENERAL INFORMATION:
5 APPLICANT: Basi, Gurig
6 APPLICANT: Saldanha, Jose
7 APPLICANT: Vednock, Ted
8 TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
9 TITLE OF INVENTION: BETA-AMLOID PEPTIDE
10 FILE REFERENCE: EBN-002CP
11 CURRENT APPLICATION NUMBER: US/10/789,273
12 CURRENT FILING DATE: 2004-02-27

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PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 138
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized 3D6 light chain variable region
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-789-273-12

Query Match 76.6%; Score 118; DB 1; Length 138;
Best Local Similarity 73.3%; Pred. No. 5,3e-08;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVHPGSRSLKLSGAGSGFTFS 30
DB 20 EVQLLESGGGLVQPGSLRLSCAASGFTFS 49

RESULT 15
US-11-144-248-46
Sequence 46, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvatan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-46

Query Match 76.6%; Score 118; DB 7; Length 470;
Best Local Similarity 73.3%; Pred. No. 1,5e-07;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVHPGSRSLKLSGAGSGFTFS 30
DB 20 EVQLLESGGGLVQPGSLRLSCAASGFTFS 49

Search completed: November 21, 2005, 12:33:52
Job time : 0.649451 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:32 ; Search time 6.69414 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-159
Perfect score: 32
Sequence: 1 DYDMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	32 100.0	5	ADR38765	Adi38765 Mouse hea
2	32 100.0	5	ADR38761	Adi38761 Mouse hea
3	32 100.0	5	ADR38757	Adi38757 Mouse hea
4	32 100.0	5	ADR38769	Adi38769 Mouse hea
5	32 100.0	142	3 AAG00943	Aag00943 Human bec
6	32 100.0	144	3 ABG20497	Abg20497 Novel hum
7	32 100.0	180	6 ABU70539	Abu70539 Human adi
8	32 100.0	253	8 ADS09256	Ads09256 Human c-M
9	32 100.0	319	8 ADS44811	Ads44811 Bacterial
10	32 100.0	341	8 ABM68679	Abm68679 Photocarb
11	32 100.0	457	8 ADS41979	Ads41979 Bacterial
12	32 100.0	465	8 ADN18693	Adn18693 Bacterial
13	32 100.0	473	5 ABB92826	Abb92826 Herbicida
14	32 100.0	493	4 AAM93283	Aam93283 Human pol
15	32 100.0	493	8 ADI30731	Adi30731 Human pro
16	32 100.0	525	5 ABB97214	Abb97214 Novel hum
17	32 100.0	564	3 AAY68726	Aay68726 Short cna
18	32 100.0	564	3 AAB3224	Aab3224 Human ORF
19	32 100.0	564	3 AAY69295	Aay69295 A human h
20	32 100.0	564	8 ADF08477	Adf08477 Human HSP
21	32 100.0	564	8 ABM62354	Abm62354 Tumour-as
22	32 100.0	579	7 ADE09984	Ade09984 Novel pro
23	32 100.0	581	3 AAB58463	Aab58463 lung can
24	32 100.0	585	4 ABG11793	Abg11793 Novel hum

25	32	100.0	596	4	ABG04416
26	32	100.0	607	6	ADA54819
27	32	100.0	640	4	ABG20499
28	32	100.0	858	4	ABB66508
29	32	100.0	973	4	AAY97696
30	32	100.0	973	8	ADR21541
31	29	90.6	20	4	AAB57691
32	29	90.6	20	4	AAB58101
33	29	90.6	20	4	AAB55829
34	29	90.6	20	5	ABJ05221
35	29	90.6	20	5	ABP63246
36	29	90.6	50	6	AAY40779
37	29	90.6	50	6	ABM37298
38	29	90.6	85	5	ABB04486
39	29	90.6	139	4	AAB63457
40	29	90.6	139	4	AAB63286
41	29	90.6	282	5	ABP25940
42	29	90.6	293	3	AAG52812
43	29	90.6	303	3	AAG52811
44	29	90.6	392	3	AAG52810
45	29	90.6	397	8	ADY04516

ALIGNMENTS

RESULT 1
ADR38765 standard; peptide; 5 AA.

ADR38765;

02-DEC-2004 (first entry)

Mouse heavy chain anti-BoNT-antibody CDR1 seqid 167.

antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;

BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

CDR1; complementarity determining region 1.

OS Mus sp.

US2004175385-A1.

09-SEP-2004.

01-AUG-2003; 2003US-00632706.

31-AUG-1998; 98US-00144886.

01-AUG-2002; 2002US-0400721P.

(REGC) UNIV CALIFORNIA.

Marke JD, Amersdorfer P;

WPI; 2004-652009/63.

New isolated antibody that neutralizes botulinum neurotoxin type A,

useful for diagnosing botulism or for treating pathologies associated

with botulinum neurotoxin poisoning.

Example 4; SEQ ID NO 167; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds

to an epitope specifically bound by an antibody expressed by a specific

clone where (I) binds to and neutralizes botulinum neurotoxin type A

(BoNT/A). An isolated antibody (I) that specifically binds to an epitope

specifically bound by an antibody expressed by a clone chosen from clone

S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI (V), WRI (T), 3-1,

3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum

neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)

comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BONT-antibody CRD1.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 32; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYDMH 5
 1 DYDMH 5
 DB 1 DYDMH 5
 RESULT 2
 ADR38761
 ID ADR38761 standard; peptide; 5 AA.
 AC ADR38761;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Mouse heavy chain anti-BONT-antibody CRD1 seqid 163.
 XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW CRD1; complementarity determining region 1.
 XX
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Marks JD, Amersdorfer P;
 PI WPI; 2004-652009/63.
 XX
 DR WPI; 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX
 PS Example 4; SEQ ID NO 163; 110pp; English.
 XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C33, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BONT-antibody CRD1.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 32; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYDMH 5
 1 DYDMH 5
 DB 1 DYDMH 5
 RESULT 3
 ADR38757
 ID ADR38757 standard; peptide; 5 AA.
 AC ADR38757;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Mouse heavy chain anti-BONT-antibody CRD1 seqid 159.
 XX
 KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
 KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW CRD1; complementarity determining region 1.
 XX
 OS Mus sp.
 XX
 PN US2004175385-A1.
 XX
 PD 09-SEP-2004.
 XX
 PF 01-AUG-2003; 2003US-00632706.
 XX
 PR 31-AUG-1998; 98US-00144886.
 PR 01-AUG-2002; 2002US-0400721P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Marks JD, Amersdorfer P;
 PI WPI; 2004-652009/63.
 XX
 DR WPI; 2004-652009/63.
 XX
 PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.
 XX
 PS Example 4; SEQ ID NO 159; 110pp; English.
 XX
 CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone

CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising a botulinum neurotoxin which
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which (I) is
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody CRD1.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
 Db 1 DYDMH 5

RESULT 4

ID ADR38769 standard; peptide; 5 AA.

XX ADR38769;

XX 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody CDRI seqid 171.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A.

KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KM toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;

XX CDRI; complementarity determining region 1.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,

XX useful for diagnosing botulism or for treating pathologies associated

XX with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 171, 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising a botulinum neurotoxin which
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody CRD1.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
 Db 1 DYDMH 5

RESULT 5

ID AAG00943 standard; protein; 142 AA.

XX AAG00943;

XX 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 5024.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

KM gene therapy; chromosome mapping.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GENEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX N-PSDB; AAC00949.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

XX diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 5024; 71pp + Sequence listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of

XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were

XX prepared from total human RNAs or polyA+ RNAs derived from 30 different

CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX SQ Sequence 142 AA;

XX Query Match 100.0%; Score 32; DB 3; Length 142;
XX Best Local Similarity 100.0%; Pred. No. 63;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|||
Db 22 DYDMH 26

RESULT 6
ABG20497
ID ABG20497 standard; protein, 144 AA.

XX AC ABG20497;
XX 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #20488.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
XX DR N-PSDB; AAS84684.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.

XX PS Claim 20; SEQ ID NO 50856; 103bp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC pathto acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 144 AA;

XX Query Match 100.0%; Score 32; DB 4; Length 144;
XX Best Local Similarity 100.0%; Pred. No. 64;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|||
Db 26 DYDMH 30

RESULT 7
ABU70539
ID ABU70539 standard; protein, 180 AA.

XX AC ABU70539;
XX 10-JUN-2003 (first entry)
XX DE Human adipocyte Selected Interacting domain, SID, #170.
XX KW Human; prey; adipocyte; SID; selected interacting domain; anorectic;
XX antidiabetic; protein-protein interaction; diabetes;
XX yeast 2-hybrid assay; metabolic disorder; obesity.
XX OS Homo sapiens.
XX PN WO200286122-A2.
XX PD 31-OCT-2002.
XX PF 14-MAR-2002; 2002WO-EP003768.
XX PR 14-MAR-2001; 2001US-0275734P.
XX PA (HYBR-) HYBRIGENICS.
XX PI Legrain P, Davlet L;
XX WPI: 2003-103412/09.
XX DR N-PSDB; ACA57083.
XX PT New complex between two interacting proteins in adipocyte cells, useful
XX for identifying selected interacting domains that modulate protein
XX interactions, or for preventing or treating metabolic disorders such as
XX obesity or diabetes.

XX PS Claim 6; Page 163; 382bp; English.

XX CC The invention relates to a complex between two interacting proteins in
XX adipocyte cells, given in the specification. The proteins are identified
XX by selecting a bait protein from a known adipocyte marker and then
XX performing a yeast 2-hybrid selection to isolate prey proteins encoded by
XX members of an adipocyte cDNA library. The proteins are designated SID
XX (RIM) (selected interacting domains) proteins. Also included are a
XX polynucleotide encoding a polypeptide in the adipocyte cells, a
XX recombinant host cell expressing at least one of the interacting
XX polypeptides of the complex, selecting a modulating compound in adipocyte
XX cells, a SID (RIM) polypeptide comprising any of the 738 amino acid
XX sequences given in the specification (including its fragment or variant),
XX a SID (RIM) polynucleotide comprising any of the 738 nucleotide sequences
XX given in the specification (including its fragment or variant), a vector
XX comprising the SID (RIM) polynucleotide, a recombinant host cell
XX comprising the vector, a protein chip comprising the polypeptides and a

CC record comprising all or part of the data, listed in the specification.
CC The complex, polypeptides, polynucleotides and compounds are useful for
CC preventing or treating metabolic disorders such as obesity or diabetes.
CC The polynucleotides are useful as probes or primers. The complex is
CC particularly useful for identifying selected interacting domains (SID
CC (RMI)) for screening drugs that modulate the protein interaction, thus
CC exhibiting the therapeutic effect. The present sequence represents a SID
CC (prey) protein of the invention
XX
SQ Sequence 180 AA;
Query Match 100.0%; Score 32; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYDMH 5
DB 22 DYDMH 26
RESULT 8
ADS09256
ID ADS09256 standard; protein; 253 AA.
AC ADS09256;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human c-Met protein tyrosine kinase antibody, PG1A-2-A4.
XX
KW c-Met; tyrosine kinase antibody; antigen binding; cytostatic;
KW ophthalmological; antiinflammatory; analgesic; vasotropic; antipsoriatic;
KW osteopathic; cancer; tumour; ophthalmic disease; glaucoma; retinitis;
KW retinopathy; uveitis; ocular photophobia; macular degeneration; pain;
KW acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;
KW psoriasis; HGF; osteoporosis; cancer.
XX
OS Homo sapiens.
XX
PN WO2004072117-A2.
XX
PD 26-AUG-2004.
XX
PF 11-FEB-2004; 2004WO-1B000503.
XX
PR 13-FEB-2003; 2003US-0447073P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Morton PA, Arbuckle JA, Evans ML, Joy WD, Kahn LB, Shieh JU;
XX
DR MPI: 2004-616044/59.
XX
N-PSDB; ADS09316.
XX
PT Novel c-Met protein tyrosine kinase antibody or its antigen-binding
PT portion specifically binding to c-Met, useful for manufacture of
PT medicament for treating cancer or tumor and for treatment of ophthalmic
PT diseases such as glaucoma.
XX
PS Claim 1, SEQ ID NO 18; 303pp; English.
XX
XX The invention relates to a novel c-Met protein tyrosine kinase antibody
CC or its antigen binding portion that specifically binds to c-Met. The c-
CC Met antibody comprises any one of 1-60 fully defined sequence of 238,
CC 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino
CC acids as given in the specification, or its fragment. The invention
CC further comprises: a pharmaceutical composition comprising the c-Met
CC protein tyrosine kinase antibody and a carrier; an isolated cell that
CC produces the c-Met protein tyrosine kinase antibody; and an isolated
CC nucleic acid molecule that comprises a nucleic acid sequence that encodes
CC a heavy chain or its antigen-binding portion or light chain or its
CC antigen-binding portion of the c-Met protein tyrosine kinase antibody.
CC The c-Met protein tyrosine kinase antibody has cytostatic,

CC ophthalmological, antiinflammatory, analgesic, vasotropic, antipsoriatic,
CC and osteopathic activities. The c-Met protein tyrosine kinase antibody is
CC useful for the manufacture of medicament for the treatment of cancer or
CC tumour. The c-Met protein tyrosine kinase antibody is useful for
CC diagnosing the presence or ligand of c-Met expressing tissue. The c-Met
CC protein tyrosine kinase antibody is useful for detecting c-Met in a
CC biological sample in vitro or in vivo. The c-Met protein tyrosine kinase
CC antibody is also useful in the treatment or prevention of ophthalmic
CC diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic
CC retinopathy), uveitis, ocular photophobia, macular degeneration and pain
CC associated with acute injury to the eye. The pharmaceutical composition
CC is useful for the treatment of hyperproliferative disorders such as
CC restenosis after angioplasty, and psoriasis, and for the treatment of
CC animals that lack sufficient HGF, e.g. osteoporosis and cancer. This
CC sequence represents the protein of a phase display generated human c-Met
CC antibody of the invention.
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 32; DB 8; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYDMH 5
DB 31 DYDMH 35
RESULT 9
ADS44811
ID ADS44811 standard; protein; 319 AA.
AC ADS44811;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #23241.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR MPI: 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1, SEQ ID NO 23241; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 319 AA;

Query Match 100.0%; Score 32; DB 8; Length 319;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 195 DYDMH 199

RESULT 10

ID ABM68679 standard; protein; 341 AA.

XX ABM68679;

XX 20-NOV-2003 (first entry)

XX Photorhabdus luminescens protein sequence #1776.

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
XX detection; food; gene expression; plant; animal; microorganism; toxin;
XX antibiotic; biopesticide; virulence factor; disease model; plague;
XX whooping cough.

XX Photorhabdus luminescens.

XX MO200294867-A2.

XX 28-NOV-2002.

XX 07-FEB-2002; 2002MO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.

XX (INSP) INST PASTEUR.

XX (CNRS) CNRS CENT NAT RECH SCT.

XX Duchaud E, Taourit S, Glaeser P, Frangeul L, Kunst F, Danchin A;

XX Buchrieser C;

XX WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 2; SEQ ID NO 1776; 1205BP; French.

CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms, for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterial proteins useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins

XX Sequence 341 AA;

Query Match 100.0%; Score 32; DB 6; Length 341;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 194 DYDMH 198

RESULT 11

ID ADS41979 standard; protein; 457 AA.

XX ADS41979;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #20409.

XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 20409; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 457 AA;

Query Match 100.0%; Score 32; DB 8; Length 457;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYDNH 5

DB 235 DYDNH 239

RESULT 12

ID ADN18693 standard; protein; 465 AA.

XX AC ADN18693;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #1346.

KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX (CAO Y.
XX (HINKLE G J.
XX (SLATER S C.
XX (CHEN X.
XX (GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX DR WPI; 2004-061375/06.

XX PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 1346; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 465 AA;

Query Match 100.0%; Score 32; DB 8; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DYDNH 5

DB 241 DYDNH 245

RESULT 13

ID ABB92826 standard; protein; 473 AA.

XX AC ABB92826;

XX DT 31-MAY-2002 (first entry)

XX DE Herbicidally active polypeptide SEQ ID NO 2037.

XX OS Herbicidal; plant; agriculture; herbicide.

XX PN Arabidopsis thaliana.

XX PD WO200210210-A2.

XX PF 07-FEB-2002.

XX PR 26-AUG-2001; 2001WO-BP009892.

XX (FARB) BAYER AG.

XX Tietjen K, Weidner M;

DR WPI; 2002-269010/31.
XX
XX Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.
XX
XX Claim 5; SEQ ID NO 2037; 261pp + Sequence Listing; English.
PS
CC The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides
XX
XX Sequence 473 AA;
SQ
Query Match 100.0%; Score 32; DB 5; Length 473;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYDMH 5
DB 62 DYDMH 66
RESULT 14
AAAG3283
ID AAM93283 standard; protein; 493 AA.
XX
AC AAM93283;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 2764.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2001-524255/58.
DR
DR N-PSDB; AAK94202.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
XX Disclosure; SEQ ID NO 2764; 1380pp + Sequence Listing; English.
PS
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesizing the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA

CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide provided in the
CC specification. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in CD-ROM format directly
CC from EPO
XX
XX Sequence 493 AA;
SQ
Query Match 100.0%; Score 32; DB 4; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYDMH 5
DB 50 DYDMH 54
RESULT 15
ADL30731
ID ADL30731 standard; protein; 493 AA.
XX
AC ADL30731;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein encoded by a full length cDNA clone seqid 2764.
XX
XX human; medicine; signal transduction; glycoprotein; transcription;
KW oligo-capping method.
XX
OS Homo sapiens.
XX
PN EP1396543-A2.
XX
PD 10-MAR-2004.
XX
PF 07-JUL-2000; 2003EP-00025638.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Oca T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
XX WPI; 2004-204755/20.
DR
DR N-PSDB; ADL30730.
XX
PT New oligonucleotide primers (830 cDNAs) Useful for synthesizing full
PT length human cDNAs.
XX
XX Example 1; SEQ ID NO 2764; 1340pp; English.
PS
CC This invention relates to a novel primer useful for synthesizing full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction,
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polypeptide sequence is a full
CC length human protein of the invention.
XX
XX Sequence 493 AA;
SQ
Query Match 100.0%; Score 32; DB 8; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDWH 5
|||
Db 50 DYDWH 54

Search completed: November 21, 2005, 12:20:05
Job time : 8.69414 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:36 ; Search time 1.21795 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-159

Perfect score: 32

Sequence: 1 DYDMH 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	93	2 A37263	Ig heavy chain V r
2	32	100.0	101	2 I37262	Ig heavy chain V r
3	32	100.0	319	2 A69675	6-phosphofructokin
4	32	100.0	465	2 F71213	probable H(+)-tran
5	32	100.0	473	2 D85041	hypothetical prote
6	32	100.0	984	2 AB0290	insecticidal toxin
7	29	90.6	204	2 T04491	hypothetical prote
8	29	90.6	286	2 AB4797	hypothetical prote
9	29	90.6	301	2 AH3431	cobalt-zinc-cadm
10	29	90.6	495	2 A26396	T-cell surface gly
11	29	90.6	824	2 T36818	probable secreted
12	29	90.6	825	2 A59296	alpha-L-arabinofur
13	29	90.6	986	2 A65116	hypothetical prote
14	29	90.6	1016	2 T25433	hypothetical prote
15	29	90.6	1266	2 AF0911	probable exported
16	29	90.6	1266	2 A85989	hypothetical prote
17	29	90.6	1266	2 F91143	hypothetical prote
18	28	87.5	80	2 PH1166	Ig heavy chain V r
19	28	87.5	149	2 AB0812	conserved hypotet
20	28	87.5	266	2 A85114	hypothetical prote
21	28	87.5	266	2 B97983	hypothetical prote
22	28	87.5	273	2 H70849	hypothetical prote
23	28	87.5	279	2 G97143	probable membrane
24	28	87.5	298	1 WMLJLK	bel-1 protein - s1
25	28	87.5	298	1 A28260	chromosomal protei
26	28	87.5	311	2 S18740	bell protein - sim
27	28	87.5	321	2 B98200	hypothetical prote
28	28	87.5	321	2 AG3086	formyltetrahydrofo
29	28	87.5	337	2 AC1615	glycine betaine/ca

30 28 87.5 328 2 AE1252 glycine betaine/ca
31 28 87.5 354 2 A75087 acetyl ornithine d
32 28 87.5 367 2 E87340 Rieseke 2Fe-28 fami
33 28 87.5 368 2 S40627 hypothetical prote
34 28 87.5 371 2 T18558 probable mitochond
35 28 87.5 409 2 A48890 transcripion acti
36 28 87.5 448 2 AB2740 acetyl-CoA carboxy
37 28 87.5 448 2 H97520 biotin carboxylase
38 28 87.5 459 2 A13384 biotin carboxylase
39 28 87.5 473 2 H63962 two-component sens
40 28 87.5 498 2 F88359 protein Y51HA.5 f
41 28 87.5 499 2 S74396 hypothetical prote
42 28 87.5 500 2 B83364 pyoverdine biosynt
43 28 87.5 511 2 G90455 acid phosphatase
44 28 87.5 517 2 T27101 hypothetical prote
45 28 87.5 544 2 S24915 gene 18 protein -

ALIGNMENTS

RESULT 1
A37263
Ig heavy chain V region (4A9) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Aug-1991 #sequence_revision 03-Apr-1992 #text_change 16-Aug-1996
C/Accession: A37263
R/Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A/Title: Common structural features among monoclonal antibodies binding the same antigen;
A/Reference number: A38601; MUID:91115823; PMID:1703527
A/Accession: A37263
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-93 <GOS>
A/Cross-references: UNIPARC:UPI0000176AE0; GB:M57996
A/Note: the authors translated the codon CNA for residue 38 as Hle, AGA for residue 39 as
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|||||
DB 15 DYDMH 19

RESULT 2
I37262
Ig heavy chain V region (1G1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C/Accession: I37262
R/Goshorn, S.C.; Retzel, E.; Jemerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A/Title: Common structural features among monoclonal antibodies binding the same antigen;
A/Reference number: A38601; MUID:91115823; PMID:1703527
A/Accession: I37262
A/Status: Preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-101 <GOS>
A/Cross-references: UNIPARC:UPI0000115185; GB:M57995; NID:G195375; PIDN:AAA6334.1; PID:G
C/Suprafamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|||||

A:Cross-references: UNIPROT:O49574; UNIPARC:UPI00000A96C5; EMBL:AL021633
A:Experimental source: cultivar Columbia; BAC clone FBP16
C:Genetics:
A:Map position: 4
A:Note: FBP16.60

Query Match 90.6%; Score 29; DB 2; Length 204;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 188 DYDLH 192

RESULT 8

A84797
hypothetical protein At2g37780 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: A84797

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Maynard, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, U.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84797

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <STD>

A:Cross-references: UNIPROT:O7XJP2; UNIPARC:UPI00001623D2; GB:AE002093; NID:G4895206; PI

A:Genetics:

A:Gene: At2g37780

A:Map position: 2

Query Match 90.6%; Score 29; DB 2; Length 286;
Best Local Similarity 80.0%; Pred. No. 56;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 45 DYDLH 49

RESULT 9

AH3431
cobalt-zinc-cadmium resistance protein czcd [imported] - Brucella melitensis (strain 16M

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AH3431

R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,

.; Mazur, M.; Goldstein, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

A:Reference number: AD325; PMID:11756688

A:Accession: AH3431

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-301 <KUR>

A:Cross-references: UNIPROT:O8YPT2; UNIPARC:UPI0000058084; GB:AE008917; PIDN:AAL52619.1;

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI1438

A:Map position: 1

C:Superfamily: zinc transporter Znt-2

Query Match 90.6%; Score 29; DB 2; Length 301;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 111

DB 279 DYDLH 283

RESULT 10

A26396
T-cell surface glycoprotein CD5 precursor [validated] - human

N:Alternate names: TI/Lew-1 antigen

C:Species: Homo sapiens (man)

C>Date: 17-Sep-1987 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004

C:Accession: A26396

R:Jones, N.H.; Clabby, M.L.; Dialyna, D.P.; Huang, H.J.S.; Herzenberg, L.A.; Strominger,

Nature 323, 346-349, 1986

A:Title: Isolation of complementary DNA clones encoding the human lymphocyte glycoprotein

A:Reference number: A26396; MUID:87014786; PMID:3093892

A:Accession: A26396

A:Molecule type: mRNA

A:Residues: 1-495 <JON>

A:Cross-references: UNIPROT:P06127; UNIPARC:UPI0000012AD; GB:X04391; NID:G37186; PIDN:C

A:Experimental source: lymphoblastoid tumor cell line HPB-ALL

A:Note: parts of this sequence, including the amino end of the mature protein, were confi

C:Genetics:

A:Gene: GDB:CD5; LEU1

A:Cross-references: GDB:120579; OMIM:153340

A:Map position: 11q13.1

C:Superfamily: T-cell surface glycoprotein CD5; scavenger receptor cysteine-rich domain }

C:Keywords: duplication; glycoprotein; T-cell; transmembrane protein

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-495/Product: T-cell surface glycoprotein CD5 #status experimental <MAT>

F/32-133/Domain: extracellular #status predicted <EXT>

F/158-268/Domain: scavenger receptor cysteine-rich domain homology <SRC1>

F/273-368/Domain: scavenger receptor cysteine-rich domain homology <SRC3>

F/403-495/Domain: intracellular #status predicted <CYT>

F/116,241/Binding site: carbohydrate (Asn) (divalent) #status predicted

Query Match 90.6%; Score 29; DB 1; Length 495;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 486 DYDLH 490

RESULT 11

T36818
probable secreted arabinosidase - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T36818

R:Oliver, K.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21615

A:Accession: T36818

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-824 <OLI>

A:Cross-references: UNIPROT:O88043; UNIPARC:UPI00000DAD6; EMBL:AL031541; PIDN:CAA20794.1

A:Experimental source: strain AJ(2)

C:Genetics:

A:Gene: SCODB:SC135.05C

C:Superfamily: Streptomyces alpha-L-arabinofuranosidase SC135.05C

Query Match 90.6%; Score 29; DB 2; Length 824;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 634 DYDLH 638

RESULT 12

A59296
alpha-L-arabinofuranosidase I [validated] - Streptomyces chartreusis
C/Species: Streptomyces chartreusis
C/Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C/Accession: A59296
R/Matsu, N.; Kaneko, S.; Kuno, A.; Kobayashi, H.; Kusakabe, I.
Biochem. J. 346, 9-15, 2000
A/Title: Purification, characterization and gene cloning of two alpha-L-arabinofuranosidase
A/Reference number: A59296; MUID:20125575; PMID:1055733
A/Accession: A59296
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-825 <MAT>
A/Cross-references: UNIPROT:P82593; UNIPARC:UPI0000125127; GB:AB023625; PIDD:BA90771.1
C/Superfamily: Streptomyces alpha-L-arabinofuranosidase SC135.05c

Query Match 90.6%; Score 29; DB 2; Length 825;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 635 DYDLH 639

RESULT 13

G65116
hypothetical protein b3245 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: G65116
R/Battnner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Ch.
A.; Rose, D.J.; Mau, B.; Siao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: G65116
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-986 <BIAT>
A/Cross-references: UNIPROT:P46474; UNIPARC:UPI0000131619; GB:AE000403; GB:U00096; NID:G
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: Escherichia coli hypothetical protein yhdP

Query Match 90.6%; Score 29; DB 2; Length 986;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 804 DYDLH 808

RESULT 14

T25433
hypothetical protein ZK524.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T25433; T27888
R/McMurray, A.
submitted to the EMBL Data Library, May 1996
A/Reference number: Z20033

A/Accession: T25433
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1016 <WIL>
A/Cross-references: UNIPROT:Q22855; UNIPARC:UPI000007F2B3; EMBL:Z72517; PIDD:CAA96698.1;
A/Experimental source: clone T28F4
R/Gardner, A.
submitted to the EMBL Data Library, June 1996
A/Reference number: Z20435
A/Accession: T27888

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1016 <WIL>

A/Cross-references: UNIPARC:UPI000007F2B3; EMBL:Z73912; PIDD:CAA96148.1; GSPDB:GN00019; C
A/Experimental source: clone ZK524
C/Gene: ZK524.4
A/Map position: 1
A/Intons: 52/3; 91/3; 151/3; 207/1; 254/2; 288/3; 422/2; 560/2; 592/1; 623/1; 660/3; 681

Query Match 90.6%; Score 29; DB 2; Length 1016;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 107 DYDLH 111

RESULT 15

AF0911
probable exported protein [imported] - Salmonella enterica subsp. enterica serovar Typh
C/Species: Salmonella enterica subsp. enterica serovar Typh
A/Note: this species has also been called Salmonella typh
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AF0911
R/Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AF0911
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1266 <PAR>
A/Cross-references: UNIPARC:UPI00000CDBA6; GB:AL513382; PIDD:CAD07884.1; PIDD:G16504431; C
C/Gene: SRY3549
C/Superfamily: Escherichia coli hypothetical protein yhdP

Query Match 90.6%; Score 29; DB 2; Length 1266;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 1084 DYDLH 1088

Search completed: November 21, 2005, 12:22:17
Job time : 3.21795 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:45:55 ; Search time 7.39927 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-159
Perfect score: 32
Sequence: 1 DYDMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	32	100.0	123 2	Q4GYZ8_TRYP
2	32	100.0	129 2	Q4GYZ5_TRYP
3	32	100.0	276 2	Q5B0Z9_TRYP
4	32	100.0	287 2	Q5NHC6_TRYP
5	32	100.0	319 1	Q4H26_TRYP
6	32	100.0	326 2	Q4H26_TRYP
7	32	100.0	340 2	Q7N656_TRYP
8	32	100.0	462 1	Q4H26_TRYP
9	32	100.0	465 1	Q4H26_TRYP
10	32	100.0	473 2	Q4H26_TRYP
11	32	100.0	493 2	Q4H26_TRYP
12	32	100.0	521 2	Q4H26_TRYP
13	32	100.0	562 2	Q4H26_TRYP
14	32	100.0	564 1	Q4H26_TRYP
15	32	100.0	564 2	Q4H26_TRYP
16	32	100.0	564 2	Q4H26_TRYP
17	32	100.0	564 2	Q4H26_TRYP
18	32	100.0	564 2	Q4H26_TRYP
19	32	100.0	564 2	Q4H26_TRYP
20	32	100.0	564 2	Q4H26_TRYP
21	32	100.0	564 2	Q4H26_TRYP
22	32	100.0	607 2	Q4H26_TRYP
23	32	100.0	637 2	Q4H26_TRYP
24	32	100.0	641 2	Q4H26_TRYP
25	32	100.0	677 2	Q4H26_TRYP
26	32	100.0	796 2	Q4H26_TRYP
27	32	100.0	858 2	Q4H26_TRYP
28	32	100.0	973 2	Q4H26_TRYP
29	32	100.0	982 2	Q4H26_TRYP
30	32	100.0	984 2	Q4H26_TRYP
31	32	100.0	1697 2	Q4H26_TRYP

32	32	100.0	2320 2	Q4GYZ8_TRYP	Q4GYZ8_TRYP
33	29	90.6	99 2	Q531P4_TRYP	Q531P4_TRYP
34	29	90.6	131 2	Q4G346_TRYP	Q4G346_TRYP
35	29	90.6	176 2	Q4G346_TRYP	Q4G346_TRYP
36	29	90.6	204 2	Q4G346_TRYP	Q4G346_TRYP
37	29	90.6	282 2	Q4G346_TRYP	Q4G346_TRYP
38	29	90.6	282 2	Q4G346_TRYP	Q4G346_TRYP
39	29	90.6	282 2	Q4G346_TRYP	Q4G346_TRYP
40	29	90.6	282 2	Q4G346_TRYP	Q4G346_TRYP
41	29	90.6	286 2	Q4G346_TRYP	Q4G346_TRYP
42	29	90.6	297 2	Q4G346_TRYP	Q4G346_TRYP
43	29	90.6	300 2	Q4G346_TRYP	Q4G346_TRYP
44	29	90.6	301 2	Q4G346_TRYP	Q4G346_TRYP
45	29	90.6	305 2	Q4G346_TRYP	Q4G346_TRYP

ALIGNMENTS

RESULT 1
Q4GYZ8_TRYP PRELIMINARY; PRT; 123 AA.
ID Q4GYZ8_TRYP PRELIMINARY; PRT; 123 AA.
AC Q4GYZ8_TRYP
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Calpain-like protein, putative.
GN ORFNames=TB927.1.2230;
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
CX NCBI_TaxID=5691;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=927/4 GUTACT10.1;
RA Hall N., Berriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,
RA Bart-delecluse E.N., Gerrard C.S., Atkin R.J., Barron A.J., Bowman S.,
RA Bray-Allen S.P., Brington F., Clark L.N., Corion C.H., Cronin A.,
RA Davies R., Doggett J., Fraser A., Gruber E., Hall S., Harper A.D.,
RA Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabinowitch E.,
RA Reller C., Rutherford K., Saase J., Sharp S., Showkeen R.,
RA Macleod A., Taylor S., Tweedie A., Turner C.M.R., Tait A., Gull K.,
RA Barrell B., Melville S.E.;
RT "The DNA sequence of chromosome I of an African trypanosome: gene
content, chromosome organization, recombination and polymorphism";
RL Nucleic Acids Res. 31:4864-4873(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=927/4 GUTACT10.1;
RA Hertz-Fowler C., Berriman M.,
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL929603; CAJ16331.1; -; Genomic DNA.
SQ SEQUENCE 123 AA; 13535 MW; 26D0156E593E4F7 CRC64;
Query Match 100.0%; Score 32; DB 2; Length 123;
Best local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DYDMH 5
DB 55 DYDMH 59
RESULT 2
Q4GYZ5_TRYP PRELIMINARY; PRT; 129 AA.
ID Q4GYZ5_TRYP PRELIMINARY; PRT; 129 AA.
AC Q4GYZ5_TRYP
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Calpain-like protein, putative.
GN ORFNames=TB927.1.2260;
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

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OX  NCBI_TaxID=5691;
RN  NUCLEOTIDE SEQUENCE.
RC  STRAIN=927/4 GUT410.1;
RA  Hall N., Berriman M., Lennard N.J., Harris B.R., Hertz-Fowler C.,
RA  Bart-Delabesse B.N., Gerrard C.S., Atkin R.J., Barron A.J., Bowman S.,
RA  Bray-Allen S.P., Bringsrud F., Clark L.N., Corcoran C.H., Cronin A.D.,
RA  Davies R., Doggett J., Fraser A., Gruter E., Hall S., Harper A.D.,
RA  Kay M.P., Leech V., Mayes R., Price C., Quail M.A., Rabinowitch B.,
RA  Ralston C., Rutherford K., Sasse J., Sharp S., Showman R.,
RA  Macleod A., Taylor S., Turner A., Tweedie A., Turner C.M.R., Tait A., Gull K.,
RA  Barrett B., Melville S.E.;
RT  "The DNA sequence of chromosome I of an African trypanosome: gene
RT  content, chromosome organisation, recombination and polymorphism.";
RL  Nucleic Acids Res. 31:4864-4873(2003).
RN  NUCLEOTIDE SEQUENCE.
RP  STRAIN=927/4 GUT410.1;
RA  Hertz-Fowler C., Berriman M.;
RL  Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR  EMBL, AJ29603, CAJ16336.1, -; Genomic DNA.
SQ  SEQUENCE 129 AA; 14030 MW; 91C28BCF31609A1A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 54 DYDMH 58

RESULT 3
ID Q5B023 EMENI PRELIMINARY; PRT; 276 AA.
OS Q5B023;
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLREL. 30, Last annotation update)
DE Hypothetical protein.
OS ORFNames=AN5781.2;
GN Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FGSC A4;
RA Biren B., Nisbaum C., Abouneillel A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Deavellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gherre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamet A., Karakas A.,
RA Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., MacDonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneses L.,
RA Mihova T., Mienna V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Reta R., Rise R., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer S., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vasiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RL "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an

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CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL, AACD01000098; EAA62874.1, -; Genomic DNA.
KW  Hypothetical protein.
SQ  SEQUENCE 276 AA; 31803 MW; 9C1E24C76A107E74 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 92 DYDMH 96

RESULT 4
ID Q5NH60 FRATT PRELIMINARY; PRT; 287 AA.
OS Q5NH60;
DT 01-FEB-2005 (TRENBLREL. 29, Created)
DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
DE Beta-lactamase (EC 3.5.2.6).
OS OrderedLocNames=FTT061ic;
GN Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=SCHU S4 / Schu 4;
RX PubMed=15640799; DOI=10.1038/ng1499;
RA Larson P., Oyston P.C.F., Chain P., Chu M.C., Duffield M.,
RA Fuxelius H.-H., Garcia E., Haelltorp G., Johansson D., Isherwood K.E.,
RA Karp P.D., Larson E., Liu Y., Mitchell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vargas L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Foreman M.,
RA Tibball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
RT  agent of tularemia."
RL Nat. Genet. 37:153-159(2005).
DR EMBL, AJ749949; CAG45244.1, -; Genomic DNA.
DR GO; GO:0008800; F:beta-lactamase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0030655; P:beta-lactam antibiotic catabolism; IEA.
DR GO; GO:0046677; P:response to antibiotic; IEA.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR InterPro; IPR000008; C2.
DR Pfam; PF00144; Beta-lactamase; 1.
DR PRINTS; PRO0116; BLACTAMASEA.
DR PRINTS; PRO0360; C2DOMAIN.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Complete proteome; Hydrolyase.
SQ  SEQUENCE 287 AA; 31982 MW; 93FC6A24A1C0383A CRC64;

Query Match 100.0%; Score 32; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 73 DYDMH 77

RESULT 5
ID K6PF_BACSU STANDARD; PRT; 319 AA.
AC 034529;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)

```


(phosphohexokinase).
 DR Name=pfkA; Synonym=pfk; OrderedLocustNames=BSU29190;
 CC Bacillus subtilis.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OK NCBI_taxid=1423;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=168;
 RC MEDLINE=8048467; PubMed=9387221;
 RX Lapidus A., Galleron N., Sorokin A., Ehrlich S.-D.;
 RT "Sequencing and functional annotation of the Bacillus subtilis genes
 in the 200 kb rnb-dnaB region."
 RL Microbiology 143:3431-3441(1997).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=168;
 RX MEDLINE=8044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst F., Ogatawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Besieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.-K., Codani J.-J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritsch C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Gilm S.-Y., Glaeser P., Goffeau A., Gollightly B.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holtepel S., Hosono S., Hulio M.-F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Kletter-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Kontingstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Meuel C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moesl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogawa A., Oudega B.,
 RA Park S.-H., Parro T., Pohl T.M., Portetelle D., Portolillo S.,
 RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
 RA Roy M., Reynolds S., Rieger M., Rivolta C., Rocha B., Roche B.,
 RA Rose M., Sadale Y., Sato T., Scanlan B., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi Y., Sekowska A., Seror S.J., Serron P.,
 RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
 RA Vassaretto A., Viali A., Wambuit R., Wedler H., Wedler F.,
 RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamae K.,
 RA Yamaoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein E.,
 RA Yoshikawa H., Darchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis."
 RL Nature 390:249-256(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
 fructose 1,6-bisphosphate.
 CC -1- PATHWAY: key control step of glycolysis.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the phosphofructokinase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL, AF008220; AAC00342.1; -; Genomic DNA.
 DR EMBL, Z99118; CAB14879.1; -; Genomic DNA.
 DR PIR, A69675; A69675.
 DR HSSP, P00512; 3PFK.
 DR SMR, O34529; 1-319.
 DR Subtilist; BG12644; pfkA.
 DR HAMAP, MF_00339; -; 1.
 DR InterPro, IPR012003; ATP_PFK_prok.
 DR InterPro, IPR012828; pfkA_ATP.
 DR InterPro, IPR000023; pfkfructinase.
 DR PANTHER, PTHR13697; pfkfructinase; 1.

DR Pfam, PF00365; PFK; 1.
 DR PIRSF, PIRSF000532; ATP_PFK_prok; 1.
 DR PRINTS; PR00476; PFRCTKINASE.
 DR ProDom; PD000707; Pfructinase; 1.
 DR TIGRFAMs; TIGR02482; PFKA_ATP; 1.
 DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
 KW Allosteric enzyme; ATP-binding; Complete proteome; Glycolysis; Kinase;
 KW Magnesium; Metal-binding; Nucleotide-binding; Transferase.
 FT NP_BIND 21 25
 FT NP_BIND 154 158
 FT NP_BIND 171 187
 FT ACT_SITE 127 127
 FT METAL 185 185
 FT METAL 187 187
 FT BINDING 162 162
 FT BINDING 243 243
 FT BINDING 249 249
 FT BINDING 252 252
 SQ SEQUENCE 319 AA; 34254 MW; 706C8C7F9BCFCDC CRC64;
 Query Match 100.0%; Score 32; DB 1; Length 319;
 Best Local Similarity 100.0%; Pred. No. 1;je+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYDMH 5
 DB 195 DYDMH 199
 RESULT 6
 ID Q4IH26 GIBZE PRELIMINARY; PRT; 326 AA.
 AC Q4IH26;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS ORFNames=FG03162.1;
 GN Gibberella zeae PH-1.
 CC Gibberella zeae PH-1.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreales; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OK NCBI_taxid=229533;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=PH-1;
 RC Arrich H.M., Barna N., Bastien V., Bidom T., Boguslavsky L.,
 RA Arrich H.M., Barna N., Bastien V., Bidom T., Boguslavsky L.,
 RA Bouhassal B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Darelilano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris U., Eklins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., Fitzderald M., Gage D., Galagan J.,
 RA Gardina S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas L.,
 RA Kells C., Landers T., Levine R., Lindblad-Ton K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli B., McCarthy M., Meldrum J., Menus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachugap A., Ramasamy U., Raymond C., Reta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Shtinov S.,
 RA Smith C., Spencer B., Strange-Thomson N., Stojanovic N., Stubbs M.,
 RA Talama J., Tesfaye S., Theodore J., Topham K., Travers S.,
 RA Vasilev H., Venkatarman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander B.;
 RT "Fusarium graminearum genome sequence."
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

DR EMBL; AACM01000148; EAA72902.1; -; Genomic_DNA.
 KW Hypothetical protein.35576 MW; F211C78983428339 CRC64;
 SQ SEQUENCE 326 AA; 35576 MW; F211C78983428339 CRC64;
 Query Match 100.0%; Score 32; DB 2; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYDMH 5
 |||||
 Db 292 DYDMH 296

RESULT 7
 Q7N656_PHOHL
 ID Q7N656_PHOHL PRELIMINARY; PRT; 340 AA.
 AC Q7N656;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Similarities with C-terminal region of insecticidal toxin.
 GN OrderedLocNames=D1u1712;
 OS Photorhabdus luminescens (subsp. laumondii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Photorhabdus.
 NCBI_TaxID=141679;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TF01;
 RX MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
 RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
 RA Teourt S., Bocse R., Bouraux-Eude C., Chantier M., Charles J.-F.,
 RA Dassa E., Daroche R., Derzelle S., Freydisse G., Gaudriault S.,
 RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
 RA Zouine M., Glaeser P., Boemare N., Dancin A., Kunst P.,
 RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
 luminescens."
 RT Nat. Biotechnol. 21:1307-1313 (2003).
 RL EMBL; BX571864; CAE14005.1; -; Genomic_DNA.
 DR Photolite; p1u1712; -.
 KW Complete proteome.
 SQ SEQUENCE 340 AA; 37562 MW; 4CFDA1FDA20BC81B CRC64;
 Query Match 100.0%; Score 32; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYDMH 5
 |||||
 Db 194 DYDMH 198

RESULT 8
 VABT_PYRFU
 ID VABT_PYRFU STANDARD; PRT; 462 AA.
 AC OBU4A5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
 B).
 GN Name=atpB; OrderedLocNames=PF0183;
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NCBI_TaxID=2261;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.,
 RT "The complete sequence of the Pyrococcus furiosus genome."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Produces ATP from ADP in the presence of a proton

CC gradient across the membrane. The archaeal beta chain is a
 CC regulatory subunit.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AE010144; AAL80307.1; -; Genomic_DNA.
 CC HAMAP; MF_00310; -; 1.
 CC DR InterPro; IPR005724; ATP_synth_B.
 CC DR InterPro; IPR007933; ATPase_a/b_C.
 CC DR InterPro; IPR004100; ATPase_a/b_N.
 CC DR InterPro; IPR000194; ATPase_a/bcentre.
 CC DR Pfam; PF00006; ATP-synt_ab; 1.
 CC DR Pfam; PF00306; ATP-synt_ab; 1.
 CC DR Pfam; PF02874; ATP-synt_ab_N; 1.
 CC DR TIGRfam; TIGR01041; ATP_syn_B_arch; 1.
 CC DR PROSITE; PS00152; ATPASR_ALPHA_BETA; 1.
 CC KW ATP synthase; Complete proteome; Hydrogen ion transport; Hydrolase;
 CC ion transport; Transport.
 CC SEQUENCE 462 AA; 51915 MW; 5AB9F8AFA2C86283 CRC64;
 Query Match 100.0%; Score 32; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYDMH 5
 |||||
 Db 238 DYDMH 242

RESULT 9
 VABT_PYRHO
 ID VABT_PYRHO STANDARD; PRT; 465 AA.
 AC O57729;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
 B).
 GN Name=atpB; OrderedLocNames=PH1974;
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 NCBI_TaxID=53953;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyma A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kusida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.,
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
 RL DNA Res. 5:55-76 (1998).
 CC -1- FUNCTION: Produces ATP from ADP in the presence of a proton
 CC gradient across the membrane. The archaeal beta chain is a
 CC regulatory subunit.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
 CC -----
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 CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; BA000001; BAA31101.1; -, Genomic_DNA.
DR PIR; F71213; F71213.
DR HAMAP; MF_00310; -, 1.
DR InterPro; IPR005724; ATP synthase B.
DR InterPro; IPR000793; ATPase a/b_C.
DR InterPro; IPR004100; ATPase a/b_N.
DR InterPro; IPR000194; ATPase a/bcentre.
DR Pfam; PF00006; ATP-synt_ab_1.
DR Pfam; PF00306; ATP-synt_ab_C; 1.
DR Pfam; PF02874; ATP-synt_ab_N; 1.
DR TIGRFAMs; TIGR01041; ATP syn B arch; 1.
DR PROSITE; PS00152; ATPase ALPHA_BETA; 1.
KW Ion transport; Complete proteome; Hydrogen ion transport; Hydrolase;
KW Ion transport; Transport.
SQ SEQUENCE 465 AA; 52265 MW; EDAPDFAD74C2A54 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 241 DYDMH 245

RESULT 10
Q9ZRO5 ARATH PRELIMINARY; PRT; 473 AA.
AC Q9ZRO5;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein P4C21.19 (Hypothetical protein AT4903260).
GN Name=P4C21.19; Synonym=AT4903260;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN RA Habermann K., de la Bastide M., Huang B.N., Gnoj L., Schutz K.,
RA Preston R., Calma C., Martensen R., Parnell L.D., Dedhia N.,
RA McCombie W.R.;
RT "Arabidopsis thaliana BAC P4C21 from chromosome IV near 17 cM."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN RA [2]
RN RP NUCLEOTIDE SEQUENCE.
RN RA Parnell L.D.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN RA [3]
RN RP NUCLEOTIDE SEQUENCE.
RN RA Spiegel L.A., Huang B.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Maturo A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN RA [4]
RN RP NUCLEOTIDE SEQUENCE.
RN RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005275; AAD1454.1; -, Genomic_DNA.
DR EMBL; AL161496; CAB7811.1; -, Genomic_DNA.
DR PIR; D85041; D85041.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007092; LRR_SD822.
DR Pfam; PF00560; LRR_1_4_1.
DR PFAM; PRO0019; LEURICHRPT.
KW Hypothetical protein; Leucine-rich repeat; Repeat.
KW SEQUENCE 473 AA; 52344 MW; 02EF2385906D5C40 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 62 DYDMH 66

RESULT 11
O8NCL6 HUMAN
ID O8NCL6_HUMAN PRELIMINARY; PRT; 493 AA.
AC O8NCL6;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE CDNA FJ30170 f1s, clone MAMMA1000370, highly similar to Ig alpha-1
chain C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN RA [1]
RN RP NUCLEOTIDE SEQUENCE.
RN RC TISSUE=Mammary gland;
RA Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J.,
RA Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S.,
RA Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y.,
RA Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
RA Isoaga T.;
RT "Signal Sequence and Keyword Trap in silico for Selection of Full-
RT Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-
RT Capped cDNA Libraries."
RL DNA Ref. 12:117-126(2005).
DR EMBL; AK074651; BAC1114.1; -, mRNA.
DR HSSP; P01876; 10M0.
DR SMR; O8NCL6; 263-471.
DR InterPro; IPR007110; Ig-1Lk.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7B094777101 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
DB 50 DYDMH 54

RESULT 12
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ID Q64BJ3_9ARCH PRELIMINARY; PRT; 521 AA.
AC Q64BJ3;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=GZ27A8_54;
OS uncultured archaean GZf0527A8.
OC Archaea; environmental samples.
OX NCBI_TaxID=285382;
RN RA [1]
RN RP NUCLEOTIDE SEQUENCE.

RX		PubMed=15358601; DOI=10.1126/science.1100025;
RA	Hillam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,	
RB	Richardson P.M., DeLong E.F.	
RT	"Reverse methanogenesis: testing the hypothesis with environmental genomics."	
RL	science 305:1457-1462(2004).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RA	Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.; Submitted (AUG-2004) to the EMBL/Genebank/DBJ databases. KM EMBL; AY174844; AAU93234.1; -, Genomic_DNA. KW Hypothetical protein. SQ SEQUENCE 521 AA; 59736 MW; 2ABBDPFBEBBDEIF CRC64; 	
OY	1 DYDMH 5 Best Local Similarity 100.0%; Score 32; DB 2; Length 521; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dn	247 DYDMH 251	
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ID Q6E878_XENTR PRELIMINARY; PRF; 562 AA.		
AC O6P878;		
DT 05-JUL-2004 (TREMBLrel .27, Created)		
DT 05-JUN-2004 (TREMBLrel .27, Last sequence update)		
DT 05-JUN-2004 (TREMBLrel .27, Last annotation update)		
DE Hypothetical protein MGCT5896.		
CN Name=MGCT5896;		
CS Xenopus tropicalis (Western clawed frog) (<i>Xilurana tropicalis</i>). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; OC Xenopodinae; Xenopus; Silurana. OX NCBI_Taxid=8364; []		
NP NUCLEOTIDE SEQUENCE.		
RP TISSUE=Embryo;		
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschuler R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D., Kutschera S.F., Zeeberg B., Bueltow K.H., Scheefel C.F., Butler N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Marzella K., Farmer A.A., Rubin G.M., Hong L., Stepien M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein W.J., Ustin T.B., Toshynski S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Boesak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulik S.W., Villation D.K., Mazny D.M., Sodergren E.O., Lu X., Gibbs R.A., Fahey J., Helton E., Kettleman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakealey R.C., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywnicki M.I., Skalske U., Smalusz D.E., Schnerch A., Schein J.R., Jones G.J.M., Barra M.A., RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2] RN NUCLEOTIDE SEQUENCE. RC TISSE=Embryo; RA Klein S., Gerhard D.S.; Submitted (NOV-2003) to the EMBL/genBank/DBSJ databaeses. RU EMBL; BC061351; AAA61351.1; -, mRNA. KW Hypothetical proteim. SQ SEQUENCE 562 AA; 66612 MW; C0393E711095E3D1 CRC64; 		
Query March	100.0%;	Score 32; DB 2; Length 562;
Best Loccal Similarity	100.0%; Pred. NO. 2.4e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

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DR InterPro; IPR011990; TPR-like_helical.
 KM Protein biosynthesis.
 SQ SEQUENCE 564 AA; 66727 MW; ECD32192D96E3FE CRC64;

Query Match 100.0%; Score 32; DB 1; Length 564
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
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 DB 22 DYDMH 26

RESULT 15

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 ID OSQTRL_HUMAN PRELIMINARY; PRT; 564 AA.
 AC OSQTRL;
 DT 01-FEB-2005 (TRENBLrel. 29, Created)
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
 DE MSTRP005.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Aorta;
 RA Hui R.T., Liu Y.Q., Liu B., Zhao B., Meng X.M., Sheng H., Xu Y.Y.,
 RA Wang X.Y., Ye J., Song L., Gao Y., Wei Y.J., Zhang C.L., Zhang J.,
 RA Chai M.Q., Chen J.Z., Sun Y.H., Zhou X.L., Jiang Y.X., Zhao X.W.,
 RA Liu S., Cao H.Q., Zhao Y., Liu D.Q., Ding J.F., Liu L.S., Gao R.L.,
 RA Wu Q.Y., Qiang B.Q., Yuan J.G., Liew C.C., Zhao M.S.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF109359; AAQ13507.1; -; mRNA.
 SQ SEQUENCE 564 AA; 66739 MW; 415F13C1FEB8C4DB CRC64;

Query Match 100.0%; Score 32; DB 2; Length 564;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
 |||||
 DB 22 DYDMH 26

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 Job time : 9.39927 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:49:31 / Search time 1.88645 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-159

Perfect score: 32
Sequence: 1 DYDMH 5

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	93	2	US-09-621-976-5904 Sequence 5904, Ap
2	32	100.0	142	2	US-09-513-999C-5024 Sequence 5024, Ap
3	32	100.0	149	2	US-09-621-976-5116 Sequence 5116, Ap
4	32	100.0	150	2	US-09-621-976-5112 Sequence 5112, Ap
5	32	100.0	150	2	US-09-621-976-5117 Sequence 5117, Ap
6	32	100.0	160	2	US-09-621-976-5115 Sequence 5115, Ap
7	32	100.0	161	2	US-09-621-976-5114 Sequence 5114, Ap
8	32	100.0	176	2	US-09-621-976-5113 Sequence 5113, Ap
9	32	100.0	163	2	US-09-621-976-5111 Sequence 5111, Ap
10	29	90.6	20	2	US-09-688-017-216 Sequence 216, App
11	29	90.6	528	2	US-09-543-681A-6551 Sequence 6551, A
12	29	90.6	1019	2	US-09-902-540-15897 Sequence 15897, A
13	29	90.6	1279	2	US-09-489-039A-13602 Sequence 13602, A
14	28	87.5	60	2	US-09-331-930A-27 Sequence 27, Appl
15	28	87.5	94	2	US-09-331-930A-27 Sequence 60718, A
16	28	87.5	120	2	US-10-092-246-9 Sequence 9, Appl1
17	28	87.5	120	2	US-10-096-246A-9 Sequence 45241, A
18	28	87.5	156	2	US-09-270-767-45241 Sequence 45241, A
19	28	87.5	205	2	US-09-270-767-58524 Sequence 58524, A
20	28	87.5	231	2	US-09-328-352-49108 Sequence 49108, Ap
21	28	87.5	262	2	US-09-583-110-5208 Sequence 5208, Ap
22	28	87.5	266	2	US-09-134-000C-5984 Sequence 5984, Ap
23	28	87.5	433	2	US-09-270-767-43555 Sequence 43555, A
24	28	87.5	446	2	US-09-543-681A-7270 Sequence 7270, Ap
25	28	87.5	517	2	US-09-252-991A-25364 Sequence 25364, A
26	28	87.5	527	2	US-09-270-767-45390 Sequence 45390, A
27	27	84.4	97	2	US-09-534-717-615 Sequence 615, App

ALIGNMENTS

28	27	84.4	99	2	US-09-270-767-60648	Sequence 60648, A
29	27	84.4	116	1	US-07-634-278-56	Sequence 56, Appl
30	27	84.4	116	1	US-07-634-278-57	Sequence 57, Appl
31	27	84.4	116	1	US-07-634-278-73	Sequence 73, Appl
32	27	84.4	116	1	US-08-477-728-56	Sequence 56, Appl
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34	27	84.4	116	1	US-08-477-728-73	Sequence 73, Appl
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36	27	84.4	116	1	US-08-474-040-57	Sequence 57, Appl
37	27	84.4	116	1	US-08-474-040-73	Sequence 73, Appl
38	27	84.4	116	1	US-08-487-200-56	Sequence 56, Appl
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40	27	84.4	116	1	US-08-487-200-73	Sequence 73, Appl
41	27	84.4	116	2	US-08-545-809A-101	Sequence 101, App
42	27	84.4	116	2	US-08-484-537-56	Sequence 56, Appl
43	27	84.4	116	2	US-08-484-537-57	Sequence 57, Appl
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45	27	84.4	116	2	US-09-515-697-101	Sequence 101, App

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RESULT 1
US-09-621-976-5904
; Sequence 5904, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5904
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -82...-1
; US-09-621-976-5904

Query Match      100.0%; Score 32; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DYDMH 5
Db      22 DYDMH 26

RESULT 2
US-09-513-999C-5024
; Sequence 5024, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122.487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5024

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LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-5024

Query Match 100.0%; Score 32; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 22 DYDMH 26

RESULT 3
US-09-621-976-5116
Sequence 5116, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5116
LENGTH: 149
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-5116

Query Match 100.0%; Score 32; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 22 DYDMH 26

RESULT 4
US-09-621-976-5112
Sequence 5112, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5112
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-5112

Query Match 100.0%; Score 32; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 22 DYDMH 26

RESULT 5

US-09-621-976-5117
Sequence 5117, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5117
LENGTH: 150
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 134
OTHER INFORMATION: Xaa = Asp,Glu
NAME/KEY: UNSURE
LOCATION: 66
OTHER INFORMATION: Xaa = Leu,Met
US-09-621-976-5117

Query Match 100.0%; Score 32; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 22 DYDMH 26

RESULT 6
US-09-621-976-5115
Sequence 5115, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5115
LENGTH: 160
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-5115

Query Match 100.0%; Score 32; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 22 DYDMH 26

RESULT 7
US-09-621-976-5114
Sequence 5114, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5114
LENGTH: 161
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-5114

Query Match 100.0%; Score 32; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 22 DYDMH 26

RESULT 8
US-09-621-976-5113
Sequence 5113, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5113
LENGTH: 163
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURB
LOCATION: 148
OTHER INFORMATION: Xaa = His, Pro
US-09-621-976-5113

Query Match 100.0%; Score 32; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 22 DYDMH 26

RESULT 9
US-09-621-976-5111
Sequence 5111, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5111
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-5111

Query Match 100.0%; Score 32; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 22 DYDMH 26

RESULT 10
US-09-688-017-216
Sequence 216, Application US/09688017
Patent No. 6942861
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweitzer, Johannes
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: 020054-001110US
CURRENT APPLICATION NUMBER: US/09/688.017
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/134,114
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/134,118
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/170,453
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,460
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,527
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: US 60/196,528
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 383
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 216
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: AA49L CDS PL peptide
US-09-688-017-216

Query Match 90.6%; Score 29; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 13;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 11 DYDLH 15

RESULT 11
US-09-543-681A-6551
Sequence 6551, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6551
LENGTH: 528
TYPE: PRT
ORGANISM: *Proteus mirabilis*
US-09-543-681A-6551

Query Match 90.6%; Score 29; DB 2; Length 528;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 231 DYDLH 235

RESULT 12
US-09-502-540-15897
Sequence 15897, Application US/0902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
FILE REFERENCE: 38-101(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,863
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15897
LENGTH: 1019
TYPE: PRT
ORGANISM: *Myxococcus xanthus*
US-09-502-540-15897

Query Match 90.6%; Score 29; DB 2; Length 1019;
Best Local Similarity 80.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 658 DYDLH 662

RESULT 13
US-09-489-039A-13602
Sequence 13602, Application US/09489039A
Patent No. 6610835
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *KLEBSIELLA*
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13602
LENGTH: 1279
TYPE: PRT
ORGANISM: *Klebsiella pneumoniae*
US-09-489-039A-13602

Query Match 90.6%; Score 29; DB 2; Length 1279;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 1097 DYDLH 1101

RESULT 14
US-09-331-930A-27
Sequence 27, Application US/09331930A
Patent No. 643670
GENERAL INFORMATION:
APPLICANT: ZIMMET, PAUL Z.
APPLICANT: COLLIER, GREGORY
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
FILE REFERENCE: 22975-20007.00
CURRENT APPLICATION NUMBER: US/09/331,930A
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: PCT/AU98/00902
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: AU P0117/97
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: AU P0323/97
PRIOR FILING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 60
TYPE: PRT
ORGANISM: *Arabidopsis thaliana*
US-09-331-930A-27

Query Match 87.5%; Score 28; DB 2; Length 60;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 49 DYDLH 53

RESULT 15
US-09-270-767-60718
Sequence 60718, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60718
LENGTH: 94
TYPE: PRT
ORGANISM: *Drosophila melanogaster*
US-09-270-767-60718

Query Match 87.5%; Score 28; DB 2; Length 94;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 35 DYDLH 39

Search completed: November 21, 2005, 12:07:40
Job time : 2.88645 secs

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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51 ; Search time 6.19048 Seconds
(without alignments)
337.478 Million cell updates/sec

Title: US-10-632-706-159
Perfect score: 32
Sequence: 1 DYDMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	5	US-10-632-706-159	Sequence 159, App
2	32	100.0	5	US-10-632-706-163	Sequence 163, App
3	32	100.0	5	US-10-632-706-167	Sequence 167, App
4	32	100.0	5	US-10-632-706-171	Sequence 171, App
5	32	100.0	73	US-10-424-599-176475	Sequence 176475, A
6	32	100.0	144	US-10-450-763-50856	Sequence 50856, A
7	32	100.0	253	US-10-779-461-18	Sequence 18, App1
8	32	100.0	319	US-10-369-493-23241	Sequence 23241, A
9	32	100.0	457	US-10-369-493-20409	Sequence 20409, A
10	32	100.0	465	US-10-369-493-1346	Sequence 1346, App
11	32	100.0	564	US-10-514-150-10	Sequence 10, App1
12	32	100.0	581	US-09-925-302-801	Sequence 801, App
13	32	100.0	581	US-09-925-302-801	Sequence 801, App
14	32	100.0	585	US-10-450-763-42152	Sequence 42152, A
15	32	100.0	596	US-10-450-763-34775	Sequence 34775, A
16	32	100.0	607	US-10-094-749-2387	Sequence 2387, App
17	32	100.0	640	US-10-450-763-50858	Sequence 50858, A
18	32	100.0	858	US-11-097-143-26316	Sequence 26316, A
19	32	100.0	973	US-10-754-115-61	Sequence 61, App1
20	29	90.6	20	US-10-938-249-456	Sequence 456, App
21	29	90.6	20	US-11-131-054-216	Sequence 216, App
22	29	90.6	20	US-11-131-042-216	Sequence 216, App
23	29	90.6	80	US-10-425-115-323622	Sequence 323622, A
24	29	90.6	195	US-10-425-115-187817	Sequence 187817, A
25	29	90.6	259	US-10-424-599-199590	Sequence 199590, A
26	29	90.6	282	US-10-474-192-472	Sequence 472, App
27	29	90.6	389	US-10-424-599-206539	Sequence 206539, A

28	29	90.6	394	4	US-10-425-115-359544	Sequence 359544, A
29	29	90.6	397	4	US-10-425-114-60331	Sequence 60331, A
30	29	90.6	422	6	US-11-097-143-318	Sequence 318, App
31	29	90.6	495	4	US-10-207-655-93	Sequence 93, App1
32	29	90.6	495	4	US-10-116-275-251	Sequence 251, App
33	29	90.6	511	4	US-10-437-963-143624	Sequence 143624, A
34	29	90.6	513	4	US-10-425-114-50246	Sequence 50246, A
35	29	90.6	646	4	US-10-437-963-161859	Sequence 161859, A
36	29	90.6	747	4	US-10-371-877-44	Sequence 44, App1
37	29	90.6	965	4	US-10-437-963-201115	Sequence 201115, A
38	29	90.6	970	4	US-10-282-122A-59736	Sequence 59736, A
39	29	90.6	986	4	US-10-282-122A-42808	Sequence 42808, A
40	29	90.6	1259	4	US-10-282-122A-56089	Sequence 56089, A
41	29	90.6	1266	4	US-10-282-122A-75669	Sequence 75669, A
42	29	90.6	2064	4	US-10-437-963-137624	Sequence 137624, A
43	29	90.6	2590	4	US-10-072-012-490	Sequence 490, App
44	29	90.6	4473	4	US-10-437-963-201113	Sequence 201113, A
45	29	90.6	4737	4	US-10-437-963-201116	Sequence 201116, A

ALIGNMENTS

```

RESULT 1
US-10-632-706-159
; Sequence 159, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-159
;
; Query Match      100.0%; Score 32; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 1.7e+06;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      1 DYDMH 5
; DB      1 DYDMH 5
;
; RESULT 2
US-10-632-706-163
; Sequence 163, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806

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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-163

Query Match 100.0%; Score 32; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 1 DYDMH 5

RESULT 3
US-10-632-706-167
; Sequence 167; Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSOORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 167
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-167

Query Match 100.0%; Score 32; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 1 DYDMH 5

RESULT 4
US-10-632-706-171
; Sequence 171; Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; APPLICANT: AMERSOORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 171
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-171

Query Match 100.0%; Score 32; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 1 DYDMH 5

RESULT 5
US-10-424-599-176475
; Sequence 176475; Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 176475
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) . (73)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130375C.1.pep
US-10-424-599-176475

Query Match 100.0%; Score 32; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 47 DYDMH 51

RESULT 6
US-10-450-763-50856
; Sequence 50856; Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 50856
; LENGTH: 144

TYPE: PRT
ORGANISM: Homo sapiens
US-10-450-763-50856

Query Match 100.0%; Score 32; DB 5; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 26 DYDMH 30

RESULT 7
US-10-779-461-18
Sequence 18, Application US/10779461
Publication No. US20040166544A1
GENERAL INFORMATION:
APPLICANT: Morton, Philip A
TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
FILE REFERENCE: 00980/1
CURRENT APPLICATION NUMBER: US/10/779,461
CURRENT FILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: 60/447,073
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 253
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: phage display generated human antibody
US-10-779-461-18

Query Match 100.0%; Score 32; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 31 DYDMH 35

RESULT 8
US-10-369-493-23241
Sequence 23241, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 23241
LENGTH: 319
TYPE: PRT
ORGANISM: Bacillus subtilis
US-10-369-493-23241

Query Match 100.0%; Score 32; DB 4; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5

Db 195 DYDMH 199

RESULT 9
US-10-369-493-20409
Sequence 20409, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20409
LENGTH: 457
TYPE: PRT
ORGANISM: Pyrococcus horikoshii
US-10-369-493-20409

Query Match 100.0%; Score 32; DB 4; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 235 DYDMH 239

RESULT 10
US-10-369-493-1346
Sequence 1346, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1346
LENGTH: 465
TYPE: PRT
ORGANISM: Pyrococcus horikoshii
US-10-369-493-1346

Query Match 100.0%; Score 32; DB 4; Length 465;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
Db 241 DYDMH 245

RESULT 11
US-10-514-150-10
Sequence 10, Application US/10514150

```
/ Publication No. US20050233957A1
/ GENERAL INFORMATION:
/ APPLICANT: UNIVERSITY COLLEGE LONDON
/ APPLICANT: Kenji OKUSE
/ APPLICANT: Mark BAKER
/ APPLICANT: Louise POON
/ APPLICANT: John Nicholas WOOD
/ APPLICANT: Misha Malik-HALL
/ TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
/ FILE REFERENCE: 117-528 / N.88745B GCM
/ CURRENT APPLICATION NUMBER: US/10/514,150
/ PRIOR FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: PCT/GB03/02225
/ PRIOR FILING DATE: 2003-05-22
/ PRIOR APPLICATION NUMBER: GB 0211833.9
/ PRIOR FILING DATE: 2002-05-22
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-514-150-10
```

```
Query Match          100.0%; Score 32; DB 5; Length 564;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYDMH 5
        |||||
Db      22 DYDMH 26
```

```
RESULT 12
US-09-925-302-801
/ Sequence 801, Application US/09925302
/ Patent No. US20020044941A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 896
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 801
/ LENGTH: 581
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-801
```

```
Query Match          100.0%; Score 32; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYDMH 5
        |||||
Db      39 DYDMH 43
```

```
RESULT 13
US-09-925-302-801
/ Sequence 801, Application US/09925302
/ Publication No. US20030064072A9
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1999-03-12
/ NUMBER OF SEQ ID NOS: 896
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 801
/ LENGTH: 581
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: SITE
/ LOCATION: (1)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-801
```

```
Query Match          100.0%; Score 32; DB 3; Length 581;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYDMH 5
        |||||
Db      39 DYDMH 43
```

```
RESULT 14
US-10-450-763-42152
/ Sequence 42152, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ PRIOR FILING DATE: 2003-06-11
/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO 42152
/ LENGTH: 585
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(585)
/ OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-42152
```

```
Query Match          100.0%; Score 32; DB 5; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DYDMH 5
        |||||
Db      22 DYDMH 26
```

```
RESULT 15
US-10-450-763-34775
/ Sequence 34775, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
```

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 34775
LENGTH: 596
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(596)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-34775

Query Match 100.0%; Score 32; DB 5; Length 596;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|||
Db 22 DYDMH 26

Search completed: November 21, 2005, 12:33:39
Job time : 8.19048 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 12:04:27 ; Search time 0.0915751 Seconds
(without alignments)
61.686 Million cell updates/sec

Title: US-10-632-706-159

Perfect score: 32

Sequence: 1 DYDMH 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 8323 seqs, 1129788 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	78.1	153	1	US-10-522-883-2
2	25	78.1	173	1	US-10-522-883-19
3	25	78.1	173	1	US-10-522-883-23
4	25	78.1	177	1	US-10-522-883-4
5	25	78.1	177	1	US-10-522-883-13
6	25	78.1	179	1	US-10-522-883-17
7	25	78.1	179	1	US-10-522-883-21
8	25	78.1	179	1	US-10-522-883-17
9	25	78.1	552	1	US-10-131-826A-332
10	25	78.1	552	1	US-10-131-826A-290
11	25	78.1	275	1	US-10-510-386-100
12	25	78.1	278	1	US-10-131-826A-136
13	25	78.1	293	1	US-10-131-826A-456
14	25	78.1	296	1	US-11-179-977-8
15	25	78.1	628	7	US-11-074-176-244
16	25	78.1	634	1	US-10-632-150-26
17	25	78.1	937	1	US-11-057-058-55
18	25	78.1	106	7	US-11-144-248-26
19	25	78.1	213	7	US-11-172-320-8
20	25	78.1	213	7	US-11-174-186-42
21	25	78.1	227	1	US-10-986-501-136
22	25	78.1	236	7	US-11-144-248-47
23	25	78.1	236	7	US-11-144-248-48
24	25	78.1	236	7	US-11-144-248-51
25	25	78.1	236	7	US-11-144-248-52

26	22	68.8	299	7	US-11-074-176-198	Sequence 198, App
27	22	68.8	329	1	US-10-510-386-36	Sequence 36, Appl
28	22	68.8	330	1	US-10-510-386-196	Sequence 196, App
29	22	68.8	444	1	US-10-131-826A-198	Sequence 498, App
30	22	68.8	902	7	US-11-057-058-64	Sequence 64, Appl
31	22	68.8	1827	7	US-11-057-058-62	Sequence 62, Appl
32	22	68.8	1841	7	US-11-057-058-63	Sequence 63, Appl
33	22	68.8	1857	7	US-11-057-058-60	Sequence 60, Appl
34	22	68.8	1857	7	US-11-057-058-61	Sequence 61, Appl
35	21	65.6	13	1	US-10-509-170-3	Sequence 3, Appl1
36	21	65.6	138	7	US-11-008-727-2	Sequence 2, Appl1
37	21	65.6	204	1	US-10-131-826A-288	Sequence 288, App
38	21	65.6	234	1	US-10-997-697-47	Sequence 47, Appl
39	21	65.6	296	1	US-10-510-386-58	Sequence 58, Appl
40	21	65.6	304	7	US-10-074-176-262	Sequence 262, App
41	21	65.6	316	1	US-10-131-826A-80	Sequence 80, Appl
42	21	65.6	420	7	US-11-074-176-48	Sequence 48, Appl
43	21	65.6	468	1	US-10-131-826A-90	Sequence 90, Appl
44	21	65.6	470	7	US-11-008-727-20	Sequence 20, Appl
45	21	65.6	476	1	US-10-997-697-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-10-522-883-2
Sequence 2, Application US/10522883
Publication No. US20050249701A1
GENERAL INFORMATION:
APPLICANT: CYTHERIS
TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
FILE REFERENCE: B0131W0
CURRENT APPLICATION NUMBER: US/10/522,883
CURRENT FILING DATE: 2005-02-02
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 153
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: r-hil-7 CDNA
US-10-522-883-2

Query Match 78.1%, Score 25; DB 1; Length 153;
Best Local Similarity 60.0%, Pred. No. 6.1;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 75 DFIDLH 79

RESULT 2
US-10-522-883-19
Sequence 19, Application US/10522883
Publication No. US20050249701A1
GENERAL INFORMATION:
APPLICANT: CYTHERIS
TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
FILE REFERENCE: B0131W0
CURRENT APPLICATION NUMBER: US/10/522,883
CURRENT FILING DATE: 2005-02-02
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 173
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: HMM38PS-r-hil-7 CDNA
US-10-522-883-19

Query Match 78.1%; Score 25; DB 1; Length 173;
Best Local Similarity 60.0%; Pred. No. 7;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|:|:|
Db 95 DFDLH 99

RESULT 3
US-10-522-883-23
; Sequence 23, Application US/10522883
; Publication No. US20050249701A1
; GENERAL INFORMATION:

APPLICANT: CYTHERIS
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
; FILE REFERENCE: B0131WO
; CURRENT APPLICATION NUMBER: US/10/522,883
; CURRENT FILING DATE: 2005-02-02

NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23

LENGTH: 173

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: HMM38PS-sIL-7

US-10-522-883-23

Query Match 78.1%; Score 25; DB 1; Length 173;
Best Local Similarity 60.0%; Pred. No. 7;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|:|:|
Db 95 DFDLH 99

RESULT 4
US-10-522-883-4
; Sequence 4, Application US/10522883
; Publication No. US20050249701A1
; GENERAL INFORMATION:

APPLICANT: CYTHERIS
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
; FILE REFERENCE: B0131WO
; CURRENT APPLICATION NUMBER: US/10/522,883
; CURRENT FILING DATE: 2005-02-02

NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

LENGTH: 177

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: r-hIL-7 cDNA

US-10-522-883-4

Query Match 78.1%; Score 25; DB 1; Length 177;
Best Local Similarity 60.0%; Pred. No. 7.1;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|:|:|
Db 99 DFDLH 103

RESULT 5
US-10-522-883-13
; Sequence 13, Application US/10522883
; Publication No. US20050249701A1
; GENERAL INFORMATION:

APPLICANT: CYTHERIS
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
; FILE REFERENCE: B0131WO
; CURRENT APPLICATION NUMBER: US/10/522,883
; CURRENT FILING DATE: 2005-02-02

NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13

LENGTH: 177

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: PS-sIL-7 cDNA

US-10-522-883-13

Query Match 78.1%; Score 25; DB 1; Length 177;
Best Local Similarity 60.0%; Pred. No. 7.1;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|:|:|
Db 99 DFDLH 103

RESULT 6
US-10-522-883-17
; Sequence 17, Application US/10522883
; Publication No. US20050249701A1
; GENERAL INFORMATION:

APPLICANT: CYTHERIS
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
; FILE REFERENCE: B0131WO
; CURRENT APPLICATION NUMBER: US/10/522,883
; CURRENT FILING DATE: 2005-02-02

NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17

LENGTH: 179

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: EPOPS-r-hIL-7 cDNA

US-10-522-883-17

Query Match 78.1%; Score 25; DB 1; Length 179;
Best Local Similarity 60.0%; Pred. No. 7.2;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYDMH 5
|:|:|
Db 101 DFDLH 105

RESULT 7
US-10-522-883-21
; Sequence 21, Application US/10522883
; Publication No. US20050249701A1
; GENERAL INFORMATION:

APPLICANT: CYTHERIS
; TITLE OF INVENTION: IL-7 drug substance, composition, preparation and uses.
; FILE REFERENCE: B0131WO
; CURRENT APPLICATION NUMBER: US/10/522,883
; CURRENT FILING DATE: 2005-02-02

NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21

LENGTH: 179

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: EPOPS-sIL-7 cDNA

US-10-522-883-21

Query Match 78.1%; Score 25; DB 1; Length 179;
Best Local Similarity 60.0%; Pred. No. 7.2;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDM 5
Db 101 DYDM 105

RESULT 8

US-10-131-826A-332
Sequence 332, Application US/10131826A

Publication No. US20050245730A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zhen
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131, 826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 332
LENGTH: 552
TYPE: PRT
ORGANISM: Homo Sapien

US-10-131-826A-332

Query Match 78.1%; Score 25; DB 1; Length 552;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDM 5
Db 268 DYDM 272

RESULT 9

US-11-082-389-290
Sequence 290, Application US/11082389

Publication No. US20050244935A1
GENERAL INFORMATION:

APPLICANT: Pompeius, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schröder, Hartwig
APPLICANT: Zelder, Oskar
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
FILE REFERENCE: BGI-131CPCN
CURRENT APPLICATION NUMBER: US/11/082, 389
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930487.4
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931549.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931550.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932134.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 290
LENGTH: 503
TYPE: PRT
ORGANISM: Corynebacterium glutamicum

US-11-082-389-290

Query Match 75.0%; Score 24; DB 7; Length 503;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDM 4
Db 400 DYDM 403

RESULT 10

US-10-510-386-100
Sequence 100, Application US/10510386

Publication No. US20050244932A1
GENERAL INFORMATION:

APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Peter Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3
SEQ ID NO 100
LENGTH: 275
TYPE: PRT
ORGANISM: Bacillus licheniformis

US-10-510-386-100

US-10-510-386-100

Query Match 71.9%; Score 23; DB 1; Length 275;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 86 DYDLY 90

RESULT 11

US-10-131-826A-136
; Sequence 136, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 136
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-136

Query Match 71.9%; Score 23; DB 1; Length 278;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 109 DYSLH 113

RESULT 12

US-10-131-826A-456
; Sequence 456, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 456
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-456

Query Match 71.9%; Score 23; DB 1; Length 293;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DYDMH 5
Db 72 DCDMH 76

RESULT 13

US-11-179-977-8
; Sequence 8, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes

```

; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 8
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-8

```

```

Query Match      71.9%; Score 23; DB 7; Length 296;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 3; Conservative 1; Mismatches 0; Gaps 0;

```

```

QY      2 YDMH 5
        ||:|
DB      190 YDLH 193

```

```

RESULT 14
US-11-074-176-244
; Sequence 244, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Kjaerhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 244
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-244

```

```

Query Match      71.9%; Score 23; DB 7; Length 628;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DYDMH 5
        |.:|
DB      145 DHDH 149

```

```

RESULT 15
US-10-632-150-26
; Sequence 26, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chlaui, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449

```

```

; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 26
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: all Xaa positions
; OTHER INFORMATION: Xaa=unknown amino acid residue
US-10-632-150-26

```

```

Query Match      71.9%; Score 23; DB 1; Length 634;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 YDMH 5
        ||:|
DB      621 YDLH 624

```

```

Search completed: November 21, 2005, 12:33:52
Job time : 0.191575 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:32 ; Search time 42.8425 Seconds
(without alignments)
328.182 Million cell updates/sec

Title: US-10-632-706-196

Perfect score: 155
Sequence: 1 RPTISRDNSKNTLFLQMSLRADPTAVYCAR 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Geneseqp21:1*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003s:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	165	100.0	32	8	ADR38791	Adx38791 Mouse hea
2	165	100.0	32	8	ADR38794	Adx38794 Mouse hea
3	165	100.0	32	8	ADR38797	Adx38797 Mouse hea
4	165	100.0	32	8	ADR38800	Adx38800 Mouse hea
5	162	98.2	113	4	AATU2529	Naou2529 Anti-adip
6	162	98.2	116	5	ABG30486	Abg30486 Human ant
7	162	98.2	117	5	ABG30484	Abg30484 Human ant
8	162	98.2	118	5	ADW08865	Adw08865 IGF-IR an
9	162	98.2	126	4	AAg93640	AAg93640 Human ant
10	162	98.2	126	6	ABO27447	ABO27447 Anti-Rh(D
11	162	98.2	127	4	AAg93627	AAg93627 Human ant
12	162	98.2	127	6	ABO27434	ABO27434 Anti-Rh(D
13	162	98.2	127	7	ADG30422	Adg30422 Human GMB
14	161	97.6	115	8	ADP22238	Adp22238 Human ant
15	161	97.6	121	8	ADO36356	Ado36356 Intracell
16	161	97.6	121	8	ADQ75229	Adq75229 Immunoglo
17	161	97.6	122	8	ADP22252	Adp22252 Human ant
18	161	97.6	122	8	ADP22308	Adp22308 Human ant
19	161	97.6	123	7	ADL91329	ADL91329 VH chain
20	161	97.6	463	3	AAV93701	AAV93701 The heavy
21	161	97.6	463	3	AAV93727	AAV93727 The heavy
22	161	97.6	463	3	AAV93728	AAV93728 The heavy
23	161	97.6	463	6	AAE35882	AAE35882 Human 4.1
24	161	97.6	463	6	AAE35883	AAE35883 Human 4.1

25	159	96.4	120	4	AAU02508	AAU02508 Anti-adip
26	158	95.8	32	2	AAE87051	AAE87051 Human gro
27	158	95.8	32	5	AAE19693	AAE19693 Human gro
28	158	95.8	32	5	AAU70472	AAU70472 Human hea
29	158	95.8	32	8	ADL93533	ADL93533 Human CD4
30	158	95.8	32	8	ADL93671	ADL93671 Human CD4
31	158	95.8	32	8	ADQ90726	Adq90726 Anti-VEGF
32	158	95.8	32	8	ADW96725	Adw96725 Anti-EGFR
33	158	95.8	32	9	ADW96738	Adw96738 Anti-EGFR
34	158	95.8	32	9	ADW80310	Adw80310 Human ant
35	158	95.8	32	9	ADW80297	Adw80297 Human ant
36	158	95.8	32	9	ADX27039	Adx27039 Human gro
37	158	95.8	32	9	ADY31524	Ady31524 Human ant
38	158	95.8	32	9	ADY31503	Ady31503 Human ant
39	158	95.8	32	9	ADY31398	Ady31398 Human ant
40	158	95.8	32	9	ADY31371	Ady31371 Human ant
41	158	95.8	32	9	ADY31506	Ady31506 Human ant
42	158	95.8	32	9	ADY31392	Ady31392 Human ant
43	158	95.8	32	9	ADY31374	Ady31374 Human ant
44	158	95.8	32	9	ADY31530	Ady31530 Human ant
45	158	95.8	32	9	AEA21479	AEA21479 Human ant

ALIGNMENTS

RESULT 1
ID ADR38791 standard; peptide; 32 AA.
AC ADR38791;
DT 02-DEC-2004 (first entry)
DE Mouse heavy chain anti-BONT-antibody framework 3 seqid 193.
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX framework 3.
XX OS Mus sp.
XX FN US2004175385-A1.
XX PD 09-SEP-2004.
XX PP 01-AUG-2003; 2003US-00632706.
XX PR 31-AUG-1998; 98US-00144886.
XX PR 01-AUG-2002; 2002US-0400721P.
XX PA (REGC) UNIV CALIFORNIA.
XX PI Marks JD, Amersdorfer P;
XX WPI; 2004-652009/63.
XX PT New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX PS Example 4; SEQ ID NO 193; 110pp; English.
XX CC The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C35, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,
XX 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
XX comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I) and a composition (II) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I) and a kit comprising (I). (I) is useful for neutralising
CC BONT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BONT-antibody framework region 3.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 165; DB 8; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
RESULT 2
ID ADR38794 standard; peptide; 32 AA.
XX ADR38794;
AC
XX 02-DEC-2004 (first entry)
DT
XX
XX Mouse heavy chain anti-BONT-antibody framework 3 seqid 196.
XX
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX framework 3.
XX
XX Mus sp.
OS
XX US2004175385-A1.
PN
XX 09-SEP-2004.
PD
XX 01-AUG-2003; 2003US-00632706.
PF
XX 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
XX (REGC) UNITV CALIFORNIA.
XX
XX Marke JD, Amerdorfer P;
PI
XX WPI; 2004-652009/63.
DR
XX
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
PT
XX
XX Example 4; SEQ ID NO 196, 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX 8S5, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ari, Ar2, WRI(V), WRI(T), 3-1,
XX 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
XX

CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I) and a composition (II) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I) and a kit comprising (I). (I) is useful for neutralising
CC BONT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BONT-antibody framework region 3.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 165; DB 8; Length 32;
Best Local Similarity 100.0%; Pred. No. 9.9e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
RESULT 3
ID ADR38797 standard; peptide; 32 AA.
XX ADR38797;
AC
XX 02-DEC-2004 (first entry)
DT
XX
XX Mouse heavy chain anti-BONT-antibody framework 3 seqid 199.
XX
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX framework 3.
XX
XX Mus sp.
OS
XX US2004175385-A1.
PN
XX 09-SEP-2004.
PD
XX 01-AUG-2003; 2003US-00632706.
PF
XX 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
XX (REGC) UNITV CALIFORNIA.
XX
XX Marke JD, Amerdorfer P;
PI
XX WPI; 2004-652009/63.
DR
XX
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
PT
XX
XX Example 4; SEQ ID NO 199, 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX

CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surpluss. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surpluss, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surpluss. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin (I)
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulinum. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody framework region 3.

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 165; DB 8; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTSRDNRKNTLFLQNSLRADPTAVYYCAR 32
 DB 1 RFTSRDNRKNTLFLQNSLRADPTAVYYCAR 32

RESULT 4

ID ADR38800 standard; peptide; 32 AA.

XX ADR38800;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain anti-BoNT-antibody framework 3 seqid 202.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW framework 3.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amerdorter P.

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulinum or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 202; 110p; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A

CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC 525, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surpluss. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surpluss, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surpluss. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin (I)
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulinum. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody framework region 3.

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 165; DB 8; Length 32;
 Best Local Similarity 100.0%; Pred. No. 9.9e-16;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTSRDNRKNTLFLQNSLRADPTAVYYCAR 32
 DB 1 RFTSRDNRKNTLFLQNSLRADPTAVYYCAR 32

RESULT 5

ID AAU02529 standard; protein; 113 AA.

XX AAU02529;

XX 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody heavy chain, FAT 19.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TV;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03429.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 111; 182p; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the

CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

XX Sequence 113 AA;
SQ

Query Match 98.2%; Score 162; DB 4; Length 113;
Best Local Similarity 96.9%; Pred. No. 1.1e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDN SKNTLFLQMSLRADDTAVYYCAR 32
ID |||||
ABG30486 ABG30486 standard; protein; 116 AA.

XX AC ABG30486;
XX

DT 07-OCT-2002 (first entry)

DE Human anti-CD40 monoclonal antibody 12D9 heavy chain #1.

XX Human; heavy chain; CD40; autoimmune disease; multiple sclerosis;
KM systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
KM Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
KM non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
KW proliferation.

XX Homo sapiens.
OS

XX WO200228904-A2.
PN

XX 11-APR-2002.
PD

XX 02-OCT-2001; 2001WO-US030857.
PF

XX 02-OCT-2000; 2000US-0237556P.
PR

XX (CHIR) CHIRON CORP.
PA

XX Chu K, Wang C, Yoshihara C, Donnelly JJ;
PI

XX WPI; 2002-405169/43.
DR

XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT proliferation, growth or differentiation of a normal human B cells and
PT treating autoimmune disease such as rheumatoid arthritis or systemic
PT lupus erythematosus.

XX Claim 8; Fig 6; 75pp; English.
PS

XX The invention relates to a human monoclonal antibody or fragment capable
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC on the surface of human B cells), where the antibody or fragment is free
CC of significant agonistic activity when it binds to the CD40 antigen, and
CC the growth or differentiation is inhibited. The fragments comprise the
CC complementarily determining region (CDR) of the light and heavy chains of
CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
CC 20C4, 12D9, 9F7 and 13B4. Also included are the nucleic acids encoding

CC the antibody (or fragments). The antibodies or fragments are used for
CC inhibiting proliferation, growth or differentiation of a normal human B
CC cells and to inhibit antibody production by B cells. They may also be
CC useful for treating autoimmune diseases, such as systemic lupus
CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
CC Hodgkin's lymphoma). The present sequence represents the antibody 12D9
CC heavy chain

XX Sequence 116 AA;
SQ

Query Match 98.2%; Score 162; DB 5; Length 116;
Best Local Similarity 96.9%; Pred. No. 1.2e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDN SKNTLFLQMSLRADDTAVYYCAR 32
ID |||||
ABG30484 ABG30484 standard; protein; 117 AA.

XX AC ABG30484;
XX

DT 07-OCT-2002 (first entry)

DE Human anti-CD40 monoclonal antibody 9F7 heavy chain #1.

XX Human; heavy chain; CD40; autoimmune disease; multiple sclerosis;
KM systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
KM Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
KM non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
KW proliferation.

XX Homo sapiens.
OS

XX WO200228904-A2.
PN

XX 11-APR-2002.
PD

XX 02-OCT-2001; 2001WO-US030857.
PF

XX 02-OCT-2000; 2000US-0237556P.
PR

XX (CHIR) CHIRON CORP.
PA

XX Chu K, Wang C, Yoshihara C, Donnelly JJ;
PI

XX WPI; 2002-405169/43.
DR

XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT proliferation, growth or differentiation of a normal human B cells and
PT treating autoimmune disease such as rheumatoid arthritis or systemic
PT lupus erythematosus.

XX Claim 6; Fig 6; 75pp; English.
PS

XX The invention relates to a human monoclonal antibody or fragment capable
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC on the surface of human B cells), where the antibody or fragment is free
CC of significant agonistic activity when it binds to the CD40 antigen, and
CC the growth or differentiation is inhibited. The fragments comprise the
CC complementarily determining region (CDR) of the light and heavy chains of
CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
CC 20C4, 12D9, 9F7 and 13B4. Also included are the nucleic acids encoding
CC the antibody (or fragments). The antibodies or fragments are used for
CC inhibiting proliferation, growth or differentiation of a normal human B
CC cells and to inhibit antibody production by B cells. They may also be
CC useful for treating autoimmune diseases, such as systemic lupus
CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
 DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

RESULT 10

ID ABO27447 standard; protein; 126 AA.

AC ABO27447;

DT 12-SEP-2003 (first entry)

XX Anti-Rh(D) heavy chain SH54.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;
 KM magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

PF 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX 29-JAN-1999; 99US-00240274.

XX (UYPR-) UNIV PENNSYLVANIA.

XX S1egel DL;

XX WPI; 2003-512273/48.

XX N-PSDB; ACD45361.

XX New human Rh(D)-binding protein useful for various diagnostic and
 PT therapeutic applications, including typing of blood or blood products.

XX Claim 4; Page 49; 187pp; English.

XX The invention relates to an isolated Rh(D) binding protein. The protein
 CC can be used for magnetically activated cell sorting. The protein is
 CC useful in various diagnostic and therapeutic applications in humans,
 CC including typing of blood or blood products. The present sequence
 CC represents the amino acid sequence of a human anti-Rh(D) chain

XX Sequence 126 AA;

Query Match 98.2%; Score 162; DB 6; Length 126;
 Best Local Similarity 96.9%; Pred. No. 1.3e-14;

Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32

DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

RESULT 11

ID AAG93627 standard; protein; 127 AA.

XX AAG93627;

DT 14-SEP-2001 (first entry)

XX Human anti-Rh(D) antibody clone SH10 protein sequence.

XX Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
 KM red blood cell; Rh phenotype; diagnosis; therapeutic.

XX red blood cell; Rh phenotype; diagnosis; therapeutic.

XX Homo sapiens.
 XX US6255455-B1.

XX 03-JUL-2001.

XX 29-JAN-1999; 99US-00240274.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

XX (UYPR-) UNIV PENNSYLVANIA.

XX S1egel DL;

XX WPI; 2001-388931/41.

XX N-PSDB; AAH68684.

XX Claim 1; Col 65; 162pp; English.

XX The present invention describes an isolated Rh(D) binding protein,
 CC preferably a human antibody, (I) having an amino acid sequence comprising
 CC one of the sequences (S) given in AAG93658 to AAG93669. (I) has
 CC immunostimulant activity, and can be used as an immune system stimulant.

CC (I) can be used in diagnostic and therapeutic medicine. The antibodies
 CC are used in diagnostics that require human antibodies instead of animal
 CC antibodies, such as determine the Rh phenotype of human red blood cells.

CC AAH68615 to AAH68726 represent the nucleotide sequence which encode
 CC AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
 CC chain CDR3 amino acid sequences which are given in the exemplification of
 CC the present invention

XX Sequence 127 AA;

Query Match 98.2%; Score 162; DB 4; Length 127;
 Best Local Similarity 96.9%; Pred. No. 1.3e-14;

Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32

DB 68 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 99

RESULT 12

ID ABO27434 standard; protein; 127 AA.

XX ABO27434;

DT 12-SEP-2003 (first entry)

XX Anti-Rh(D) heavy chain SH10.

XX Human; RH(D) binding protein; blood typing; blood product; antibody;
 KM magnetically activated cell sorting.

XX Homo sapiens.

XX US2003040605-A1.

XX 27-FEB-2003.

XX 04-MAY-2001; 2001US-00848798.

XX 11-OCT-1996; 96US-0028550P.

XX 27-JUN-1997; 97US-00884045.

XX 10-APR-1998; 98US-0081380P.

PR 29-JAN-1999; 99US-00240274.
XX
XX (UYPR-) UNIV PENNSYLVANIA.
XX
XX
PI Siegel DL;
XX
XX WPI; 2003-512273/48.
DR N-PSDB; ACD45348.
XX
XX New human Rh(D)-binding protein useful for various diagnostic and
PT therapeutic applications, including typing of blood or blood products.
XX
XX
XX Claim 4; Page 48; 187pp; English.
XX
XX The invention relates to an isolated Rh(D) binding protein. The protein
CC can be used for magnetically activated cell sorting. The protein is
CC useful in various diagnostic and therapeutic applications in humans,
CC including typing of blood or blood products. The present sequence
CC represents the amino acid sequence of a human anti-Rh(D) chain
XX
SQ Sequence 127 AA;
XX
Query Match 98.2%; Score 162; DB 6; Length 127;
Best Local Similarity 96.9%; Pred. No. 1.3e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
CY 1 RFTISRDNSKNTLFLQNNSLRADPTAVYYCAR 32
68 RFTISRDNSKNTLYLQNNSLRADPTAVYYCAR 99
DB
RESULT 13
ADG30422
ID ADG30422 standard; protein; 244 AA.
XX
XX ADG30422;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Human GMB619 scFv protein.
DE
XX
XX GMB619; VH; CDR; complementarity determining region; VL; scFv;
KW single chain antibody; antidiabetic; type II diabetes; human; GMB619.
XX
XX Homo sapiens.
OS
XX
XX WO2003085093-A2.
PN
XX
XX 16-OCT-2003.
PD
XX
XX 28-MAR-2003; 2003WO-US009625.
PF
XX
XX 01-APR-2002; 2002US-0368813P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Baker KP, Albert VR, Chowdhury P;
PI
XX
XX WPI; 2003-804305/75.
DR N-PSDB; ADG30519.
DR
XX
XX New antibody that specifically binds to GMB619 polypeptide, useful for
PT diagnosing, monitoring, treating, preventing or ameliorating type II
PT diabetes.
XX
XX Claim 2; SEQ ID NO 55; 410pp; English.
XX
XX The invention relates to a novel antibody that specifically binds to a
CC GMB619 polypeptide comprising a first amino acid sequence that is at least
CC 95% identical to a second amino acid sequence of a VH CDR
CC (complementarity determining region) or VL CDR of an scFv (single chain
CC antibody molecule). The antibody of the invention demonstrates
CC antidiabetic activity and may be useful for diagnosing, monitoring,

CC treating, preventing or ameliorating type II diabetes. The current
CC sequence is that of the human scFv protein of the invention.
XX
XX
SQ Sequence 244 AA;
XX
Query Match 98.2%; Score 162; DB 7; Length 244;
Best Local Similarity 96.9%; Pred. No. 2.7e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
CY 1 RFTISRDNSKNTLFLQNNSLRADPTAVYYCAR 32
67 RFTISRDNSKNTLYLQNNSLRADPTAVYYCAR 98
DB
RESULT 14
ADP22238
ID ADP22238 standard; protein; 115 AA.
XX
XX
XX ADP22238;
AC
XX
XX 09-SEP-2004 (first entry)
DT
XX
XX Human anti-TNFA antibody light chain variable region SEQ ID NO:144.
DE
XX
XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
KW anti-TNFA antibody; antibody; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipapillary; antithrombotic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotoxic;
KW neuroprotective; vasoregulatory; antiapoptotic; TNFA antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis.
XX
XX Homo sapiens.
OS
XX
XX WO2004050683-A2.
PN
XX
XX 17-JUN-2004.
PD
XX
XX 02-DEC-2003; 2003WO-US038281.
PF
XX
XX 02-DEC-2002; 2002US-0430729P.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Babcock JS, Kang JS, Poord O, Green U, Peng X, Klakamp S;
PI Haek-Frendscho W, Rathnaswami P, Pigott C, Liang ML, Lee R;
PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
XX WPI; 2004-480601/45.
DR N-PSDB; ADP22237.
DR
XX
XX New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancer, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
XX
XX Example 10; SEQ ID NO 144; 213pp; English.
XX
XX The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFA in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFA in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a

CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (1); and (4) inhibiting (M3) TNF α induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNF α induced apoptosis by administering the human monoclonal antibody of
CC (1). (1) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipaprotic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic, and
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNF α antagonist. The antibody (1) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence represents a human anti-TNF α
CC antibody light chain variable region, which is used in the
CC exemplification of the present invention.

SQ Sequence 115 AA;

Query Match 97.6%; Score 161; DB 8; Length 115;
Best Local Similarity 96.9%; Pred. No. 1.6e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSSKNTLFLQNSIRADDTAVYYCAR 32
Db 66 RFTISRDNSSKNTLFLQNSIRADDTAVYYCAR 97

RESULT 15
ADO36356 standard; protein; 121 AA.

AC ADO36356;
DT 26-AUG-2004 (first entry)
DE Intracellular interaction-related scfv protein SeqID20.
XX
XX Immunoglobulin single domain; intracellular environment;
KM intracellular interaction; immunoglobulin domain; scfv;
KW single chain variable fragment.
XX
XX Unidentified.
OS
XX WC2004046185-A2.
PN
XX
XX 03-JUN-2004.
PD
XX
XX 14-NOV-2003; 2003WO-GB004942.
PF
XX 15-NOV-2002; 2002GB-00026729.
PR
XX (MED1-) MEDICAL RES COUNCIL.
PA
XX Rabbits TH, Tanaka T;
PI
XX
XX WPI; 2004-431946/40.
DR
XX
XX
XX Determining the ability of an immunoglobulin single domain to bind to a
PT target in an intracellular environment by assessing the intracellular
PT interaction between the immunoglobulin domain and the target by
PT monitoring the signal.
XX
XX
XX Disclosure; SEQ ID NO 20; 66pp; English.

CC This invention relates to a novel method of determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment comprising assessing the intracellular interaction between
CC the immunoglobulin domain and the target by monitoring the signal. The

CC method comprises providing a first molecule and a second molecule, where
CC stable interaction of the first and second molecules leads to the
CC generation of a signal; providing a single intracellular immunoglobulin
CC domain which is associated with the first molecule, where the single
CC immunoglobulin domain is free of complementary immunoglobulin domains;
CC providing an intracellular target which is associated with the second
CC molecule, such that association of the immunoglobulin domain and the
CC target leads to stable interaction of the first and second molecules and
CC generation of the signal; and assessing the intracellular interaction
CC between the immunoglobulin domain and the target by monitoring the
CC signal. The methods are useful for determining the ability of an
CC immunoglobulin single domain to bind to a target in an intracellular
CC environment. The present sequence is that of a single chain variable
CC fragment (scfv) protein which was used to illustrate the method of the
CC invention.

SQ Sequence 121 AA;

Query Match 97.6%; Score 161; DB 8; Length 121;
Best Local Similarity 96.9%; Pred. No. 1.7e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSSKNTLFLQNSIRADDTAVYYCAR 32
Db 67 RFTISRDNSSKNTLFLQNSIRADDTAVYYCAR 98

Search completed: November 21, 2005, 12:20:06
Job time : 43.8425 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:36 / Search time 7.79487 Seconds
(without alignments)
394.995 Million cell updates/sec

Title: US-10-632-706-196

Perfect score: 165
Sequence: 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	158	95.8	97	2	S26935 Ig heavy chain V r
2	158	95.8	97	2	S46462 Ig heavy chain V r
3	158	95.8	98	2	S28546 Ig heavy chain V r
4	158	95.8	105	2	S24249 Ig heavy chain V r
5	158	95.8	108	2	PH1642 Ig heavy chain V r
6	158	95.8	109	2	PH1646 Ig heavy chain V r
7	158	95.8	109	2	PH1644 Ig heavy chain V r
8	158	95.8	111	2	PH1645 Ig heavy chain V r
9	158	95.8	114	2	S46390 Ig heavy chain V r
10	158	95.8	114	2	S46391 Ig heavy chain V r
11	158	95.8	114	2	S46392 Ig heavy chain V r
12	158	95.8	116	2	B28966 Ig heavy chain pre
13	158	95.8	119	2	S31111 Ig heavy chain - h
14	158	95.8	119	2	F36005 Ig heavy chain V r
15	158	95.8	121	2	G36005 Ig heavy chain V r
16	158	95.8	122	2	S31117 Ig heavy chain - h
17	158	95.8	122	2	E36005 Ig heavy chain V r
18	158	95.8	123	2	S38493 Ig heavy chain - h
19	158	95.8	128	2	S48797 Ig heavy chain V r
20	158	95.8	130	2	S31601 Ig heavy chain V r
21	158	95.8	133	2	A49028 Ig heavy chain V-I
22	158	95.8	134	2	S31679 Ig heavy chain V r
23	158	95.8	140	2	S70442 Ig heavy chain pre
24	157	95.2	133	2	S31510 Ig heavy chain - h
25	155	93.9	52	2	S21591 Ig heavy chain V r
26	155	93.9	76	2	S31592 Ig heavy chain V r
27	155	93.9	98	2	S26889 Ig heavy chain V-I
28	155	93.9	98	2	PL0121 Ig heavy chain V-I
29	155	93.9	98	2	PL0116 Ig heavy chain V-I

30	155	93.9	98	2	S29545 Ig heavy chain V r
31	155	93.9	98	2	S29543 Ig heavy chain V r
32	155	93.9	98	2	S26896 Ig heavy chain V r
33	155	93.9	99	2	S24259 Ig heavy chain V r
34	155	93.9	100	2	S24258 Ig heavy chain V r
35	155	93.9	101	2	S24257 Ig heavy chain V r
36	155	93.9	102	2	S24256 Ig heavy chain V r
37	155	93.9	104	2	S24255 Ig heavy chain V r
38	155	93.9	106	2	S24256 Ig heavy chain V r
39	155	93.9	108	2	PH1648 Ig heavy chain V r
40	155	93.9	109	2	PH1649 Ig heavy chain V r
41	155	93.9	111	2	PH1643 Ig heavy chain V r
42	155	93.9	112	2	PH1647 Ig heavy chain V r
43	155	93.9	117	1	H3H026 Ig heavy chain pre
44	155	93.9	117	2	A45953 Ig heavy chain pre
45	155	93.9	117	2	A34964 Ig heavy chain pre

ALIGNMENTS

RESULT 1

S26935
Ig heavy chain V region (DP-42) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S26935
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Ulewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V.
A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26935
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-97 <TOM>
A/Cross-references: UNIPARC:UPI0000116408; EMBL:Z12342; NID:G32905; PIDN:CAA78212.1; PID:
C/Species: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F,15-97/Domain: Immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 97;
Best Local Similarity 93.8%; Pred. No. 9.6e-15;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32
Db 66 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 97

RESULT 2

S46462
Ig heavy chain V region (YAC-5) - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C/Accession: S46462
R/Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Wint
R/Cook, G.P.; Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Wint
Nature Genet. 7, 162-168, 1994
A/Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telome
A/Reference number: S46460; MUID:95004581; PMID:7920635
A/Accession: S46462
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-97 <COO>
A/Cross-references: UNIPARC:UPI00001165D9; EMBL:Z27504; NID:G505430; PIDN:CAA81824.1; PIT
C/Species: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F,15-97/Domain: Immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 97;
Best Local Similarity 93.8%; Pred. No. 9.6e-15;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32

Db 66 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 97
|||||

RESULT 3

S29546

Ig heavy chain V region (COS-8 / DP-46) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-Jan-1994 #sequence_rev1510-1995 #text_change 23-Jul-1999

C/Accession: S29546; S26888

R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.

Submitted to the EMBL Data Library, October 1992

A/Reference number: S29543

A/Accession: S29546

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:932843; PIDD:CA78997.1; PII

A/Note: designated COS-8

R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A/Reference number: S26885, MUID:93021117, PMID:1404388

A/Accession: S26888

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-98 <TOM>

A/Note: designated DP-46

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 98;
Best Local Similarity 93.8%; Pred. No. 9.7e-15;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 32
|||||

Db 67 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 98
|||||

RESULT 4

S24249

Ig heavy chain V region (VH26-DN1-DXPI-JH4) - human

C/Species: Homo sapiens (man)

C/Date: 19-Feb-1994 #sequence_rev1510-Nov-1995 #text_change 30-May-1997

C/Accession: S24249

R/Stewart, A.K.; Huang, C.; Scollard, B.D.; Schwartz, R.S.

Submitted to the EMBL Data Library, June 1992

A/Description: A single VH gene predominates in the rearranged and expressed human B cell

A/Reference number: S24247

A/Accession: S24249

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-105 <STW>

A/Cross-references: UNIPARC:UPI0000176E3E; EMBL:X67070

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/10-92/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 105;
Best Local Similarity 93.8%; Pred. No. 1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 32
|||||

Db 61 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 92
|||||

RESULT 5

PH1642

Ig heavy chain V region (clone 5A10) - human (fragment)

C/Species: Homo sapiens (man)

Query Match 95.8%; Score 158; DB 2; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

C/Date: 24-Feb-1994 #sequence_rev1510-1994 #text_change 31-Dec-2004

C/Accession: PH1642

R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1642

A/Molecule type: mRNA

A/Residues: 1-108 <HIL>

A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B78

C/Superfamily: immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 108;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 32
|||||

Db 59 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 90
|||||

RESULT 6

PH1646

Ig heavy chain V region (clone 6H12) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence_rev1510-1994 #text_change 31-Dec-2004

C/Accession: PH1646

R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1646

A/Molecule type: mRNA

A/Residues: 1-109 <HIL>

A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B7C

C/Superfamily: immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 32
|||||

Db 59 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 90
|||||

RESULT 7

PH1644

Ig heavy chain V region (clone 5D11) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence_rev1510-1994 #text_change 31-Dec-2004

C/Accession: PH1644

R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saaso, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1644

A/Molecule type: mRNA

A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B7A

C/Superfamily: immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 109;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQMNLSRAEDTAVYYCAR 32
|||||

Db 59 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 90

RESULT 8

PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C/Accession: PH1645
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasse, R.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylococcal protein A
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1645
A/Molecule type: mRNA
A/Residues: 1-111 <H11>
A/Cross-references: UNIPROT:Q8WTK1; UNIPARC:UPI000017687B
C/Superfamily: immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 114;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32
Db 59 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 90

RESULT 9

S46390
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C/Accession: S46390
R/Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display
A/Reference number: S46390; MUID:94254092; PMID:8196048
A/Accession: S46390
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <Fig>
A/Cross-references: UNIPARC:UPI000011663F; EMBL:Z31686; NID:G509782; PIDN:CAA83491.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 114;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32
Db 67 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

RESULT 10

S46391
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C/Accession: S46391
R/Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display
A/Reference number: S46390; MUID:94254092; PMID:8196048
A/Accession: S46391
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <Fig>

A/Cross-references: UNIPARC:UPI00001137D5; EMBL:Z31687; NID:G509784; PIDN:CAA83492.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 114;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32
Db 67 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

RESULT 11

S46392
Ig heavy chain V region (VH-28) - human
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C/Accession: S46392
R/Figini, M.; Marke, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display
A/Reference number: S46390; MUID:94254092; PMID:8196048
A/Accession: S46392
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <Fig>
A/Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:G499306; PIDN:CAA83493.1; PII
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 114;
Best Local Similarity 93.8%; Pred. No. 1.1e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32
Db 67 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 98

RESULT 12

B28966
Ig heavy chain precursor V-region chain 5A - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Aug-1996
C/Accession: B28966; A32782
R/Wilson, M.R.; Middleton, D.; Warr, G.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 1566-1570, 1988
A/Title: Immunoglobulin heavy chain variable region gene evolution: structure and family
A/Reference number: A28966; MUID:88144476; PMID:3125551
A/Accession: B28966
A/Molecule type: DNA
A/Residues: 1-116 <H11>
A/Cross-references: UNIPARC:UPI000012CDE
R/Wilson, M.R.; Middleton, D.; Warr, G.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 3276, 1989
A/Reference number: A32782
A/Contents: annotation; erratum
A/Note: The authors note that this sequence is of higher primate (probably human) origin
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 116;
Best Local Similarity 93.8%; Pred. No. 1.2e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 32
Db 85 RFTISRDNKNTLYLQWNSLRADTAIVYCAR 116

RESULT 13

g31111
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: g31111
R/Schroeder, P.M.; Timmers, B.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Bur, J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31111
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-119 <RHA>
A/Cross-references: UNIPARC:UPI0000176DC2; EMBL:X62959
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 119;
Best Local Similarity 93.8%; Pred. No. 1.2e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32

DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

RESULT 14

F36005
Ig heavy chain V region (M49) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C/Accession: F36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:9034577; PMID:2117273
A/Accession: F36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 119;
Best Local Similarity 93.8%; Pred. No. 1.2e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32

DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

RESULT 15

G36005
Ig heavy chain V region (M74) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C/Accession: G36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:9034577; PMID:2117273
A/Accession: G36005

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-121 <SCH>
A/Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C2C; GB:M34021
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 95.8%; Score 158; DB 2; Length 121;
Best Local Similarity 93.8%; Pred. No. 1.2e-14;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32

DB 67 RFTISRDNKNTLYLQNSLRADDTAVYYCAR 98

Search completed: November 21, 2005, 12:22:17
Job time : 7.79487 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:45:55 ; Search time 47.3553 Seconds
(without alignments)
476.756 Million cell updates/sec

Title: US-10-632-706-196
Perfect score: 165
Sequence: 1 RPTISRDNKXKTLFLQNNSLRADPTAVYYCAR 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	158	95.8	112 2 Q9UGP3_HUMAN	Q9UGP3 homo sapien
2	158	95.8	116 1 HV05_CARAU	P19181 carassius a
3	158	95.8	240 2 Q6SZC9_HUMAN	Q6SZC9 homo sapien
4	158	95.8	466 2 Q6TNT8_HUMAN	Q6TNT8 homo sapien
5	155	93.9	113 2 Q9UL90_HUMAN	Q9UL90 homo sapien
6	155	93.9	117 1 HV3C_HUMAN	P01764 homo sapien
7	155	93.9	613 2 Q8WUK1_HUMAN	Q8WUK1 homo sapien
8	153	92.7	118 2 Q9UL72_HUMAN	Q9UL72 homo sapien
9	151	91.5	112 2 Q9HCC1_HUMAN	Q9HCC1 homo sapien
10	151	91.5	118 2 Q9UL91_HUMAN	Q9UL91 homo sapien
11	151	91.5	470 2 Q6RJH4_HUMAN	Q6RJH4 homo sapien
12	151	91.5	478 2 Q6P181_HUMAN	Q6P181 homo sapien
13	151	91.5	494 2 Q96K68_HUMAN	Q96K68 homo sapien
14	151	91.5	606 2 Q6GMV2_HUMAN	Q6GMV2 homo sapien
15	150	90.9	116 2 Q9UL93_HUMAN	Q9UL93 homo sapien
16	150	90.9	122 1 HV3G_HUMAN	P01768 homo sapien
17	150	90.9	466 2 Q6N096_HUMAN	Q6N096 homo sapien
18	148	89.7	121 2 Q9UL71_HUMAN	Q9UL71 homo sapien
19	148	89.7	473 2 Q6MZV7_HUMAN	Q6MZV7 homo sapien
20	147	89.1	597 2 Q96BB9_HUMAN	Q96BB9 homo sapien
21	146	88.5	119 2 Q5F218_MOUSE	Q5F218 mus musculu
22	146	88.5	464 2 Q6MZU6_HUMAN	Q6MZU6 homo sapien
23	146	88.5	469 2 Q569P4_HUMAN	Q569P4 homo sapien
24	146	88.5	473 2 Q91Z05_MOUSE	Q91Z05 mus musculu
25	146	88.5	483 2 Q6MZK9_HUMAN	Q6MZK9 homo sapien
26	146	88.5	485 2 Q6PDB8_MOUSE	Q6PDB8 mus musculu
27	146	88.5	493 2 Q6GMX2_HUMAN	Q6GMX2 homo sapien
28	146	88.5	544 2 Q6P395_HUMAN	Q6P395 homo sapien
29	145	87.9	104 2 Q9UL87_HUMAN	Q9UL87 homo sapien
30	145	87.9	147 2 Q9Y509_HUMAN	Q9Y509 homo sapien
31	145	87.9	465 2 Q6PEC4_HUMAN	Q6PEC4 homo sapien

32	145	87.9	573	2	Q8WU38_HUMAN	Q8WU38 homo sapien
33	144	87.3	116	1	HV3T_HUMAN	P01781 homo sapien
34	144	87.3	121	1	HV3J_HUMAN	P01771 homo sapien
35	144	87.3	136	1	HV16_MOUSE	P01783 mus musculu
36	144	87.3	472	2	Q6N089_HUMAN	Q6N089 homo sapien
37	144	87.3	483	2	Q566J7_MOUSE	Q566J7 mus musculu
38	144	87.3	499	2	Q8N5K4_HUMAN	Q8N5K4 homo sapien
39	143	86.7	120	1	HV3E_HUMAN	P01766 homo sapien
40	143	86.7	126	1	HV3K_HUMAN	P01772 homo sapien
41	143	86.7	417	2	Q6N093_HUMAN	Q6N093 homo sapien
42	142	86.1	95	2	Q9ULB6_HUMAN	Q9ULB6 homo sapien
43	142	86.1	480	2	Q6N094_HUMAN	Q6N094 homo sapien
44	141	85.5	114	1	HV3B_HUMAN	P01763 homo sapien
45	141	85.5	115	1	HV3F_HUMAN	P01767 homo sapien

ALIGNMENTS

```

RESULT 1
Q9UGP3_HUMAN                                PRT; 112 AA.
ID Q9UGP3_HUMAN PRELIMINARY;
AC Q9UGP3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
GN Name=IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zafiroopoulos A., Kandiloglaniaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA Krambovitis E.;
RL EMBL; AJ132560; CAB65078.1; -; mRNA.
DR HSSP; P01783; IIGC.
DR SMR; Q9UGP3; 1-105.
DR Ensembl; ENSG0000018443; Homo sapiens.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;

Query Match 95.8%; Score 158; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 4,7e-15;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPTISRDNKXKTLFLQNNSLRADPTAVYYCAR 32
DB 50 RPTISRDNKXKTLFLQNNSLRADPTAVYYCAR 81

RESULT 2
HV05_CARAU                                STANDARD; PRT; 116 AA.
ID HV05_CARAU
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88144476; PubMed=3125551;
 RA Wilson M.R., Middleton D., Watt G.W.;
 RT "Immunoglobulin heavy chain variable region gene evolution: structure
 and family relationships of two genes and a pseudogene in a teleost
 fish";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC HSP, P01783, 1IGC.
 DR SMR; P19181; 20-116.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KM Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL
 FT CHAIN 1
 FT REGION 20 116 Ig heavy chain V region 5A.
 FT REGION 20 49 Framework-1.
 FT REGION 50 54 Complementarity-determining-1.
 FT REGION 55 68 Framework-2.
 FT REGION 69 84 Complementarity-determining-2.
 FT REGION 85 116 Framework-3.
 FT DISULFID 41 114 By similarity.
 FT NON_TER 116 116
 SO SEQUENCE 116 AA; 12808 MM; 9C2279E2DF199B12 CRC64;
 Query Match 95.8%; Score 158; DB 1; Length 116;
 Best Local Similarity 93.8%; Pred. No. 4.9e-15;
 Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RFTISRDNKNTLFLQNSLRADTAVYYCAR 32
 Db 85 RFTISRDNKNTLFLQNSLRADTAVYYCAR 116
 RESULT 3
 ID 065ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
 AC 065ZC9;
 DT 25-OCT-2004 (TrEMBLrel. 28; Created)
 DT 25-OCT-2004 (TrEMBLrel. 28; Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28; Last annotation update)
 DE Single-chain Fv (Fragment).
 GN Name=scFv;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C1q/7;
 RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diabodies";
 RL Nat. Biotechnol. 15:629-631(1997).
 DR EMBL; Y13056; CA73499.1; -; mRNA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON_TER 1
 FT NON_TER 1
 SO SEQUENCE 240 AA; 25569 MM; FDCFD3645F64B373 CRC64;

Query Match 95.8%; Score 158; DB 2; Length 240;
 Best Local Similarity 93.8%; Pred. No. 1.1e-14;
 Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RFTISRDNKNTLFLQNSLRADTAVYYCAR 32
 Db 67 RFTISRDNKNTLFLQNSLRADTAVYYCAR 98
 RESULT 4
 ID 06IN78_HUMAN PRELIMINARY; PRT; 466 AA.
 AC 06IN78;
 DT 05-JUL-2004 (TrEMBLrel. 27; Created)
 DT 05-JUL-2004 (TrEMBLrel. 27; Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27; Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Cassavatt T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzinski M.I., Skalka U., Skalka U., Skalka U.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072419; AAH72419.1; -; mRNA.
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-sect; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN_2.
 SO SEQUENCE 466 AA; 50854 MM; 53EB0BCBDE81076E CRC64;
 Query Match 95.8%; Score 158; DB 2; Length 466;
 Best Local Similarity 93.8%; Pred. No. 2.3e-14;
 Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RFTISRDNKNTLFLQNSLRADTAVYYCAR 32

Db 85 RFTISRDNSKNTLYLQWNSLRADPTAVYYCAR 116

RESULT 5

Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.

DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DE Myosin-reactive immunoglobulin heavy chain variable region (fragment).

OS Homo sapiens (Human); Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Euarchontoglires; Primates; Catarrhini; Homnidae; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

OC NCBT_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=9614934; DOI=10.1006/clim.1998.4531; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M., Young D.C., Van der Merwe P.L., Kalis N.N., Berny S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

RN [2] NUCLEOTIDE SEQUENCE.

RA PubMed=1730252; Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M., Raaphorst F.M.,

RT "Restricted utilization of germ-line VH3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements."

RL Eur. J. Immunol. 22:247-251(1992).

DR EMBL; AF035024; AAD56260.1; -; mRNA.

DR HSSP; P01772; 2FB4.

DR SMR; G9UL90; 1-113.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON TER 1

FT SEQUENCE 113 AA; 12437 MW; ED57PDD19086D07F CRC64;

Query Match 93.9%; Score 155; DB 2; Length 113;

Best Local Similarity 90.6%; Pred. No. 1.3e-14;

Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLYLQWNSLRADPTAVYYCAR 32

DB 67 RFTISRDNSKNTLYLQWNSLRADPTAVYYCAR 98

RESULT 6

Q8WTK1 HUMAN PRELIMINARY; PRT; 117 AA.

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Ig heavy chain V-III region VH26 precursor.

OS Homo sapiens (Human); Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Euarchontoglires; Primates; Catarrhini; Homnidae; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

OC NCBT_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=81101090; PubMed=6450418; Matthyssens G., Rabbitts T.H.,

RT "Structure and multiplicity of genes for the human immunoglobulin

RT heavy chain variable region."

RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).

RN [2] NUCLEOTIDE SEQUENCE OF 20-117.

RA MEDLINE=93209281; PubMed=7681398;

RT "Nucleotide sequence analysis of the variable domains of four human monoclonal IgM with an antibody activity to myelin-associated glycoprotein."

RL Eur. J. Immunol. 23:846-851(1993).

RN [3] 3D-STRUCTURE MODELING OF 20-117.

RA MEDLINE=86094276; PubMed=3866244;

RT "Organization and sequences of the diversity, joining, and constant region genes of the human T-cell receptor beta chain."

RL Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628(1985).

CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.

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CC EMBL; J00236; AAA53516.1; -; Unassigned DNA.

DR EMBL; M35415; AAA58735.1; -; Genomic DNA.

DR PIR; A02047; H3H026.

DR PDB; 1H0J; Model; H=20-117.

DR HGNC; HGNC:5545; IGHV0.

DR GO; GO:0005576; C:extracellular region; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW 3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117

FT DOMAIN 20 >117

FT NON TER 117

FT SEQUENCE 117 AA; 12582 MW; B826733F1A3CB0F1 CRC64;

Query Match 93.9%; Score 155; DB 1; Length 117;

Best Local Similarity 90.6%; Pred. No. 1.3e-14;

Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLYLQWNSLRADPTAVYYCAR 32

DB 86 RFTISRDNSKNTLYLQWNSLRADPTAVYYCAR 117

RESULT 7

Q8WTK1 HUMAN PRELIMINARY; PRT; 613 AA.

DT 01-MAR-2002 (TREMblrel. 20, Created)

DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DE IGHM protein.

OS Homo sapiens (Human); Chordata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Euarchontoglires; Primates; Catarrhini; Homnidae; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

OC NCBT_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RA TISSUE=Primary B-Cells; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold R.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,


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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.U.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC NIH MGC Project.
RG TISSUE=Primary B-Cells;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AA18747.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR SMR; O6PUA4; 20-470.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 5176 MM; 7849556A11PD799 CRC64;

Query Match 91.5%; Score 151; DB 2; Length 470;
Best Local Similarity 87.5%; Pred. No. 2.5e-13;
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTFLQNSLRADDTAVYYCAR 32
DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117

RESULT 12
Q6P181_HUMAN PRELIMINARY; PRT; 478 AA.
ID Q6P181_HUMAN PRELIMINARY;
AC Q6P181;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG MBLIN=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Datchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Vedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltón E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.U.M., Matra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC NIH MGC Project.
RG TISSUE=Primary B-Cells;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AA41037.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 478 AA; 52667 MM; 178D38D917970D6 CRC64;

Query Match 91.5%; Score 151; DB 2; Length 478;
Best Local Similarity 87.5%; Pred. No. 2.5e-13;
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTFLQNSLRADDTAVYYCAR 32
DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117

RESULT 13
Q6K68_HUMAN PRELIMINARY; PRT; 494 AA.
ID Q6K68_HUMAN PRELIMINARY;
AC Q6K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ14473.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RG PubMed=14702039; DOI=10.1038/ng1285;
RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku T., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa K.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togiyama S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Iino N., Mutsaers S., Yuuki F., Hara R., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Taniguchi A., Fujisawa T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

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RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuko Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RU Nat. Genet. 36:40-45(2004).
 RN [2]
 RP PROTEIN SEQUENCE.
 RX PubMed=1555592;
 RA Makiya R., Stigbrand T.;
 RT "Placental alkaline phosphatase has a binding site for the human
 RT immunoglobulin-G FC portion";
 RL Eur. J. Biochem. 205:341-345(1992).
 DR EMBL; AK027379; BAB55072.1; -; mRNA.
 DR PIR; S21205; S21205.
 DR HSSP; P01876; 10M0.
 DR SMR; Q96K68; 264-472.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AE4C0E CRC64;
 OY Query Match 91.5%; Score 151; DB 2; Length 494;
 Best Local Similarity 87.5%; Pred. No. 2.6e-13;
 Matches 28; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 DB 86 RFTISRDNAKNSLYIQWNSLRADTAVYYCAR 117
 OY 1 RFTISRDNSKNTLFLOWNSLRADTAVYYCAR 32
 ID 06GMV2 HUMAN PRELIMINARY; PRT; 606 AA.
 AC O6GMV2
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE IGHM protein.
 DE Name=IGHM;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX TISUS=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straussberg R.D., Feingold B.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan T., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettmann M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Tuchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.B., Jones S.J.M., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX TISUS=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073758; AAH73758.1; -; mRNA.
 DR SMR; Q6GMV2; 20-256.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; CI-set; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 606 AA; 66185 MW; B6B38B5114E4C55 CRC64;
 OY Query Match 91.5%; Score 151; DB 2; Length 606;
 Best Local Similarity 87.5%; Pred. No. 3.3e-13;
 Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 DB 86 RFTISRDNAKNSLYIQWNSLRADTAVYYCAR 117
 OY 1 RFTISRDNSKNTLFLOWNSLRADTAVYYCAR 32
 ID 09UL93 HUMAN PRELIMINARY; PRT; 116 AA.
 AC 09UL93;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalish N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
 RA Hillson J.L., Kair N.S., Opplinger I.R., Mannik M., Sasso B.H.,
 RT "The structural basis of germline-encoded VHS immunoglobulin binding
 RT to staphylococcal protein A";
 RL J. Exp. Med. 178:331-336(1993).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=2840480;
 RA Bird J., Gallili N., Link M., Stiles D., Sklar J.;
 RT "Continuing rearrangement but absence of somatic hypermutation in
 RT immunoglobulin genes of human B cell precursor leukemia";
 RL J. Exp. Med. 168:229-245(1988).
 DR EMBL; AF035021; AAD56257.1; -; mRNA.
 DR PIR; PH1644; PH1644.
 DR PIR; P01020; P01020.
 DR HSSP; P01772; 2F84.
 DR SMR; Q9UL93; 1-116.
 DR InterPro; IPR007110; Ig-1like.
 DR InterPro; IPR003596; Ig_v.

DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
FT	NON_TER 1 1
FT	NON_TER 116 116
SQ	SEQUENCE 116 AA; 12434 MW; ODA0348154DD6061 CRC64;

Search completed: November 21, 2005, 12:04:14
Job time : 47.3553 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 21, 2005, 11:49:31 ; Search time 12.0733 Seconds
(without alignments)
219.131 Million cell updates/sec

Title: US-10-632-706-196

Perfect score: 165
Sequence: 1 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 32

Scoring table: BIOSIM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	162	98.2	126	2	US-09-240-274-152 Sequence 152, App
2	162	98.2	126	2	US-09-848-798-152 Sequence 152, App
3	162	98.2	127	2	US-09-240-274-139 Sequence 139, App
4	162	98.2	127	2	US-09-848-798-139 Sequence 139, App
5	161	97.6	167	2	US-09-472-087-74 Sequence 74, Appl
6	161	97.6	463	2	US-09-472-087-11 Sequence 1, Appl
7	161	97.6	463	2	US-09-472-087-63 Sequence 63, Appl
8	161	97.6	463	2	US-09-472-087-64 Sequence 64, Appl
9	158	95.8	32	1	US-08-471-780C-82 Sequence 82, Appl
10	158	95.8	32	1	US-08-467-282B-82 Sequence 82, Appl
11	158	95.8	32	1	US-08-471-282A-82 Sequence 82, Appl
12	158	95.8	32	1	US-08-466-710C-82 Sequence 82, Appl
13	158	95.8	32	1	US-08-470-138-21 Sequence 21, Appl
14	158	95.8	32	1	US-08-468-739C-82 Sequence 82, Appl
15	158	95.8	32	2	US-09-563-222C-142 Sequence 142, App
16	158	95.8	32	2	US-09-855-271-21 Sequence 21, Appl
17	158	95.8	32	2	US-09-293-769A-82 Sequence 82, Appl
18	158	95.8	32	2	US-08-537-871A-64 Sequence 64, Appl
19	158	95.8	32	2	US-09-472-087-72 Sequence 72, Appl
20	158	95.8	89	2	US-09-043-514-2 Sequence 2, Appl
21	158	95.8	95	2	US-10-194-975-29 Sequence 29, Appl
22	158	95.8	97	2	US-10-194-975-31 Sequence 31, Appl
23	158	95.8	97	2	US-09-534-717-629 Sequence 629, App
24	158	95.8	97	2	US-08-211-202-118 Sequence 118, App
25	158	95.8	98	1	US-10-194-975-24 Sequence 24, Appl
26	158	95.8	98	2	US-10-194-975-26 Sequence 26, Appl

ALIGNMENTS

28	158	95.8	98	2	US-10-194-975-30 Sequence 30, Appl
29	158	95.8	98	2	US-09-534-717-624 Sequence 624, App
30	158	95.8	98	2	US-09-534-717-625 Sequence 625, App
31	158	95.8	98	2	US-09-534-717-627 Sequence 627, App
32	158	95.8	98	2	US-09-534-717-628 Sequence 628, App
33	158	95.8	98	2	US-09-534-717-629 Sequence 629, App
34	158	95.8	98	2	US-09-534-717-630 Sequence 630, App
35	158	95.8	98	2	US-09-534-717-631 Sequence 631, App
36	158	95.8	98	2	US-09-534-717-632 Sequence 632, App
37	158	95.8	98	2	US-09-534-717-633 Sequence 633, App
38	158	95.8	98	2	US-09-534-717-636 Sequence 636, App
39	158	95.8	98	2	US-09-534-717-641 Sequence 641, App
40	158	95.8	98	2	US-09-534-717-642 Sequence 642, App
41	158	95.8	98	2	US-09-534-717-643 Sequence 643, App
42	158	95.8	98	2	US-09-534-717-644 Sequence 644, App
43	158	95.8	98	2	US-09-534-717-646 Sequence 646, App
44	158	95.8	98	2	US-09-534-717-647 Sequence 647, App
45	158	95.8	98	2	US-09-534-717-651 Sequence 651, App

RESULT 1
US-09-240-274-152
; Sequence 152, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEIN AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-152
Query Match 98.2%; Score 162; DB 2; Length 126;
Best Local Similarity 96.9%; Pred. No. 1e-15; 0; Indels 0; Gaps 0;
Matches 31; Conservative 1; Mismatches 98
QY 1 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 32
DB 67 RFTISRDNKNTLFLQNNSLRADDTAVYYCAR 98
RESULT 2
US-09-848-798-152
; Sequence 152, Application US/09848798
; Patent No. 6658719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEIN AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT FILING DATE: 2001-05-04
; CURRENT APPLICATION NUMBER: US/09/848,798
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-152

Query Match          98.2%; Score 162; DB 2; Length 126;
Best Local Similarity 96.9%; Pred. No. 1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 98

RESULT 3
US-09-240-274-139
; Sequence 139, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH10
US-09-240-274-139

Query Match          98.2%; Score 162; DB 2; Length 127;
Best Local Similarity 96.9%; Pred. No. 1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db 68 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 99

RESULT 4
US-09-848-798-139
; Sequence 139, Application US/09848798
; Patent No. 6658719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH10
US-09-848-798-139

Query Match          98.2%; Score 162; DB 2; Length 127;
Best Local Similarity 96.9%; Pred. No. 1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db 68 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 99

RESULT 5
US-09-472-087-74
; Sequence 74, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-74

Query Match          97.6%; Score 161; DB 2; Length 167;
Best Local Similarity 96.9%; Pred. No. 1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db 58 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 89

RESULT 6
US-09-472-087-1
; Sequence 1, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-1

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Query Match 97.6%; Score 161; DB 2; Length 463;
Best Local Similarity 96.9%; Pred. No. 6.1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 32
Db 86 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 117

RESULT 7

US-09-472-087-63
; Sequence 63, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALLAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-63

Query Match 97.6%; Score 161; DB 2; Length 463;
Best Local Similarity 96.9%; Pred. No. 6.1e-15;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 32
Db 86 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 117

RESULT 8

US-09-472-087-64
; Sequence 64, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALLAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-64

Query Match 97.6%; Score 161; DB 2; Length 463;
Best Local Similarity 96.9%; Pred. No. 6.1e-15;

Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 32
Db 86 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 117

RESULT 9

US-08-471-780C-82
; Sequence 82, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flinnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1100 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471.780C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane R.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-780C-82

Query Match 95.8%; Score 158; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 32
Db 1 RFTISRDSKNTLFLQWNSLRADTAVYYCAR 32

RESULT 10

US-08-467-282B-82
; Sequence 82, Application US/08467282B
; Patent No. 5800988
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains

NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,282B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-282B-82

Query Match 95.8%; Score 158; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
DB 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32

RESULT 11
US-08-471-282A-82
Sequence 82, Application US/08471282A
Patent No. 5840853
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
ADDRESSEE: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,282A

FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-282A-82

Query Match 95.8%; Score 158; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
DB 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32

RESULT 12
US-08-466-710C-82
Sequence 82, Application US/08466710C
Patent No. 5874541
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
ADDRESSEE: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-466-710C-82

Query Match 95.8%; Score 158; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32
DB 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32

RESULT 13
US-08-470-139-21
Sequence 21, Application US/08470139
Patent No. 5998586
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
NUMBER OF SEQUENCES: 28
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,139
FILING DATE: 06 JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: TRUITILO, DOREEN YATKO
REGISTRATION/DOCKET NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0044
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-139-21

Query Match 95.8%; Score 158; DB 1; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32
DB 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32

RESULT 14
US-08-468-739C-82
Sequence 82, Application US/08468739C
Patent No. 6015695
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hanera, Raymond
TITLE OF INVENTION: Immunoglobulins devoid of light chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pottery, Jane E.R.
REGISTRATION/DOCKET NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 82:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-739C-82

Query Match 95.8%; Score 158; DB 2; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32
DB 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32

RESULT 15
US-09-347-061-21
Sequence 21, Application US/09347061
Patent No. 6316227
GENERAL INFORMATION:
APPLICANT: Bodmer, Mark
APPLICANT: Athwal, Diljeet Singh
APPLICANT: Emtage, John Spencer
TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
FILE REFERENCE: CARP-0071
CURRENT APPLICATION NUMBER: US/09/347,061
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Consensus
US-09-347-061-21

Query Match 95.8%; Score 158; DB 2; Length 32;
Best Local Similarity 93.8%; Pred. No. 7.8e-16;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32
DB 1 RFTISRDNSKNTLFIQNMNSLRADDTAVYYCAR 32

Db 1 RFTISRDNSKNTLYLQNNSLRAEDTAVYYCAR 32

Search completed: November 21, 2005, 12:07:40
Job time : 12.0733 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 21, 2005, 11:50:51, Search time 39.619 Seconds
(without alignments)
337,478 Million cell updates/sec

Title: US-10-632-706-196
Perfect score: 165
Sequence: 1 RFTISRDNKNTLFLQNNSLRADTAVYYCAR 32

Scoring table:
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Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	165	100.0	32 4 US-10-632-706-193	Sequence 193, App
2	165	100.0	32 4 US-10-632-706-196	Sequence 196, App
3	165	100.0	32 4 US-10-632-706-199	Sequence 199, App
4	165	100.0	32 4 US-10-632-706-202	Sequence 202, App
5	162	98.2	118 5 US-10-886-838-3	Sequence 3, App1
6	162	98.2	126 3 US-09-848-798-152	Sequence 152, App
7	162	98.2	127 3 US-09-848-798-139	Sequence 139, App
8	162	98.2	244 5 US-10-935-229-55	Sequence 55, App1
9	161	97.6	115 5 US-10-727-155-144	Sequence 144, App
10	161	97.6	122 5 US-10-727-155-198	Sequence 198, App
11	161	97.6	122 5 US-10-612-497-214	Sequence 214, App
12	161	97.6	167 5 US-10-612-497-74	Sequence 74, App1
13	161	97.6	167 5 US-10-776-648-74	Sequence 74, App1
14	161	97.6	463 4 US-10-153-382-3	Sequence 3, App1
15	161	97.6	463 4 US-10-153-382-5	Sequence 5, App1
16	161	97.6	463 5 US-10-612-497-1	Sequence 63, App1
17	161	97.6	463 5 US-10-612-497-63	Sequence 64, App1
18	161	97.6	463 5 US-10-612-497-64	Sequence 1, App1
19	161	97.6	463 5 US-10-776-648-1	Sequence 63, App1
20	161	97.6	463 5 US-10-776-648-63	Sequence 64, App1
21	161	97.6	463 5 US-10-776-648-64	Sequence 64, App1
22	161	97.6	463 6 US-11-085-368-3	Sequence 3, App1
23	161	97.6	463 6 US-11-085-368-5	Sequence 5, App1
24	161	97.6	463 6 US-11-085-368-41	Sequence 41, App1
25	158	95.8	32 3 US-09-855-271-21	Sequence 21, App1
26	158	95.8	32 3 US-09-849-559-123	Sequence 123, App
27	158	95.8	32 3 US-09-873-221A-123	Sequence 123, App

28	158	95.8	32 3 US-09-563-212-152	Sequence 152, App
29	158	95.8	32 4 US-10-663-244-28	Sequence 28, App1
30	158	95.8	32 4 US-10-783-950-142	Sequence 142, App1
31	158	95.8	32 5 US-10-764-428-30	Sequence 30, App1
32	158	95.8	32 5 US-10-751-826-82	Sequence 82, App1
33	158	95.8	32 5 US-10-728-4208-108	Sequence 108, App
34	158	95.8	32 5 US-10-923-068-203	Sequence 203, App
35	158	95.8	32 5 US-10-923-068-206	Sequence 206, App
36	158	95.8	32 5 US-10-923-068-224	Sequence 224, App
37	158	95.8	32 5 US-10-923-068-230	Sequence 230, App
38	158	95.8	32 5 US-10-923-068-235	Sequence 235, App
39	158	95.8	32 5 US-10-923-068-338	Sequence 338, App
40	158	95.8	32 5 US-10-923-068-356	Sequence 356, App
41	158	95.8	32 5 US-10-923-068-362	Sequence 362, App
42	158	95.8	32 5 US-10-914-015-108	Sequence 108, App
43	158	95.8	32 5 US-10-877-773-111	Sequence 111, App
44	158	95.8	32 5 US-10-877-773-124	Sequence 124, App
45	158	95.8	32 5 US-10-877-774-111	Sequence 111, App

ALIGNMENTS

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RESULT 1
US-10-632-706-193
; Sequence 193, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOBER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 193
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-193
Query Match      100.0%; Score 165, DB 4; Length 32;
Best local similarity 100.0%; Pred. No. 3,4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RFTISRDNKNTLFLQNNSLRADTAVYYCAR 32
Db      1 RFTISRDNKNTLFLQNNSLRADTAVYYCAR 32

RESULT 2
US-10-632-706-196
; Sequence 196, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806

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/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 196
/ LENGTH: 32
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-196

Query Match      100.0%; Score 165; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32

RESULT 3
US-10-632-706-199
/ Sequence 199, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ APPLICANT: AMERSORFER, PETER
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 199
/ LENGTH: 32
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-199

Query Match      100.0%; Score 165; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32

RESULT 4
US-10-632-706-202
/ Sequence 202, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ APPLICANT: AMERSORFER, PETER
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: PatentIn version 3.2
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/ SEQ ID NO 202
/ LENGTH: 32
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-202

Query Match      100.0%; Score 165; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32

RESULT 5
US-10-886-838-3
/ Sequence 3, Application US/10886838
/ Publication No. US20050008642A1
/ GENERAL INFORMATION:
/ APPLICANT: Hoffmann-La Roche Inc.
/ TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
/ FILE REFERENCE: 21695
/ CURRENT APPLICATION NUMBER: US/10/886,838
/ PRIOR FILING DATE: 2004-07-08
/ PRIOR APPLICATION NUMBER: EP 03015526
/ PRIOR FILING DATE: 2003-07-10
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-886-838-3

Query Match      98.2%; Score 162; DB 5; Length 118;
Best Local Similarity 96.9%; Pred. No. 3.6e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
Db      67 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 98

RESULT 6
US-09-848-798-152
/ Sequence 152, Application US/09848798
/ Publication No. US20030040605A1
/ GENERAL INFORMATION:
/ APPLICANT: Siegel, Donald L.
/ TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
/ FILE REFERENCE: 09596-42U2
/ CURRENT APPLICATION NUMBER: US/09/848,798
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
/ PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
/ NUMBER OF SEQ ID NOS: 224
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 152
/ LENGTH: 126
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-848-798-152

Query Match      98.2%; Score 162; DB 3; Length 126;
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Best Local Similarity 96.9%; Pred. No. 3.9e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 98

RESULT 7

US-09-848-798-139
; Sequence 139, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OR INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH10
US-09-848-798-139

Query Match 98.2%; Score 162; DB 3; Length 127;
Best Local Similarity 96.9%; Pred. No. 3.9e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 68 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 99

RESULT 8

US-10-935-290-55
; Sequence 55, Application US/10935290
; Publication No. US20050069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMD
; FILE REFERENCE: PFS64P1
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 55
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv protein GMB619
US-10-935-290-55

Query Match 98.2%; Score 162; DB 5; Length 244;
Best Local Similarity 96.9%; Pred. No. 8e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 98

RESULT 9

US-10-727-155-144
; Sequence 144, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Poord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Palaniswami Rathnaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OR INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX 073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-144

Query Match 97.6%; Score 161; DB 5; Length 115;
Best Local Similarity 96.9%; Pred. No. 4.8e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
Db 66 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 97

RESULT 10

US-10-727-155-198
; Sequence 198, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaspal S. Kang
; APPLICANT: Orit Poord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Palaniswami Rathnaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OR INVENTION: FACTOR AND USES THEREOF
; FILE REFERENCE: ABGENIX 073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-198

Query Match          97.6%; Score 161; DB 5; Length 122;
Best Local Similarity 96.9%; Pred. No. 5,1e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNSLRADTAVYYCAR 98

RESULT 11
US-10-727-155-214
; Sequence 214, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaapal S. Kang
; APPLICANT: Orlit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klamp
; APPLICANT: Mary Haak-Frendocho
; APPLICANT: Palaniswami Rathnaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenko
; APPLICANT: Raffaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; FILE REFERENCE: ABGENIX 073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-214

Query Match          97.6%; Score 161; DB 5; Length 122;
Best Local Similarity 96.9%; Pred. No. 5,1e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNSLRADTAVYYCAR 98

RESULT 12
US-10-612-497-74
; Sequence 74, Application US/10612497
; Publication No. US2004022858A1
; GENERAL INFORMATION:
; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Bileen E. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
```

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; FILE REFERENCE: ABX-PF1 DIV1
; CURRENT APPLICATION NUMBER: US/10/612,497
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-497-74

Query Match          97.6%; Score 161; DB 5; Length 167;
Best Local Similarity 96.9%; Pred. No. 7,2e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADTAVYYCAR 32
Db 58 RFTISRDNKNTLFLQNSLRADTAVYYCAR 89

RESULT 13
US-10-776-649-74
; Sequence 74, Application US/10776649
; Publication No. US2004022861A1
; GENERAL INFORMATION:
; APPLICANT: Douglas C. Hanson
; APPLICANT: Mark J. Neveu
; APPLICANT: Bileen E. Mueller
; APPLICANT: Jeffrey H. Hanke
; APPLICANT: Steven C. Gilman
; APPLICANT: C. Geoffrey Davis
; APPLICANT: Jose R. Corvalan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV2
; CURRENT APPLICATION NUMBER: US/10/776,649
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-649-74

Query Match          97.6%; Score 161; DB 5; Length 167;
Best Local Similarity 96.9%; Pred. No. 7,2e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADTAVYYCAR 32
Db 58 RFTISRDNKNTLFLQNSLRADTAVYYCAR 89

RESULT 14
US-10-153-382-3
; Sequence 3, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USBS OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
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; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-3

Query Match 97.6%; Score 161; DB 4; Length 463;
Best Local Similarity 96.9%; Pred. No. 2.2e-13;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFTISRDN SKNTLFLQMN SLRADDTAVYYCAR 32
|||
DB 86 RFTISRDN SKNTLFLQMN SLRADDTAVYYCAR 117

RESULT 15
US-10-153-382-5
; Sequence 5, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-382-5

Query Match 97.6%; Score 161; DB 4; Length 463;
Best Local Similarity 96.9%; Pred. No. 2.2e-13;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RFTISRDN SKNTLFLQMN SLRADDTAVYYCAR 32
|||
DB 86 RFTISRDN SKNTLFLQMN SLRADDTAVYYCAR 117

Search completed: November 21, 2005, 12:33:39
Job time : 39.619 secs

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OM protein - protein search, using SW model

Run on: November 21, 2005, 12:04:27 ; Search time 0.586081 Seconds

(without alignments)
61.666 Million cell updates/sec

Title: US-10-632-706-196

Perfect score: 165

Sequence: 1 RFTISRDNKNTLFLQNMNLRADDTAVYYCAR 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8323 seqs, 112978 residues

Total number of hits satisfying chosen parameters: 8323

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA_New*

- 1: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	158	95.8	102	1	US-10-997-201A-6
2	155	93.9	98	1	US-10-789-273-10
3	155	93.9	98	7	US-11-144-248-32
4	155	93.9	122	7	US-11-144-248-24
5	155	93.9	125	7	US-11-144-248-16
6	155	93.9	139	1	US-10-721-763-33
7	155	93.9	139	1	US-11-144-248-46
8	154	93.3	138	1	US-10-789-273-12
9	151	91.5	98	7	US-11-144-248-30
10	151	91.5	444	7	US-11-172-320-6
11	151	91.5	473	7	US-11-144-248-50
12	147	89.1	174	7	US-11-144-248-4
13	147	89.1	470	7	US-11-144-248-49
14	146	88.5	124	7	US-11-144-248-8
15	146	88.5	120	7	US-11-144-248-45
16	145	87.3	421	1	US-10-789-273-9
17	144	87.3	138	1	US-10-789-273-8
18	138	83.6	120	7	US-11-077-978-7
19	136	82.4	121	7	US-11-077-978-2
20	133	80.6	138	1	US-10-789-273-4
21	128	77.6	118	1	US-10-648-816-9
22	128	77.6	118	1	US-10-648-816-10
23	128	77.6	118	1	US-10-648-816-11
24	128	77.6	118	1	US-10-648-816-12
25	128	77.6	118	1	US-10-648-816-13

26	128	77.6	118	1	US-10-648-816-14	Sequence 14, Appl
27	128	77.6	121	1	US-10-648-816-15	Sequence 15, Appl
28	128	77.6	121	1	US-10-648-816-16	Sequence 16, Appl
29	128	77.6	121	7	US-11-077-978-3	Sequence 3, Appl
30	127	77.0	543	1	US-10-495-664-3	Sequence 3, Appl
31	126	76.4	114	1	US-10-726-554-8	Sequence 8, Appl
32	119	72.1	119	7	US-11-010-954-5	Sequence 5, Appl
33	119	72.1	263	1	US-10-512-184-29	Sequence 29, Appl
34	119	72.1	250	1	US-10-512-184-27	Sequence 27, Appl
35	118	71.5	258	1	US-10-512-184-26	Sequence 26, Appl
36	114	69.1	327	1	US-10-512-184-64	Sequence 64, Appl
37	114	69.1	327	1	US-10-512-184-63	Sequence 63, Appl
38	114	69.1	328	1	US-10-512-184-64	Sequence 64, Appl
39	114	69.1	576	1	US-10-512-184-65	Sequence 65, Appl
40	114	69.1	625	1	US-10-512-184-67	Sequence 47, Appl
41	113	68.5	119	1	US-10-502-145-25	Sequence 25, Appl
42	111	67.3	118	7	US-11-012-393-71	Sequence 71, Appl
43	110	66.7	261	1	US-10-512-184-35	Sequence 35, Appl
44	110	66.7	313	1	US-10-512-184-72	Sequence 72, Appl
45	108	65.5	118	7	US-11-012-353-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-10-997-201A-6 Application US/10997201A
; Sequence 6, Appl
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; TITLE OF INVENTION: Anticodules Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997, 201A
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524, 840
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-6

Query Match 95.8% Score 158; DB 1; Length 102;
Best Local Similarity 93.8% Pred. No. 4.2e-13;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMNLRADDTAVYYCAR 32
Db 57 RFTISRDNKNTLFLQNMNLRADDTAVYYCAR 86

RESULT 2
US-10-789-273-10
; Sequence 10, Appl
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: EIM-002CP
; CURRENT APPLICATION NUMBER: US/10/789, 273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388, 389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010, 942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251, 892

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/ PRIOR FILING DATE: 2000-12-06
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-789-273-10
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Query Match          93.9%; Score 155; DB 1; Length 98;
Best Local Similarity 90.6%; Pred. No. 1.9e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQMSLRADDTAVYYCAK 98
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RESULT 3

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US-11-144-248-32
/ Sequence 32, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 32
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-32
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Query Match          93.9%; Score 155; DB 7; Length 98;
Best Local Similarity 90.6%; Pred. No. 1.9e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQMSLRADDTAVYYCAK 98
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RESULT 4

```
US-11-144-248-24
/ Sequence 24, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
```

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/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-24
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Query Match          93.9%; Score 155; DB 7; Length 122;
Best Local Similarity 90.6%; Pred. No. 2.4e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQMSLRADDTAVYYCAK 98
```

RESULT 5

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US-11-144-248-16
/ Sequence 16, Application US/11144248
/ Publication No. US20050244408A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Bruce D.
/ APPLICANT: Beebe, Jean
/ APPLICANT: Miller, Penelope E.
/ APPLICANT: Moyer, James D.
/ APPLICANT: Corvalan, Jose R.
/ APPLICANT: Gallo, Michael
/ TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
/ FILE REFERENCE: ABX-PF2
/ CURRENT APPLICATION NUMBER: US/11/144,248
/ PRIOR FILING DATE: 2005-06-02
/ PRIOR APPLICATION NUMBER: US/10/038,591
/ PRIOR FILING DATE: 2002-01-04
/ PRIOR APPLICATION NUMBER: 60/259,927
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-248-16
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Query Match          93.9%; Score 155; DB 7; Length 125;
Best Local Similarity 90.6%; Pred. No. 2.4e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RFTISRDNKNTLYLQMSLRADDTAVYYCAR 32
Db 67 RFTISRDNKNTLYLQMSLRADDTAVYYCAK 98
```

RESULT 6

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US-10-721-763-33
/ Sequence 33, Application US/10721763
/ Publication No. US20050249729A1
/ GENERAL INFORMATION:
/ APPLICANT: KIRIN BEER KABUSHIKI KAISHA
/ TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
/ FILE REFERENCE: PH-1573-PCF
/ CURRENT APPLICATION NUMBER: US/10/721,763
/ PRIOR FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: JP2001-150213
/ PRIOR FILING DATE: 2001-05-18
/ PRIOR APPLICATION NUMBER: JP2001-243040
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: JP2001-314489
/ PRIOR FILING DATE: 2001-10-11
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 33
/ LENGTH: 139
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;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-721-763-33

Query Match 93.9%; Score 155; DB 1; Length 139;
Best Local Similarity 90.6%; Pred. No. 2.7e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32
Db 86 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 117

RESULT 7
US-11-144-248-46
; Sequence 46, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-46

Query Match 93.9%; Score 155; DB 7; Length 470;
Best Local Similarity 90.6%; Pred. No. 8.3e-12;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32
Db 86 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 117

RESULT 8
US-10-789-273-12
; Sequence 12, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurliq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: EBN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 138
; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Humanized 3D6 light chain variable region
;; NAME/KEY: SIGNAL
;; LOCATION: (1)...(19)
US-10-789-273-12

Query Match 93.3%; Score 154; DB 1; Length 138;
Best Local Similarity 90.6%; Pred. No. 3.4e-12;
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32
Db 86 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 117

RESULT 9
US-11-144-248-30
; Sequence 30, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-30

Query Match 91.5%; Score 151; DB 7; Length 98;
Best Local Similarity 87.5%; Pred. No. 5.5e-12;
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 32
Db 67 RFTISRDNKNTLFLQNMSLRADPTAVYYCAR 98

RESULT 10
US-11-172-320-6
; Sequence 6, Application US/11172320
; Publication No. US20050244413A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Guenther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunocjugates and
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/11/172,320
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/645,215
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002

NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Humanised Murine Antibody B1W4 4 Heavy Chain
US-11-172-320-6

Query Match 91.5%; Score 151; DB 7; Length 444;
Best Local Similarity 87.5%; Pred. No. 2,2e-11;
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
DB 67 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 98

RESULT 11

US-11-144-248-50
Sequence 50, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
PRIOR FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 50
LENGTH: 473
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-50

Query Match 91.5%; Score 151; DB 7; Length 473;
Best Local Similarity 87.5%; Pred. No. 2,3e-11;
Matches 28; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117

RESULT 12

US-11-144-248-4
Sequence 4, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
PRIOR FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927

PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-4

Query Match 89.1%; Score 147; DB 7; Length 174;
Best Local Similarity 84.4%; Pred. No. 2,6e-11;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
DB 59 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 90

RESULT 13

US-11-144-248-49
Sequence 49, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
PRIOR FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 49
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-49

Query Match 89.1%; Score 147; DB 7; Length 470;
Best Local Similarity 84.4%; Pred. No. 6,6e-11;
Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQNSLRADDTAVYYCAR 32
DB 86 RFTISRDNKNSLYLQNSLRADDTAVYYCAR 117

RESULT 14

US-11-144-248-8
Sequence 8, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
PRIOR FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927

NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 8
 LENGTH: 124
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-144-248-8

Query Match 88.5% Score 146; DB 7; Length 124;
 Best Local Similarity 84.4% Pred. No. 2.5e-11;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
 DB 66 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 97

RESULT 15
 US-11-144-248-45
 Sequence 45, Application US/11144248
 Publication No. US2005024408A1
 GENERAL INFORMATION:
 APPLICANT: Cohen, Bruce D.
 APPLICANT: Beebe, Jean
 APPLICANT: Miller, Penelope E.
 APPLICANT: Moyer, James D.
 APPLICANT: Corvalan, Jose R.
 APPLICANT: Gallo, Michael
 TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
 FILE REFERENCE: ABX-PF2
 CURRENT APPLICATION NUMBER: US/11/144,248
 CURRENT FILING DATE: 2005-06-02
 PRIOR APPLICATION NUMBER: US/10/038,591
 PRIOR FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 60/259,927
 PRIOR FILING DATE: 2001-01-05
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 45
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-144-248-45

Query Match 88.5% Score 146; DB 7; Length 470;
 Best Local Similarity 84.4% Pred. No. 8.5e-11;
 Matches 27; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 32
 DB 66 RFTISRDNKNTLFLQMSLRADDTAVYYCAR 117

Search completed: November 21, 2005, 12:33:52
 Job time : 0.686081 secs

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